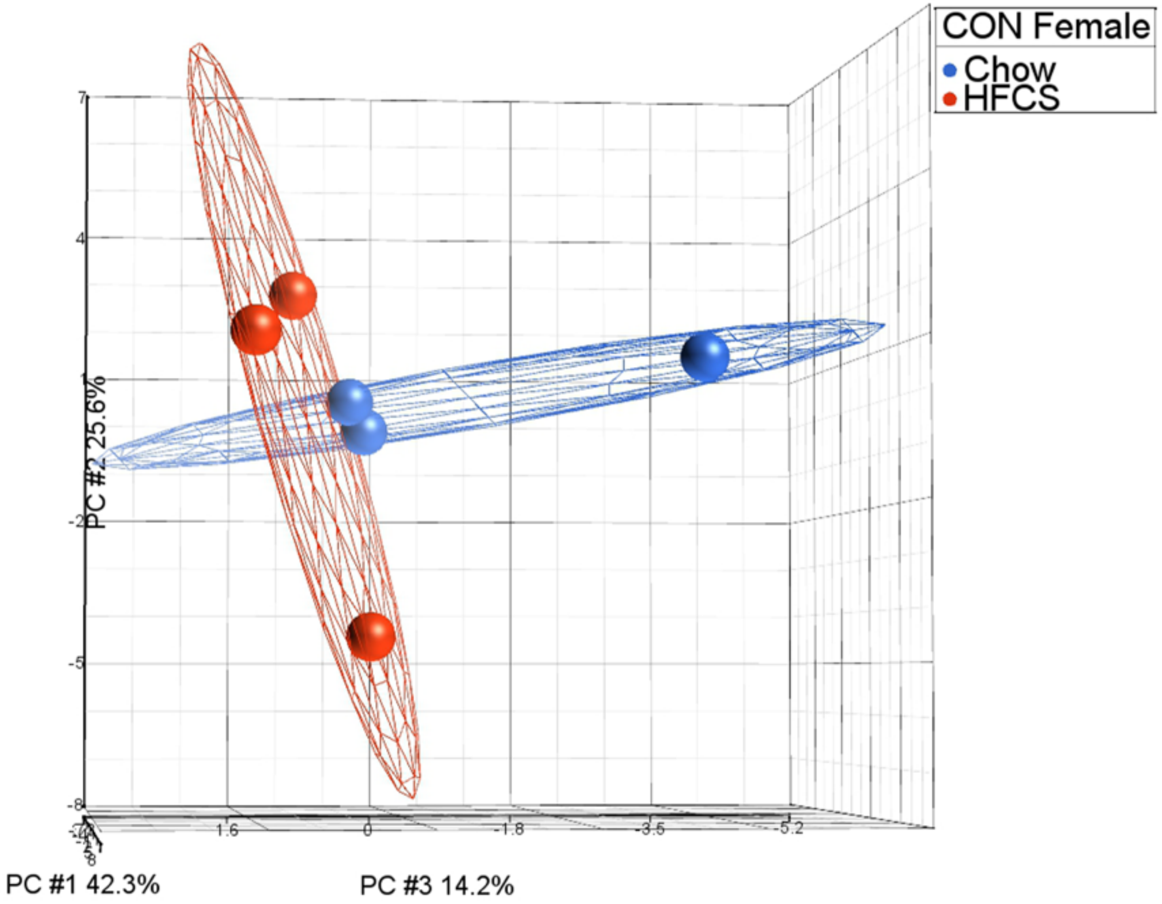
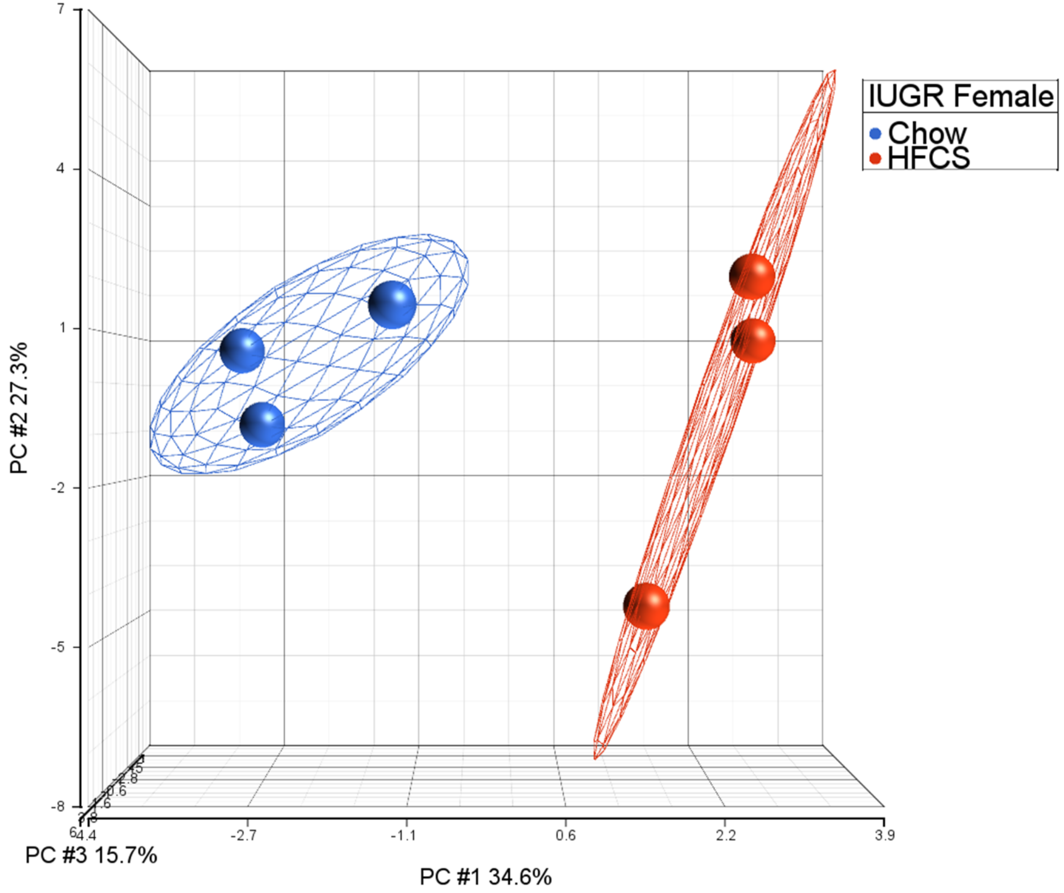
Supplemental Figure 1





Supplementary Table 1: IUGR vs CON Chow Diet Gene Expression							Nephron Segment-Specific		
Gene Symbol	**Gene Name**	**Accession No.**	**CON Chow F Mean**	**IUGR Chow F Mean**	**pval IUGR v CON F Chow**	**Ratio IUGR v CON F Chow**	**REFSEQ ID**	**NEPHRON (MEAN RPKM)**	**COLLECTING DUCT (MEAN RPKM)**
Xist	X inactive specific transcript (non-protein coding)(XIST)	NR_001564	599.6	836.2	0.0001	1.3			
GTPBP6	GTP binding protein 6 (putative)(GTPBP6)	NM_012227	244.8	183	0.0002	0.69			
CSDE1	cold shock domain containing E1(CSDE1)	NM_001007553	143	131.3	0.0003	0.75			
CSDE1	cold shock domain containing E1(CSDE1)	NM_001007553	187.8	156.9	0.0003	0.75			
OSTM1	osteopetrosis associated transmembrane protein 1(OSTM1)	NM_014028	91.4	131.6	0.0003	1.28			
		BQ186959	111.6	106.8	0.0004	0.88			
		DB336481	147.3	135.5	0.0004	0.82	NM_017193	356.13	8.18
UBC	ubiquitin C(UBC)	NM_021009	10602.5	9244.7	0.0005	0.68	NM_017193	356.13	8.18

UBC	ubiquitin C(UBC)	NM_021009	12020.7	11235.1	0.0005	0.68	NM_017193	356.13	8.18
ODC1	ornithine decarboxylase 1(ODC1)	NM_002539	463.8	725.5	0.0006	1.42			
PCDHA3	protocadherin alpha 3(PCDHA3)	NM_018906	105.8	136.8	0.0006	1.15			
SREBF1	sterol regulatory element binding transcription factor 1(SREBF1)	NM_004176	150.6	118.2	0.0008	0.73			
UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1(UAP1L1)	NM_207309	134.5	114.8	0.0008	0.78			
DNAJB6	DnaJ heat shock protein family (Hsp40) member B6(DNAJB6)	NM_005494	206	182.1	0.0011	0.79			
UBE3C	ubiquitin protein ligase E3C(UBE3C)	NM_014671	160.3	131.2	0.0013	0.75			
UBE3C	ubiquitin protein ligase E3C(UBE3C)	NM_014671	478.2	511.9	0.0013	0.75			
		XM_941684	297.7	538.9	0.0014	1.65			

PAH	phenylalanine hydroxylase(PAH)	NM_000277	126.8	100.9	0.0015	0.75
ZNF467	zinc finger protein 467(ZNF467)	NM_207336	264.2	193.3	0.0015	0.67
CYB5D2	cytochrome b5 domain containing 2(CYB5D2)	NM_144611	125.3	170.6	0.0016	1.18
NDUFB11	NADH:ubiquinone oxidoreductase subunit B11(NDUFB11)	NM_019056	1498.6	1222.1	0.0018	0.75
APOE	apolipoprotein E(APOE)	NM_000041	2789.9	1250.2	0.0021	0.39
LGMN	legumain(LGMN)	NM_001008530	135.2	143.9	0.0021	0.41
LGMN	legumain(LGMN)	NM_001008530	203.6	186.1	0.0021	0.41
LGMN	legumain(LGMN)	NM_001008530	1731.9	783.9	0.0021	0.41
		XM_941785	110.7	106.4	0.0022	0.88
NUMA1	nuclear mitotic apparatus protein 1(NUMA1)	NM_006185	123	158	0.0024	1.3
NUMA1	nuclear mitotic apparatus protein 1(NUMA1)	NM_006185	252	368.7	0.0024	1.3

MID1IP1	MID1 interacting protein 1(MID1IP1)	NM_021242	116	115.3	0.0028	0.72
MID1IP1	MID1 interacting protein 1(MID1IP1)	NM_021242	199.5	158.2	0.0028	0.72
SRSF12	serine and arginine rich splicing factor 12(SRSF12)	NM_080743	97.8	136.2	0.0028	1.23
		XM_0017199540	114.6	150.1	0.0029	1.14
BAG3	BCL2 associated athanogene 3(BAG3)	NM_004281	291.2	149.3	0.0031	0.47
USP21	ubiquitin specific peptidase 21(USP21)	NM_012475	133.7	142.8	0.0032	1.24
USP21	ubiquitin specific peptidase 21(USP21)	NM_012475	150	217.3	0.0032	1.24
CASKIN2	CASK interacting protein 2(CASKIN2)	NM_020753	116.9	106.8	0.0034	0.85
		XM_933893	108.3	149.8	0.0034	1.2
TIPARP	TCDD inducible poly(ADP-ribose) polymerase(TIPARP)	NM_015508	396.4	319.1	0.0036	0.75

XYLT1	xylosyltransferase 1(XYLT1)	NM_022166	95.4	125.5	0.0036	1.18
		BX111977	112.6	145.7	0.0036	1.14
		XM_934376	115.9	149.6	0.0037	1.13
SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1(SBDSP1)	NR_001588	336.4	258.4	0.0038	0.68
SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1(SBDSP1)	NR_001588	415.5	362.7	0.0038	0.68
DCUN1D2	defective in cullin neddylation 1 domain containing 2(DCUN1D2)	NM_001014283	205	190.3	0.0039	0.82
ELMOD2	ELMO domain containing 2(ELMOD2)	NM_153702	160.2	132.5	0.0041	0.77
SCARA3	scavenger receptor class A member 3(SCARA3)	NM_016240	97.4	131.1	0.0041	1.19
OR6N2	olfactory receptor family 6 subfamily N member 2(OR6N2)	NM_001005278	105.4	134	0.0044	1.14

		XR_019029	129.5	175.5	0.0044	1.18
ARHGEF37	Rho guanine nucleotide exchange factor 37(ARHGEF37)	NM_001001669	124.1	173.1	0.0047	1.21
CDCA7	cell division cycle associated 7(CDCA7)	NM_031942	128.6	214.8	0.0049	1.45
		XR_039439	111.5	155.4	0.0049	1.21
		XR_039439	1038.8	1435	0.0049	1.21
DPCD	deleted in primary ciliary dyskinesia homolog (mouse)(DPCD)	NM_015448	281.5	229.7	0.005	0.72
SEL1L3	SEL1L family member 3(SEL1L3)	NM_015187	113.5	162.3	0.0053	1.23
		XR_038700	102.2	149.8	0.0053	1.26
		XR_018838	192.5	163.3	0.0056	0.77
MRPL53	mitochondrial ribosomal protein L53(MRPL53)	NM_053050	231.1	205	0.0057	0.77

KCNJ14	potassium voltage-gated channel subfamily J member 14(KCNJ14)	NM_170720	120.1	162.7	0.0059	1.18			
KMT2C	lysine methyltransferase 2C(KMT2C)	NM_170606	127.7	200.7	0.0059	1.34			
KMT2C	lysine methyltransferase 2C(KMT2C)	NM_170606	138.7	155.8	0.0059	1.34			
TRAPPC2	trafficking protein particle complex 2(TRAPPC2)	NM_001011658	108.3	140.7	0.006	1.14			
c1orf216	chromosome 1 open reading frame 216(C1orf216)	NM_152374	123.1	162	0.0061	1.15			
HAUS4	HAUS augmin like complex subunit 4(HAUS4)	NM_017815	164.4	138.2	0.0062	0.76	NM_053502	4.02	18.01
SCAPER	S-phase cyclin A associated protein in the ER(SCAPER)	NM_020843	200.8	181.1	0.0063	0.78	NM_053502	4.02	18.01

c3p1	complement component 3 precursor pseudogene(C3P1)	NM_001013640	125.7	168.7	0.0066	1.17	NM_053502	4.02	18.01
		AK129699	141.4	332	0.0069	2.08			
PEX2	peroxisomal biogenesis factor 2(PEX2)	NM_000318	242.1	194.7	0.007	0.71			
		XM_928619	183.9	175	0.007	0.86			
MIR939	microRNA 939(MIR939)	NR_030635	137.4	183.9	0.0071	1.16			
KLF10	Kruppel like factor 10(KLF10)	NM_005655	154.5	164.7	0.0072	0.78			
KLF10	Kruppel like factor 10(KLF10)	NM_005655	192.8	164.2	0.0072	0.78	NM_001009670	33.30	2.04
PTK2	protein tyrosine kinase 2(PTK2)	NM_153831	119	119.9	0.0072	0.9			
TMEM184C	transmembrane protein 184C(TMEM184C)	NM_018241	110.5	106.7	0.0072	0.89			
TMEM184C	transmembrane protein 184C(TMEM184C)	NM_018241	331.1	360.5	0.0072	0.89			
RNF146	ring finger protein 146(RNF146)	NM_030963	117.2	104.6	0.0073	0.82			
RNF146	ring finger protein 146(RNF146)	NM_030963	152.3	156.8	0.0073	0.82			

FAM174A	family with sequence similarity 174 member A(FAM174A)	NM_198507	283.1	227.5	0.0076	0.71
SLC41A3	solute carrier family 41 member 3(SLC41A3)	NM_001008485	612.9	375.5	0.0076	0.58
TBC1D8B	TBC1 domain family member 8B(TBC1D8B)	NM_017752	113.6	121.8	0.0076	0.81
TBC1D8B	TBC1 domain family member 8B(TBC1D8B)	NM_017752	176.8	157.7	0.0076	0.81
RPL17P39	ribosomal protein L17 pseudogene 39(RPL17P39)	NM_001093733	519.6	880.1	0.0078	1.57
RRAGB	Ras related GTP binding B(RRAGB)	NM_006064	98.7	152.4	0.0079	1.36
RRAGB	Ras related GTP binding B(RRAGB)	NM_006064	126.7	129.2	0.0079	1.36
CNEP1R1	CTD nuclear envelope phosphatase 1 regulatory subunit 1(CNEP1R1)	NM_153261	111.5	147.8	0.008	1.18
ARHGAP1	Rho GTPase activating protein 1(ARHGAP1)	NM_004308	1017.5	907.2	0.0081	0.83

ATP6V0D1	ATPase H+ transporting V0 subunit d1(ATP6V0D1)	NM_004691	430.6	338.6	0.0083	0.73
GAPDH	glyceraldehyde-3-phosphate dehydrogenase(GAPDH)	NM_002046	142.9	141.5	0.0085	0.43
GAPDH	glyceraldehyde-3-phosphate dehydrogenase(GAPDH)	NM_002046	1842.1	1026.5	0.0085	0.43
GAPDH	glyceraldehyde-3-phosphate dehydrogenase(GAPDH)	NM_002046	3640.2	1836.1	0.0085	0.43
TYMS	thymidylate synthetase(TYMS)	NM_001071	113.5	232.8	0.0086	1.72
FNTA	farnesyltransferase, CAAX box, alpha(FNTA)	NM_0010118677	302.3	399.5	0.0089	1.21
RPLP2	ribosomal protein lateral stalk subunit P2(RPLP2)	NM_001004	10890.7	9676.9	0.009	0.66

HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1(HACE1)	NM_020771	127.4	120.2	0.0091	0.86
EIF1	eukaryotic translation initiation factor 1(EIF1)	NM_005801	1591.4	202.6	0.0093	0.12
PTS	6-pyruvoyltetrahydropterin synthase(PTS)	NM_000317	316.4	243.3	0.0093	0.67
TFDP1	transcription factor Dp-1(TFDP1)	NM_007111	196.2	339.1	0.0093	1.52
TFDP1	transcription factor Dp-1(TFDP1)	NM_007111	492.5	636.7	0.0093	1.52
		XM_001718145	121.7	114.7	0.0094	0.86
		XM_927228	109.4	137.4	0.0095	1.11
HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')(HNRNPH2)	NM_019597	293.3	236.1	0.0096	0.74
		XM_938755	1571.1	2625.7	0.0097	1.49

AP2M1	adaptor related protein complex 2 mu 1 subunit(AP2M1)	NM_004068	126.6	119.3	0.0098	0.86
AP2M1	adaptor related protein complex 2 mu 1 subunit(AP2M1)	NM_004068	271	288.9	0.0098	0.86
LOC105377348	uncharacterized LOC105377348(LOC105377348)	AK093356	153.6	138.2	0.0099	0.82
STRAP	serine/threonine kinase receptor associated protein(STRAP)	NM_007178	186.5	321.8	0.01	1.5
ANXA7	annexin A7(ANXA7)	NM_004034	145	191.6	0.0101	2.02
ANXA7	annexin A7(ANXA7)	NM_004034	345.7	830.6	0.0101	2.02
GHSR	growth hormone secretagogue receptor(GHSR)	NM_004122	103.9	133.9	0.0101	1.13
PSMD5	proteasome 26S subunit, non-ATPase 5(PSMD5)	NM_005047	163.1	234.6	0.0101	1.25
		XM_001721968	107.3	141.8	0.0101	1.15

SDR42E1	short chain dehydrogenase/reductase family 42E, member 1(SDR42E1)	NM_145168	119.6	119.1	0.0105	0.9
ZBTB40	zinc finger and BTB domain containing 40(ZBTB40)	NM_001083621	148	234.5	0.0106	1.36
		XM_001722060	469.6	1000.1	0.0108	1.96
		XM_939687	1087.7	1810	0.0108	1.56
USE1	unconventional SNARE in the ER 1(USE1)	NM_018467	148.9	131.6	0.011	0.81
		XM_944813	121.9	121.3	0.011	0.9
		XR_040895	136.4	182.2	0.011	1.16
		XR_017960	91.5	123	0.0111	1.22
ACD	adrenocortical dysplasia homolog(ACD)	NM_022914	137.6	185.5	0.0113	1.17
ISG20L2	interferon stimulated exonuclease gene 20 like 2(ISG20L2)	NM_030980	144.8	199.4	0.0115	1.2

RSRC2	arginine and serine rich coiled-coil 2(RSRC2)	NM_023012	121.6	144.5	0.0115	1.29
RSRC2	arginine and serine rich coiled-coil 2(RSRC2)	NM_023012	656.4	918.9	0.0115	1.29
C11orf74	chromosome 11 open reading frame 74(C11orf74)	NM_138787	216.8	185.6	0.0116	0.76
PUM2	pumilio RNA binding family member 2(PUM2)	NM_015317	458.7	667.5	0.0118	1.33
ANKRA2	ankyrin repeat family A member 2(ANKRA2)	NM_023039	116.8	150	0.012	1.14
ANKRA2	ankyrin repeat family A member 2(ANKRA2)	NM_023039	177.1	229.6	0.012	1.14
fxyd2	FXYD domain containing ion transport regulator 2(FXYD2)	NM_001680	128.4	146.9	0.012	0.46
fxyd2	FXYD domain containing ion transport regulator 2(FXYD2)	NM_001680	12803.3	6710.8	0.012	0.46

OTUB1	OTU deubiquitinase, ubiquitin aldehyde binding 1(OTUB1)	NR_003089	148.1	139.2	0.012	0.84			
MRAP2	melanocortin 2 receptor accessory protein 2(MRAP2)	NM_138409	141.4	116.5	0.0122	0.76			
MRAP2	melanocortin 2 receptor accessory protein 2(MRAP2)	NM_138409	161.3	174.9	0.0122	0.76			
RPS6	ribosomal protein S6(RPS6)	NM_001010	2996.1	6286.2	0.0122	1.6			
RPS6	ribosomal protein S6(RPS6)	NM_001010	6172	8646.3	0.0122	1.6			
TRIM36	tripartite motif containing 36(TRIM36)	NM_001017397	103.5	133	0.0122	1.14			
PNMA1	paraneoplastic Ma antigen 1(PNMA1)	NM_006029	322.8	245.5	0.0123	0.7			
oxtr	oxytocin receptor(OXTR)	NM_000916	118.9	112.8	0.0124	0.86			
PWWP2B	PWWP domain containing 2B(PWWP2B)	NM_138499	116.1	107	0.0128	0.84	NM_001107943	0.63	112.77
PWWP2B	PWWP domain containing 2B(PWWP2B)	NM_138499	143	161.6	0.0128	0.84			

FAM127B	family with sequence similarity 127 member B(FAM127B)	NM_001078172	157.9	178.2	0.0129	0.71
FAM127B	family with sequence similarity 127 member B(FAM127B)	NM_001078172	299.4	236.3	0.0129	0.71
		XM_001726456	115.4	155	0.0129	1.16
GNG10	G protein subunit gamma 10(GNG10)	NM_001017998	897.8	460.7	0.0131	0.53
SLC25A4	solute carrier family 25 member 4(SLC25A4)	NM_001151	1239.8	632.8	0.0131	0.43
SLC25A4	solute carrier family 25 member 4(SLC25A4)	NM_001151	2794.8	1377.6	0.0131	0.43
GPATCH8	G-patch domain containing 8(GPATCH8)	NM_001002909	120.3	158.8	0.0132	1.17
STX8	syntaxin 8(STX8)	NM_004853	462.3	367.9	0.0133	0.71
		XR_015954	126	195.4	0.0134	1.36
MINK1	misshapen like kinase 1(MINK1)	NM_153827	118.2	113.2	0.0135	0.87

MINK1	misshapen like kinase 1(MINK1)	NM_153827	118.7	138.1	0.0135	0.87	NM_134372	22.51	0.03
GPR34	G protein-coupled receptor 34(GPR34)	NM_001033513	123.6	167.1	0.0136	1.17			
MZB1	marginal zone B and B1 cell specific protein(MZB1)	NM_016459	92.9	112	0.0136	2.51			
MZB1	marginal zone B and B1 cell specific protein(MZB1)	NM_016459	179.2	514.5	0.0136	2.51			
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	95.5	110.5	0.0137	1.17			
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	110.8	120.2	0.0137	1.17			
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	111.8	150.6	0.0137	1.17			
		XR_017249	103.6	146.2	0.0137	1.25			

CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1(CEACAM1)	NM_001712	120	110	0.0141	0.83
GPRC5C	G protein-coupled receptor class C group 5 member C(GPRC5C)	NM_018653	427.4	290.7	0.0141	0.61
LINC01278	long intergenic non-protein coding RNA 1278(LINC01278)	AK130294	290.9	239.4	0.0141	0.73
BUB3	BUB3, mitotic checkpoint protein(BUB3)	NM_004725	182.1	251.4	0.0142	1.73
BUB3	BUB3, mitotic checkpoint protein(BUB3)	NM_004725	261.4	499.8	0.0142	1.73
LIG3	DNA ligase 3(LIG3)	NM_013975	160.3	207.6	0.0143	1.12
FAM96B	family with sequence similarity 96 member B(FAM96B)	NM_016062	415.4	361.1	0.0144	0.79
RPL26P30	ribosomal protein L26 pseudogene 30(RPL26P30)	NM_001093761	366.6	296	0.0145	0.73

FAM127A	family with sequence similarity 127 member A(FAM127A)	NM_001078171	363	277.5	0.0146	0.7			
GLS2	glutaminase 2(GLS2)	NM_013267	122	118.8	0.0146	0.89			
AKT3	AKT serine/threonine kinase 3(AKT3)	NM_005465	91.9	117.9	0.0147	1.18			
OPRM1	opioid receptor mu 1(OPRM1)	NM_001008505	116.7	144.5	0.0147	1.09			
OPRM1	opioid receptor mu 1(OPRM1)	NM_001008505	177.5	216.2	0.0147	1.09			
RPL19P9	ribosomal protein L19 pseudogene 9(RPL19P9)	NM_001080544	429.2	660.6	0.0147	1.38			
RPL19P9	ribosomal protein L19 pseudogene 9(RPL19P9)	NM_001080544	4171.5	6597.3	0.0147	1.38			
		XM_001726945	106.8	105.8	0.0147	0.9	NM_001031645	1.93	10.04
RAB11FIP1	RAB11 family interacting protein 1(RAB11FIP1)	NM_001002814	459.8	697.6	0.0148	1.39			
E2F4	E2F transcription factor 4(E2F4)	NM_001950	289.3	407.9	0.0149	1.27			
		XR_037945	99.3	139.2	0.0149	1.23			

PHOSPHO2	phosphatase, orphan 2(PHOSPHO2)	NM_001008489	299	208	0.015	0.65
ADGRE5	adhesion G protein-coupled receptor E5(ADGRE5)	NM_078481	103.5	130.9	0.0155	1.12
ADGRE5	adhesion G protein-coupled receptor E5(ADGRE5)	NM_078481	107.1	124.5	0.0155	1.12
		XM_001133677	94.8	106.4	0.0155	1.13
		XM_001133677	106.8	138.9	0.0155	1.13
		BM987531	112.8	142.2	0.0156	1.11
FAM96A	family with sequence similarity 96 member A(FAM96A)	NM_032231	460	369.9	0.0157	0.75
PLCD4	phospholipase C delta 4(PLCD4)	NM_032726	242	179.8	0.0158	0.65
ASB8	ankyrin repeat and SOCS box containing 8(ASB8)	NM_024095	118.5	120	0.0159	0.91
ASB8	ankyrin repeat and SOCS box containing 8(ASB8)	NM_024095	121.6	122.4	0.0159	0.91

P2RY2	purinergic receptor P2Y2(P2RY2)	NM_002564	185.8	141.2	0.0159	0.67			
		XM_001723699	112.9	142.5	0.0159	1.12	NM_144748	66.99	0.14
		XR_038699	1022.6	1448.6	0.0159	1.31			
ATP6V0E1	ATPase H+ transporting V0 subunit e1(ATP6V0E1)	NM_003945	970.5	897.5	0.0162	0.85			
ATP6V0E1	ATPase H+ transporting V0 subunit e1(ATP6V0E1)	NM_003945	1668.7	1759	0.0162	0.85			
GDI2	GDP dissociation inhibitor 2(GDI2)	NM_001494	146.7	216	0.0163	1.3			
MRPL20	mitochondrial ribosomal protein L20(MRPL20)	NM_017971	482	407.1	0.0164	0.77			
ZNF622	zinc finger protein 622(ZNF622)	NM_033414	482	463.4	0.0164	0.87			
		XM_001714310	100.6	126	0.0164	1.12			
STT3A	STT3A, catalytic subunit of the oligosaccharyltransferase complex(STT3A)	NM_152713	482.8	723.5	0.0165	1.38	NM_001107793	77.29	6.85
		XR_019270	119.8	157.2	0.0165	1.13	NM_001107793	77.29	6.85

		XR_039539	113.8	109.9	0.0165	0.88	NM_001107793	77.29	6.85
HOMER2	homer scaffolding protein 2(HOMER2)	NM_199332	212.4	171.6	0.0169	0.73			
BTF3	basic transcription factor 3(BTF3)	NM_001207	1296.2	614.3	0.0172	0.49			
SCARNA20	small Cajal body-specific RNA 20(SCARNA20)	NR_002999	104.2	131.7	0.0172	1.13			
SNORA1	small nucleolar RNA, H/ACA box 1(SNORA1)	NR_003026	100.9	128.2	0.0173	1.14			
PSMB11	proteasome subunit beta 11(PSMB11)	NM_001099780	108.5	138.9	0.0178	1.13			
STEAP2	STEAP2 metalloreductase(STEAP2)	NM_152999	127.7	115.4	0.0178	0.72			
STEAP2	STEAP2 metalloreductase(STEAP2)	NM_152999	201.8	157.9	0.0178	0.72			
GLMP	glycosylated lysosomal membrane protein(GLMP)	NM_144580	845.9	613.6	0.0179	0.66			
CYBB	cytochrome b-245 beta chain(CYBB)	NM_000397	106.7	152.9	0.0183	1.26			
RPL14	ribosomal protein L14(RPL14)	NM_001034996	864.7	1435.9	0.0184	1.51			

TIGD6	tigger transposable element derived 6(TIGD6)	NM_030953	121.5	122.8	0.0184	0.91
MRPL43	mitochondrial ribosomal protein L43(MRPL43)	NM_032112	496.5	372.2	0.0186	0.68
MRPL43	mitochondrial ribosomal protein L43(MRPL43)	NM_032112	935.3	791.2	0.0186	0.68
OXA1L	OXA1L, mitochondrial inner membrane protein(OXA1L)	NM_005015	738	478.1	0.0186	0.59
		AI911349	136.7	183.5	0.0186	1.16
		XR_037977	780.1	1280.1	0.0186	1.53
ATG4B	autophagy related 4B cysteine peptidase(ATG4B)	NM_178326	173.9	164.2	0.0187	0.83
HPX	hemopexin(HPX)	NM_000613	145.1	116.2	0.0187	0.72
RAPGEF1	Rap guanine nucleotide exchange factor 1(RAPGEF1)	NM_005312	136.4	177.8	0.0188	1.14
DEFB103A	defensin beta 103A(DEFB103A)	NM_0010811551	104	136.2	0.019	1.15

DOLK	dolichol kinase(DOLK)	NM_014908	218.9	191	0.019	0.8
RAD51AP1	RAD51 associated protein 1(RAD51AP1)	NM_006479	99.3	126.4	0.019	1.15
RTN4IP1	reticulon 4 interacting protein 1(RTN4IP1)	NM_032730	199.8	190.4	0.019	0.84
METTL4	methyltransferase like 4(METTL4)	NM_022840	160.5	227.8	0.0191	1.21
SERPINB1	serpin family B member 1(SERPINB1)	NM_030666	99.8	130.8	0.0192	1.16
		XM_934839	104	138.5	0.0192	1.17
FGD1	FYVE, RhoGEF and PH domain containing 1(FGD1)	NM_004463	118.3	115.7	0.0193	0.88
BCR	BCR, RhoGEF and GTPase activating protein(BCR)	NM_004327	137	157.7	0.0196	0.74
BCR	BCR, RhoGEF and GTPase activating protein(BCR)	NM_004327	215.7	175.7	0.0196	0.74

LINC00544	long intergenic non-protein coding RNA 544(LINC00544)	NM_001099778	116	160.1	0.0196	1.2			
		XM_934553	100	124.9	0.0197	1.11			
MYH9	myosin heavy chain 9(MYH9)	NM_002473	806.9	2308.3	0.02	2.53	NM_001009603	28.32	0.90
MYH9	myosin heavy chain 9(MYH9)	NM_002473	2233.6	3165.4	0.02	2.53			
		XM_925919	112	108.5	0.02	0.88			
KCNJ13	potassium voltage-gated channel subfamily J member 13(KCNJ13)	NM_002242	107.3	104.4	0.0201	0.89			
STXBP6	syntaxin binding protein 6(STXBP6)	NM_014178	151.4	138.1	0.0201	0.82			
		XR_038898	160.3	250	0.0204	1.42			
ZNF684	zinc finger protein 684(ZNF684)	NM_152373	97.3	127.8	0.0207	1.17			
Tas2r43	taste 2 receptor member 43(TAS2R43)	NM_176884	113	110.3	0.0208	0.89			
TRAPPC13	trafficking protein particle complex 13(TRAPPC13)	NM_001093756	201.4	162.3	0.0209	0.72			

		BQ185080	112.1	145.6	0.0209	1.13
		CR748464	101.1	127.6	0.0209	1.12
		XR_017653	1485	2142.3	0.021	1.28
ZFAND6	zinc finger AN1-type containing 6(ZFAND6)	NM_019006	257.2	254.4	0.0212	0.75
ZFAND6	zinc finger AN1-type containing 6(ZFAND6)	NM_019006	509.7	405.2	0.0212	0.75
		XR_018412	106.9	132.9	0.0213	1.11
HERPUD2	HERPUD family member 2(HERPUD2)	NM_022373	109.7	139.4	0.0214	1.13
HERPUD2	HERPUD family member 2(HERPUD2)	NM_022373	120.7	132.2	0.0214	1.13
CMC1	C-X9-C motif containing 1(CMC1)	NM_182523	274.2	215.2	0.0217	0.69
CLEC11A	C-type lectin domain family 11 member A(CLEC11A)	NM_002975	176	156.4	0.0218	0.78
TPI1P2	triosephosphate isomerase 1 pseudogene 2(TPI1P2)	NR_002187	143.8	133.8	0.0218	0.84

UQCC1	ubiquinol-cytochrome c reductase complex assembly factor 1(UQCC1)	NM_199487	217.1	198.8	0.022	0.79
		DB299679	123.7	117.3	0.0223	0.86
ADCK1	aarF domain containing kinase 1(ADCK1)	NM_020421	153.3	150.7	0.0224	0.87
SH3TC1	SH3 domain and tetratricopeptide repeats 1(SH3TC1)	NM_018986	539.6	360.7	0.0224	0.62
ANGEL1	angel homolog 1(ANGEL1)	NM_015305	166.5	276	0.0226	1.45
MACROD1	MACRO domain containing 1(MACROD1)	NM_014067	552.7	291.7	0.0226	0.5
TMEM185A	transmembrane protein 185A(TMEM185A)	NM_032508	144.5	162.4	0.0227	0.83
TMEM185A	transmembrane protein 185A(TMEM185A)	NM_032508	200.1	184.3	0.0227	0.83
PSMF1	proteasome inhibitor subunit 1(PSMF1)	NM_178579	377.6	336.1	0.0228	0.79

		XM_495909	105.7	134.6	0.0228	1.14
csnk1g3	casein kinase 1 gamma 3(CSNK1G3)	NM_001031812	142.5	190.8	0.0229	1.17
ZNF385C	zinc finger protein 385C(ZNF385C)	NM_001013624	146.1	209.7	0.0229	1.23
		XM_942071	137.4	190.7	0.0229	1.21
NOTUM	NOTUM, palmitoleoyl-protein carboxylesterase(NOTUM)	NM_178493	113.6	115	0.023	0.91
RPAIN	RPA interacting protein(RPAIN)	NM_001033002	326.6	295.8	0.023	0.8
CHRNA6	cholinergic receptor nicotinic alpha 6 subunit(CHRNA6)	NM_004198	114.7	107.6	0.0232	0.86
GORASP1	golgi reassembly stacking protein 1(GORASP1)	NM_031899	169.5	129.7	0.0236	0.71
		XM_001725669	640.4	415.7	0.0237	0.61
EPB41L1	erythrocyte membrane protein band 4.1 like 1(EPB41L1)	NM_012156	326.1	273.9	0.024	0.74

		XM_926231	156.3	244.2	0.024	1.38
ARCN1	archain 1(ARCN1)	NM_001655	305	433.4	0.0241	1.29
ARRDC4	arrestin domain containing 4(ARRDC4)	NM_183376	90.1	120.7	0.0241	1.21
		XR_016385	258.3	386.7	0.0241	1.35
RPL32	ribosomal protein L32(RPL32)	NM_001007074	102.7	118.6	0.0242	1.59
RPL32	ribosomal protein L32(RPL32)	NM_001007074	1495.3	2663.2	0.0242	1.59
SPACA9	sperm acrosome associated 9(SPACA9)	NM_018956	157.3	159.6	0.0242	0.89
BBC3	BCL2 binding component 3(BBC3)	NM_014417	180.4	179.1	0.0245	0.89
LYPD6	LY6/PLAUR domain containing 6(LYPD6)	NM_194317	98.1	121.9	0.0245	1.13
		AW665973	268.9	505.5	0.0246	1.58
ADAT1	adenosine deaminase, tRNA specific 1(ADAT1)	NM_012091	116.9	118.7	0.0249	0.92
CTSF	cathepsin F(CTSF)	NM_003793	559.1	489.3	0.0249	0.81

PTPN3	protein tyrosine phosphatase, non-receptor type 3(PTPN3)	NM_002829	338.6	222.4	0.0251	0.6
PDGFA	platelet derived growth factor subunit A(PDGFA)	NM_033023	167.2	149.9	0.0252	0.8
		XR_016832	153.2	224.8	0.0252	1.28
NDUFA11	NADH:ubiquinone oxidoreductase subunit A11(NDUFA11)	NM_175614	1766.9	1305.1	0.0254	0.67
PLA1A	phospholipase A1 member A(PLA1A)	NM_015900	349.7	213.4	0.0254	0.57
TMEM189-UBE2V1	TMEM189-UBE2V1 readthrough(TMEM189-UBE2V1)	NM_003349	236.2	171.9	0.0254	0.69
MRPL34	mitochondrial ribosomal protein L34(MRPL34)	NM_023937	399.5	384.9	0.0256	0.87
PSMC1	proteasome 26S subunit, ATPase 1(PSMC1)	NM_002802	1659.8	1339.7	0.0256	0.73
PSMC1	proteasome 26S subunit, ATPase 1(PSMC1)	NM_002802	1673.9	1645.6	0.0256	0.73

SIRPG	signal regulatory protein gamma(SIRPG)	NM_001039508	102.8	157.2	0.0256	1.33
CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6(CHCHD6)	NM_032343	302.2	248.4	0.0259	0.73
fgl1	fibrinogen like 1(FGL1)	NM_201553	167.9	119.9	0.0259	0.65
		XM_944079	122.9	164.4	0.026	1.16
Cox4I1	cytochrome c oxidase subunit 4I1(COX4I1)	NM_001861	10161.5	7591.4	0.0261	0.63
FAM131B	family with sequence similarity 131 member B(FAM131B)	NM_014690	107.2	134.9	0.0261	1.11
HSPBP1	HSPA (Hsp70) binding protein 1(HSPBP1)	NM_012267	110.4	114.8	0.0261	0.87
HSPBP1	HSPA (Hsp70) binding protein 1(HSPBP1)	NM_012267	121.7	115.7	0.0261	0.87
TCEA3	transcription elongation factor A3(TCEA3)	NM_003196	704.6	419.6	0.0261	0.53

RTFDC1	replication termination factor 2 domain containing 1(RTFDC1)	NM_016407	474.5	421.8	0.0262	0.79
TRAF4	TNF receptor associated factor 4(TRAF4)	NM_004295	117.9	112.6	0.0262	0.87
ALDOA	aldolase, fructose-bisphosphate A(ALDOA)	NM_184043	4490.9	1955.6	0.0263	0.36
		XM_945148	123.5	162.6	0.0263	1.16
		XR_019429	141.7	241.6	0.0264	1.51
GLUD1	glutamate dehydrogenase 1(GLUD1)	NM_005271	111.9	110.9	0.0265	0.9
PIGL	phosphatidylinositol glycan anchor biosynthesis class L(PIGL)	NM_004278	104.4	128.1	0.0265	1.1
ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B(ANKS1B)	NM_020140	112.3	111	0.0266	0.91
slc35e2b	solute carrier family 35 member E2B(SLC35E2B)	NM_001110781	118.7	155	0.0267	1.15
		AK002088	91.1	116.5	0.0267	1.15

MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	108.3	108.6	0.0268	0.91			
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	177.3	230.5	0.0268	0.91			
		NR_003252	153.5	152.5	0.0268	0.88			
		XM_926590	99.3	128.8	0.0268	1.17			
GC	GC, vitamin D binding protein(GC)	NM_000583	172	110.3	0.027	0.58			
ESRRAP2	estrogen-related receptor alpha pseudogene 2(ESRRAP2)	NR_000033	430.1	343.1	0.0271	0.71			
SEH1L	SEH1 like nucleoporin(SEH1L)	NM_001013437	149	209.3	0.0271	1.25			
SEH1L	SEH1 like nucleoporin(SEH1L)	NM_001013437	245.1	273.8	0.0271	1.25	NM_144744	0.11	40.01
		XM_001727022	145.8	132.9	0.0271	0.83			
GORAB	golgin, RAB6 interacting(GORAB)	NM_152281	114.4	140.1	0.0272	1.09			
CORO2B	coronin 2B(CORO2B)	NM_006091	102.2	114.1	0.0273	0.83			

CORO2B	coronin 2B(CORO2B)	NM_006091	124	113.4	0.0273	0.83
TMEM206	transmembrane protein 206(TMEM206)	NM_018252	105.7	98.3	0.0274	0.86
		XM_940962	170	155.8	0.0274	0.82
CCDC106	coiled-coil domain containing 106(CCDC106)	NM_013301	349	317.4	0.0276	0.81
		XM_0017200172	494.9	722	0.0276	1.33
JADE1	jade family PHD finger 1(JADE1)	NM_024900	215	199	0.0277	0.82
ZRANB1	zinc finger RANBP2-type containing 1(ZRANB1)	NM_017580	156	154.2	0.0277	0.87
DNAJC27	DnaJ heat shock protein family (Hsp40) member C27(DNAJC27)	NM_016544	297.1	260.3	0.0278	0.76
		XM_0017144755	167.8	136.1	0.0278	0.73
ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)(ICAM4)	NM_022377	112.3	107.3	0.028	0.88

		XR_038602	1134.2	1738.1	0.0282	1.42
HOXD3	homeobox D3(HOXD3)	NM_006898	203.3	175.7	0.0285	0.79
SERPINC1	serpin family C member 1(SERPINC1)	NM_000488	329.7	175.3	0.0285	0.46
LIN7B	lin-7 homolog B, crumbs cell polarity complex component(LIN7B)	NM_022165	140.9	131.4	0.0287	0.82
HOXA11	homeobox A11(HOXA11)	NM_005523	109	131.5	0.0288	1.08
PDGFB	platelet derived growth factor subunit B(PDGFB)	NM_033016	126.5	123.4	0.0288	0.88
CYB561A3	cytochrome b561 family member A3(CYB561A3)	NM_153611	201.9	405.9	0.0289	1.77
KREMEN2	kringle containing transmembrane protein 2(KREMEN2)	NM_024507	113.8	111.5	0.0291	0.89
PAXIP1	PAX interacting protein 1(PAXIP1)	NM_007349	171.7	237.5	0.0292	1.21
TMEM67	transmembrane protein 67(TMEM67)	NM_153704	116.7	111.4	0.0292	0.88

CADM4	cell adhesion molecule 4(CADM4)	NM_145296	330.3	222.6	0.0293	0.63
		XM_944183	114.3	138.9	0.0294	1.08
IGSF9B	immunoglobulin superfamily member 9B(IGSF9B)	NM_014987	111.1	141.8	0.0295	1.13
PLAA	phospholipase A2 activating protein(PLAA)	NM_001031689	91.5	118.1	0.0295	1.16
PLAA	phospholipase A2 activating protein(PLAA)	NM_001031689	114.9	126.3	0.0295	1.16
SNX11	sorting nexin 11(SNX11)	NM_152244	376	508	0.0295	1.21
PLBD2	phospholipase B domain containing 2(PLBD2)	NM_173542	224	210.6	0.0296	0.84
TUBA3FP	tubulin alpha 3f pseudogene(TUBA3FP)	NR_003608	120.7	122.8	0.0296	0.91
CENPA	centromere protein A(CENPA)	NM_001042426	98.7	122.8	0.0297	1.14
CENPA	centromere protein A(CENPA)	NM_001042426	104.5	135.1	0.0297	1.14

		XR_019267	129.8	178.9	0.0297	1.19
SLC26A10	solute carrier family 26 member 10(SLC26A10)	NM_133489	110.1	99.9	0.0298	0.84
SLC26A10	solute carrier family 26 member 10(SLC26A10)	NM_133489	125.5	144.5	0.0298	0.84
SRP14	signal recognition particle 14(SRP14)	NM_003134	257.6	405.8	0.03	0.72
SRP14	signal recognition particle 14(SRP14)	NM_003134	4633.3	3832.9	0.03	0.72
hamp	hepcidin antimicrobial peptide(HAMP)	NM_021175	136.1	129.4	0.0301	0.84
KIF16B	kinesin family member 16B(KIF16B)	NM_024704	111.6	111.5	0.0302	0.81
KIF16B	kinesin family member 16B(KIF16B)	NM_024704	136.6	123.9	0.0302	0.81
MAN1C1	mannosidase alpha class 1C member 1(MAN1C1)	NM_020379	589.2	269	0.0302	0.41
DDX19A	DEAD-box helicase 19A(DDX19A)	NM_018332	119	127.9	0.0303	1.17

DDX19A	DEAD-box helicase 19A(DDX19A)	NM_018332	261.7	346.5	0.0303	1.17
SSTR3	somatostatin receptor 3(SSTR3)	NM_001051	107.6	105.6	0.0303	0.9
ATP5J	ATP synthase, H+ transporting, mitochondrial Fo complex subunit F6(ATP5J)	NM_001003701	4092.1	3324.4	0.0304	0.69
		AA658833	108	104.5	0.0304	0.89
		BM684558	101.2	128.4	0.0304	1.12
ASAH1	N-acylsphingosine amidohydrolase 1(ASAH1)	NM_177924	122.3	125.4	0.0307	0.92
PSMB5	proteasome subunit beta 5(PSMB5)	NM_002797	1255.4	1083.9	0.0307	0.78
RRAGD	Ras related GTP binding D(RRAGD)	NM_021244	219.1	161.2	0.0307	0.68
SARM1	sterile alpha and TIR motif containing 1(SARM1)	NM_015077	106.1	131.7	0.0308	1.1
		XR_038738	230.6	359.9	0.0308	1.41

DDAH2	dimethylarginine dimethylaminohydrolase 2(DDAH2)	NM_013974	244.6	204.9	0.031	0.76
DTD2	D-tyrosyl-tRNA deacylase 2 (putative)(DTD2)	NM_080664	119.2	112	0.031	0.84
NME6	NME/NM23 nucleoside diphosphate kinase 6(NME6)	NM_005793	114.3	147.2	0.031	1.13
NME6	NME/NM23 nucleoside diphosphate kinase 6(NME6)	NM_005793	139.1	168.6	0.031	1.13
		XR_015351	120	119.9	0.0312	0.89
NMRK2	nicotinamide riboside kinase 2(NMRK2)	NM_170678	104	92.5	0.0313	0.83
NMRK2	nicotinamide riboside kinase 2(NMRK2)	NM_170678	118.8	123.2	0.0313	0.83
PDE6H	phosphodiesterase 6H(PDE6H)	NM_006205	82.4	113.1	0.0313	1.2
MED31	mediator complex subunit 31(MED31)	NM_016060	441.8	405.1	0.0314	0.83
		XM_935907	416.3	658.5	0.0314	1.48

CCDC85C	coiled-coil domain containing 85C(CCDC85C)	AK123840	368.8	309.1	0.0316	0.73
PRMT6	protein arginine methyltransferase 6(PRMT6)	NM_018137	177.1	161.2	0.0316	0.81
PRMT6	protein arginine methyltransferase 6(PRMT6)	NM_018137	212.6	203.4	0.0316	0.81
ARSD	arylsulfatase D(ARSD)	NM_001669	970.1	728.8	0.0318	0.68
		XR_017498	151.5	232.3	0.0318	1.35
		XR_017498	458.5	519.2	0.0318	1.35
EFHD1	EF-hand domain family member D1(EFHD1)	NM_025202	600	427.1	0.0319	0.66
N4BP1	NEDD4 binding protein 1(N4BP1)	NM_153029	142.1	198.4	0.0319	1.2
UNC5C	unc-5 netrin receptor C(UNC5C)	NM_003728	110.8	111.9	0.0319	0.91
AUH	AU RNA binding methylglutaconyl-CoA hydratase(AUH)	NM_001698	505.3	369.1	0.032	0.67
CFDP1	craniofacial development protein 1(CFDP1)	NM_006324	889.4	731.3	0.032	0.77

TIMM23	translocase of inner mitochondrial membrane 23(TIMM23)	NM_006327	154.6	176	0.032	0.72
TIMM23	translocase of inner mitochondrial membrane 23(TIMM23)	NM_006327	419.4	365.1	0.032	0.72
TIMM23	translocase of inner mitochondrial membrane 23(TIMM23)	NM_006327	932.1	729.9	0.032	0.72
TIMM23	translocase of inner mitochondrial membrane 23(TIMM23)	NM_006327	1595	1344.1	0.032	0.72
FAM26D	family with sequence similarity 26 member D(FAM26D)	NM_153036	101.6	118.4	0.0325	1.09
FAM26D	family with sequence similarity 26 member D(FAM26D)	NM_153036	112.3	139.5	0.0325	1.09

OR4D6	olfactory receptor family 4 subfamily D member 6(OR4D6)	NM_001004708	126.5	161.3	0.0325	1.12
coa1	cytochrome c oxidase assembly factor 1 homolog(COA1)	NM_018224	193.7	177.5	0.0326	0.8
FBXL6	F-box and leucine rich repeat protein 6(FBXL6)	NM_012162	147.7	191.4	0.0326	1.13
		XM_001723545	108.1	135.1	0.0326	1.1
NDRG2	NDRG family member 2(NDRG2)	NM_201539	700	431.8	0.0327	0.57
RBM10	RNA binding motif protein 10(RBM10)	NM_152856	345.5	461.1	0.0329	1.24
ttll5	tubulin tyrosine ligase like 5(TTLL5)	NM_015072	179.7	252.8	0.0329	1.23
PPIP5K1	diphosphoinositol pentakisphosphate kinase 1(PPIP5K1)	NM_001024463	200.4	194	0.033	0.85
nr0b1	nuclear receptor subfamily 0 group B member 1(NR0B1)	NM_000475	108.5	96.6	0.0331	0.83

		XR_016424	2184.7	3530.7	0.0331	1.33
TMEM163	transmembrane protein 163(TMEM163)	NM_030923	138.5	191.9	0.0333	1.21
ERI1	exoribonuclease 1(ERI1)	NM_153332	159.9	208.2	0.0334	1.14
BTF3	basic transcription factor 3(BTF3)	NM_001037637	2422.2	1588.4	0.0335	0.61
TCERG1	transcription elongation regulator 1(TCERG1)	NM_006706	113.3	127.8	0.0336	1.21
TCERG1	transcription elongation regulator 1(TCERG1)	NM_006706	181.5	250.2	0.0336	1.21
TPPP3	tubulin polymerization promoting protein family member 3(TPPP3)	NM_015964	116	112.2	0.0336	0.89
		XM_942669	679.3	1229.2	0.0338	1.73
		XR_016813	114.1	155.6	0.0338	1.2
CDC123	cell division cycle 123(CDC123)	NM_006023	169.5	259.4	0.0339	1.37
		AI024182	128.9	126.5	0.034	0.88

MSI2	musashi RNA binding protein 2(MSI2)	NM_138962	111.3	117.6	0.0341	0.84			
MSI2	musashi RNA binding protein 2(MSI2)	NM_138962	188.6	182.9	0.0341	0.84			
		XR_017366	106.1	139	0.0342	1.14			
GIN1	gypsy retrotransposon integrase 1(GIN1)	NM_017676	119.6	123.6	0.0343	0.83			
GIN1	gypsy retrotransposon integrase 1(GIN1)	NM_017676	146.4	132.4	0.0343	0.83			
		XM_926898	134.4	172.2	0.0345	1.11	NM_017196	14.73	0.69
		XR_016036	194.9	302.4	0.0347	1.37	NM_017196	14.73	0.69
		XR_015255	105.7	147.3	0.0349	1.23	NM_017196	14.73	0.69
		XR_015611	139.9	213.1	0.0349	1.34			
APOO	apolipoprotein O(APOO)	NM_024122	648.6	459.8	0.035	0.65			
Fam129c	family with sequence similarity 129 member C(FAM129C)	NM_173544	111.1	141.3	0.0351	1.12			

FNDC5	fibronectin type III domain containing 5(FNDC5)	NM_153756	233.1	143.2	0.0351	0.55	NM_031356	5.43	24.53
PFKM	phosphofructokinase, muscle(PFKM)	NM_000289	1167.2	418.7	0.0351	0.32	NM_031356	5.43	24.53
		CR605357	135.1	133	0.0351	0.88			
CA10	carbonic anhydrase 10(CA10)	NM_020178	125.5	118.9	0.0354	0.86			
DPPA2	developmental pluripotency associated 2(DPPA2)	NM_138815	114.9	155.5	0.0354	1.17			
SYNGR1	synaptogyrin 1(SYNGR1)	NM_004711	135.2	123	0.0354	0.83			
DRC3	dynein regulatory complex subunit 3(DRC3)	NM_031294	127.7	113.6	0.0355	0.81			
NDUFA1	NADH:ubiquinone oxidoreductase subunit A1(NDUFA1)	NM_004541	1004.1	723.3	0.0355	0.65			
TSEN34	tRNA splicing endonuclease subunit 34(TSEN34)	NM_001077446	123.2	139.1	0.0355	0.78			

TSEN34	tRNA splicing endonuclease subunit 34(TSEN34)	NM_001077446	1078.5	938.7	0.0355	0.78			
		XM_927955	4868.5	3764.5	0.0356	0.67			
		AW364673	134.6	122.6	0.0357	0.83			
		XR_017072	119.2	177.6	0.0357	1.28			
CLIP4	CAP-Gly domain containing linker protein family member 4(CLIP4)	NM_024692	249.4	222.4	0.0359	0.79			
SAYSD1	SAYSVFN motif domain containing 1(SAYSD1)	NM_018322	94.6	119.8	0.0359	1.13			
ANKRD9	ankyrin repeat domain 9(ANKRD9)	NM_152326	107.3	115.4	0.036	0.67			
ANKRD9	ankyrin repeat domain 9(ANKRD9)	NM_152326	317	230	0.036	0.67	NM_017135	41.45	2.88
STYX	serine/threonine/tyrosine interacting protein(STYX)	NM_145251	109.1	110.1	0.0364	0.91	NM_017135	41.45	2.88
		XM_209824	111	135.6	0.0365	1.08	NM_017135	41.45	2.88

PTPN20	protein tyrosine phosphatase, non-receptor type 20(PTPN20)	NM_015605	101.9	128.9	0.0366	1.11	NM_017135	41.45	2.88
NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	NM_002530	102.8	123.3	0.0367	1.08			
TNFAIP1	TNF alpha induced protein 1(TNFAIP1)	NM_021137	171.2	263.4	0.0367	1.35			
		XM_934518	126.6	171.7	0.0367	1.17			
BYSL	bystin like(BYSL)	NM_004053	114.8	154.9	0.0369	1.17			
CCDC177	coiled-coil domain containing 177(CCDC177)	NM_020181	100.9	131.6	0.0369	1.14			
USP38	ubiquitin specific peptidase 38(USP38)	NM_032557	126	115	0.0369	0.83			
		NR_031743	108.4	138.9	0.0369	1.13	NM_001033653	43.46	1.56
TM2D1	TM2 domain containing 1(TM2D1)	NM_032027	155.4	193.9	0.0374	0.81			
TM2D1	TM2 domain containing 1(TM2D1)	NM_032027	202	178.1	0.0374	0.81			

Cox7a1	cytochrome c oxidase subunit 7A1(COX7A1)	NM_001864	710.5	487.2	0.0375	0.62
		XM_372926	2409.2	4504.4	0.0375	1.49
MGEA5	meningioma expressed antigen 5 (hyaluronidase)(MGEA5)	NM_012215	109.8	143.7	0.0376	1.14
PIAS2	protein inhibitor of activated STAT 2(PIAS2)	NM_004671	115.3	126.3	0.0376	0.87
PIAS2	protein inhibitor of activated STAT 2(PIAS2)	NM_004671	160.8	157.4	0.0376	0.87
TUBBP6	tubulin beta class I pseudogene 6(TUBBP6)	NR_003598	110.7	143.4	0.0376	1.13
		XM_928996	116.4	146.6	0.0376	1.1
CLASP1	cytoplasmic linker associated protein 1(CLASP1)	NM_015282	422.7	357.9	0.0378	0.75
RPL36	ribosomal protein L36(RPL36)	NM_033643	1083.6	1757.7	0.038	1.41
TNFRSF19	TNF receptor superfamily member 19(TNFRSF19)	NM_018647	117.1	111.3	0.038	0.85

		XM_374276	109.5	105	0.038	0.88			
		XR_018261	655.9	1141.9	0.038	1.54			
PPTC7	PTC7 protein phosphatase homolog(PPTC7)	NM_139283	282	240	0.0381	0.75			
ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2(ACAP2)	NM_012287	118.4	164.3	0.0382	1.34			
ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2(ACAP2)	NM_012287	126.2	170.7	0.0382	1.34			
ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2(ACAP2)	NM_012287	157.8	242.1	0.0382	1.34			
		XM_377426	115.4	206.1	0.0382	1.56			
STMN1	stathmin 1(STMN1)	NM_203401	102.2	147.4	0.0384	1.26			
		XM_929427	141.3	190.2	0.0384	1.16			
KEAP1	kelch like ECH associated protein 1(KEAP1)	NM_012289	249.4	238.4	0.0387	0.8	NM_134407	50.47	11.16

KEAP1	kelch like ECH associated protein 1(KEAP1)	NM_012289	329.6	296.7	0.0387	0.8
		XR_038871	541.3	964.7	0.0389	1.62
YIF1B	Yip1 interacting factor homolog B, membrane trafficking protein(YIF1B)	NM_033557	124	125.9	0.039	0.91
ZFP82	ZFP82 zinc finger protein(ZFP82)	NM_133466	125.4	162	0.039	1.12
		AW780096	100.2	119	0.039	1.08
		XR_016632	716	1233	0.039	1.62
		XR_038356	129	195.1	0.0391	1.28
NDUFB8	NADH:ubiquinone oxidoreductase subunit B8(NDUFB8)	NM_005004	5604.2	4470.4	0.0396	0.68
NCBP1	nuclear cap binding protein subunit 1(NCBP1)	NM_002486	292.3	382.8	0.0397	1.21
PDS5A	PDS5 cohesin associated factor A(PDS5A)	NM_015200	104.4	132.4	0.0398	1.14
		XR_039693	147.7	224.7	0.0398	1.34

CDC6	cell division cycle 6(CDC6)	NM_001254	106.1	136.6	0.0399	1.13			
GATB	glutamyl-tRNA amidotransferase subunit B(GATB)	NM_004564	200.2	184.2	0.0401	0.82			
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	195.7	210.8	0.0402	1.19			
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	197.7	264.4	0.0402	1.19			
UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)(UBR3)	NM_172070	199.2	199.1	0.0403	0.85			
UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)(UBR3)	NM_172070	220.9	211.2	0.0403	0.85	NM_001033706	2.42	10.86
BRD1	bromodomain containing 1(BRD1)	NM_014577	143.5	190.5	0.0404	1.16			

TRPM4	transient receptor potential cation channel subfamily M member 4(TRPM4)	NM_017636	366.4	255.3	0.0404	0.61			
CDK12	cyclin dependent kinase 12(CDK12)	NM_016507	217.3	498.7	0.0405	2.02			
ZDHHC17	zinc finger DHHC-type containing 17(ZDHHC17)	NM_015336	95.9	121.1	0.0405	1.13			
		NM_001080831	145.7	206.3	0.0405	1.23			
TRAF3IP2	TRAF3 interacting protein 2(TRAF3IP2)	NM_147686	392.8	312.2	0.0406	0.71	NM_153300	0.14	61.17
SIGLEC17P	sialic acid binding Ig like lectin 17, pseudogene(SIGLEC17P)	NR_002804	128.8	166.5	0.0407	1.12			
TMEM208	transmembrane protein 208(TMEM208)	NM_014187	250.3	237.5	0.0407	0.85	NM_032416	108.51	1.87
TMEM208	transmembrane protein 208(TMEM208)	NM_014187	299.6	302	0.0407	0.85			
Znf763	zinc finger protein 763(ZNF763)	NM_001012753	106.5	151.7	0.0407	1.23			

EI24	EI24, autophagy associated transmembrane protein(EI24)	NM_004879	206.8	173.7	0.0408	0.78
CCNDBP1	cyclin D1 binding protein 1(CCNDBP1)	NM_012142	163.9	152.5	0.0409	0.83
josd2	Josephin domain containing 2(JOSD2)	NM_138334	120.2	117.2	0.0409	0.88
NDRG4	NDRG family member 4(NDRG4)	NM_020465	117.7	128.3	0.041	0.9
NDRG4	NDRG family member 4(NDRG4)	NM_020465	119.4	120.7	0.041	0.9
SAFB2	scaffold attachment factor B2(SAFB2)	NM_014649	124.3	136.7	0.041	1.25
SAFB2	scaffold attachment factor B2(SAFB2)	NM_014649	653.9	894.6	0.041	1.25
FGF18	fibroblast growth factor 18(FGF18)	NM_003862	119.7	120.1	0.0412	0.91
APIP	APAF1 interacting protein(APIP)	NM_015957	198.8	200.5	0.0413	0.76
APIP	APAF1 interacting protein(APIP)	NM_015957	350.3	301.3	0.0413	0.76

CCT6P1	chaperonin containing TCP1 subunit 6 pseudogene 1(CCT6P1)	NR_003110	508.4	644.7	0.0413	1.16	NM_001191088	10.07	0.03
		XM_938599	503.5	827.3	0.0413	1.52	NM_001191088	10.07	0.03
ESD	esterase D(ESD)	NM_001984	247.8	204.4	0.0414	0.72			
ESD	esterase D(ESD)	NM_001984	1970.5	1884.5	0.0414	0.72			
MRPS33	mitochondrial ribosomal protein S33(MRPS33)	NM_016071	126.7	116.9	0.0414	0.84			
MRPS33	mitochondrial ribosomal protein S33(MRPS33)	NM_016071	318.9	316.3	0.0414	0.84	NM_012496	1095.39	8.76
MXD1	MAX dimerization protein 1(MXD1)	NM_002357	118.3	150.4	0.0414	1.1			
SKP2	S-phase kinase associated protein 2(SKP2)	NM_032637	103.7	135.7	0.0414	1.16			
CTLA4	cytotoxic T-lymphocyte associated protein 4(CTLA4)	NM_005214	108	156.4	0.0415	1.27			
LMOD3	leiomodin 3(LMOD3)	NM_198271	658.6	1079.3	0.0415	1.53			

P4HA1	prolyl 4-hydroxylase subunit alpha 1(P4HA1)	NM_000917	125.8	126.1	0.0415	0.9
PON3	paraoxonase 3(PON3)	NM_000940	111.4	105.6	0.0415	0.87
RANBP3	RAN binding protein 3(RANBP3)	NM_003624	103.6	130.3	0.0415	1.11
RANBP3	RAN binding protein 3(RANBP3)	NM_003624	105.5	132.3	0.0415	1.11
MTFR1L	mitochondrial fission regulator 1 like(MTFR1L)	NM_019557	193.3	171.3	0.0416	0.8
		CN479898	136.7	129.1	0.0416	0.86
		XM_001719755	116.7	150.2	0.0416	1.13
DCAF6	DDB1 and CUL4 associated factor 6(DCAF6)	NM_001017977	156.4	135.3	0.0418	0.79
DCAF6	DDB1 and CUL4 associated factor 6(DCAF6)	NM_001017977	1084.1	931.7	0.0418	0.79
TPR	translocated promoter region, nuclear basket protein(TPR)	NM_003292	357.6	500.3	0.042	1.25
		XM_940014	117.3	114.8	0.0422	0.89

MCM7	minichromosome maintenance complex component 7(MCM7)	NM_005916	107.5	138.9	0.0423	1.14
MYL6B	myosin light chain 6B(MYL6B)	NM_002475	1326.3	797.2	0.0423	0.57
PPARA	peroxisome proliferator activated receptor alpha(PPARA)	NM_001001928	143	136.8	0.0423	0.85
MICU1	mitochondrial calcium uptake 1(MICU1)	NM_006077	273.1	227	0.0424	0.72
ORC1	origin recognition complex subunit 1(ORC1)	NM_004153	126.5	163.1	0.0424	1.13
GLRX5	glutaredoxin 5(GLRX5)	NM_016417	3240.7	2238.3	0.0425	0.62
PIH1D1	PIH1 domain containing 1(PIH1D1)	NM_017916	236.8	216.1	0.0425	0.8
SDHA	succinate dehydrogenase complex flavoprotein subunit A(SDHA)	NM_004168	722	712.9	0.0425	0.51

SDHA	succinate dehydrogenase complex flavoprotein subunit A(SDHA)	NM_004168	744.3	418	0.0425	0.51
		XR_037304	109.2	101.7	0.0425	0.86
KDELR1	KDEL endoplasmic reticulum protein retention receptor 1(KDELR1)	NM_006801	130.8	170.7	0.0427	1.13
PJA1	praja ring finger ubiquitin ligase 1(PJA1)	NM_001032396	205.6	177.3	0.0428	0.78
CHMP4B	charged multivesicular body protein 4B(CHMP4B)	NM_176812	465.5	415.2	0.0429	0.8
FGA	fibrinogen alpha chain(FGA)	NM_000508	113.1	106.4	0.0429	0.87
MAPKBP1	mitogen-activated protein kinase binding protein 1(MAPKBP1)	NM_014994	107.3	134	0.043	1.11
polr2m	RNA polymerase II subunit M(POLR2M)	NM_001018102	106.2	116.4	0.043	0.82
polr2m	RNA polymerase II subunit M(POLR2M)	NM_001018102	127.1	112.7	0.043	0.82

TIMM9	translocase of inner mitochondrial membrane 9(TIMM9)	NM_012460	271.6	254.4	0.043	0.84			
UNQ6494	uncharacterized LOC100129066(UNQ6494)	NR_024280	107	133.4	0.043	1.11			
		XM_001719035	364.6	522.4	0.043	1.36			
		XR_039704	101.7	132.1	0.043	1.15			
CFAP69	cilia and flagella associated protein 69(CFAP69)	NM_001039706	171.7	153.9	0.0431	0.82	NM_013059	21.02	0.11
PALM	paralemmin(PALM)	NM_002579	107.5	113.4	0.0431	0.61			
PALM	paralemmin(PALM)	NM_002579	244	218.2	0.0431	0.61			
PALM	paralemmin(PALM)	NM_002579	1139.7	756.9	0.0431	0.61			
TMSB4X	thymosin beta 4, X-linked(TMSB4X)	NM_021109	139.5	266.2	0.0432	1.73			
TMSB4X	thymosin beta 4, X-linked(TMSB4X)	NM_021109	16760.5	17031.2	0.0432	1.73			
		AA193588	125.4	163.4	0.0433	1.13			
		XM_933938	99.3	127.8	0.0434	1.14			

KIAA0586	KIAA0586(KIAA0586)	NM_014749	118.7	117.6	0.0435	0.89			
PARP16	poly(ADP-ribose) polymerase family member 16(PARP16)	NM_017851	104.2	135.5	0.0435	1.16			
PEX7	peroxisomal biogenesis factor 7(PEX7)	NM_000288	278.2	256.5	0.0436	0.83			
FAM122A	family with sequence similarity 122A(FAM122A)	NM_138333	105.7	129.6	0.0437	1.09			
pnkd	paroxysmal nonkinesigenic dyskinesia(PNKD)	NM_015488	245.6	174.8	0.0438	0.65	NM_012816	19.78	2.28
RPL32P18	ribosomal protein L32 pseudogene 18(RPL32P18)	NM_001090027	1617.9	2874.7	0.0438	1.48	NM_012816	19.78	2.28
ZC3H18-AS1	ZC3H18 antisense RNA 1 (head to head)(ZC3H18-AS1)	NM_001001682	103.9	127.5	0.0438	1.1			
		XM_927868	845.1	653.3	0.0438	0.72			
CDK18	cyclin dependent kinase 18(CDK18)	NM_212503	151.1	146.7	0.0439	0.85			

FREM2	FRAS1 related extracellular matrix protein 2(FREM2)	NM_207361	117.9	104.5	0.044	0.81
MRPL11	mitochondrial ribosomal protein L11(MRPL11)	NM_016050	541.9	488.5	0.0441	0.83
		AI183825	117.1	117.5	0.0441	0.9
ANAPC15	anaphase promoting complex subunit 15(ANAPC15)	NM_014042	187.5	160.1	0.0442	0.75
APOA2	apolipoprotein A2(APOA2)	NM_001643	157.9	104.6	0.0442	0.6
KIAA1551	KIAA1551(KIAA1551)	NM_018169	96.6	136.8	0.0442	1.24
KIAA1551	KIAA1551(KIAA1551)	NM_018169	100.5	119.9	0.0442	1.24
PPIL6	peptidylprolyl isomerase like 6(PPIL6)	NM_173672	112.6	103.3	0.0442	0.84
		XR_018020	106.7	134.1	0.0442	1.11
ADAM8	ADAM metallopeptidase domain 8(ADAM8)	NM_001109	92.3	121.7	0.0443	1.16
GOT2	glutamic-oxaloacetic transaminase 2(GOT2)	NM_002080	1233.7	865.2	0.0443	0.65

RFX5	regulatory factor X5(RFX5)	NM_001025603	106.6	141.5	0.0443	1.17			
RPUSD3	RNA pseudouridylate synthase domain containing 3(RPUSD3)	NM_173659	260	249.8	0.0443	0.84			
HAX1	HCLS1 associated protein X-1(HAX1)	NM_006118	138.7	135.6	0.0444	0.88			
HAX1	HCLS1 associated protein X-1(HAX1)	NM_006118	334.7	354.8	0.0444	0.88			
ACTR3	ARP3 actin related protein 3 homolog(ACTR3)	NM_005721	162.5	310.8	0.0445	1.71	NM_031544	4.79	38.59
		XM_0017133657	730	488.3	0.0445	0.62	NM_031544	4.79	38.59
		XM_371878	91.6	116.4	0.0445	1.14			
FAM45A	family with sequence similarity 45 member A(FAM45A)	NM_207009	117.1	110.3	0.0446	0.84			

HAR1B	highly accelerated region 1B (non-protein coding)(HAR1B)	NR_003245	111.9	141	0.0447	1.11
PRKRIP1	PRKR interacting protein 1 (IL11 inducible)(PRKRIP1)	NM_024653	123.9	157	0.0447	1.11
USP33	ubiquitin specific peptidase 33(USP33)	NM_201624	104.6	101	0.0447	0.89
RRP1B	ribosomal RNA processing 1B(RRP1B)	NM_015056	109.3	104.6	0.0448	0.87
		XM_001724539	453.1	729.2	0.0448	1.51
		XR_016197	81.4	120.8	0.0448	1.29
CDC45	cell division cycle 45(CDC45)	NM_003504	86.1	134.6	0.0449	1.35
FGG	fibrinogen gamma chain(FGG)	NM_000509	188.8	101.8	0.0449	0.48
GPR89B	G protein-coupled receptor 89B(GPR89B)	NM_016334	150.5	138.8	0.045	0.85
		AW014327	106.7	136.9	0.045	1.12
		XM_928029	152.5	153.4	0.045	0.89

CCDC28B	coiled-coil domain containing 28B(CCDC28B)	NM_024296	119.7	125.2	0.0451	0.88
CCDC28B	coiled-coil domain containing 28B(CCDC28B)	NM_024296	140.9	139.9	0.0451	0.88
CD8A	CD8a molecule(CD8A)	NM_001768	115.5	169.7	0.0451	1.29
		XR_016732	2595.4	4667.1	0.0451	1.4
		XM_0017144765	114.2	111.8	0.0453	0.9
MPRIP	myosin phosphatase Rho interacting protein(MPRIP)	NM_201274	195	166.4	0.0454	0.78
Uqcrfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1(UQCRFS1)	NM_006003	4410.4	3323	0.0455	0.66
COPA	coatomer protein complex subunit alpha(COPA)	NM_004371	233.5	325.7	0.0456	1.25
PPP1CA	protein phosphatase 1 catalytic subunit alpha(PPP1CA)	NM_002708	121.5	125.2	0.0456	0.92

		AW028158	101	131.2	0.0457	1.15
		XM_001128975	160.9	212.8	0.0457	1.15
SLC26A8	solute carrier family 26 member 8(SLC26A8)	NM_052961	126.3	167.9	0.0458	1.16
		XM_940853	111.7	110.7	0.0458	0.91
CEBPZ	CCAAT/enhancer binding protein zeta(CEBPZ)	NM_005760	446.1	598.6	0.0461	1.23
		XM_001719341	1141.8	2040.2	0.0462	1.61
		XR_039643	131.7	193.8	0.0462	1.3
		XM_001126676	127.7	125	0.0463	0.88
		XR_040489	121.9	125.3	0.0463	0.91
ANTXR1	anthrax toxin receptor 1(ANTXR1)	NM_032208	167.3	277.1	0.0464	1.51
		XM_927511	107.3	128.4	0.0464	1.07
		XM_001717905	120	150.6	0.0465	1.1
DPH2	DPH2 homolog(DPH2)	NM_001384	169.1	165.1	0.0466	0.87
DUSP13	dual specificity phosphatase 13(DUSP13)	NM_016364	141.4	115.6	0.0466	0.73

DUSP13	dual specificity phosphatase 13(DUSP13)	NM_016364	190.8	210.7	0.0466	0.73
HSD11B2	hydroxysteroid 11-beta dehydrogenase 2(HSD11B2)	NM_000196	458.6	245.1	0.0466	0.51
TRABD	TraB domain containing(TRABD)	NM_025204	624	944	0.0467	1.38
WDR33	WD repeat domain 33(WDR33)	NM_001006623	110.6	135.3	0.0467	1.08
WDR33	WD repeat domain 33(WDR33)	NM_001006623	131.2	163.2	0.0467	1.08
ABCD3	ATP binding cassette subfamily D member 3(ABCD3)	NM_002858	148.9	126.4	0.047	0.77
SLC6A10P	solute carrier family 6 member 10, pseudogene(SLC6A10P)	NR_003083	192.7	160	0.047	0.76
		XM_941195	1831	2947.7	0.047	1.42

FAM210A	family with sequence similarity 210 member A(FAM210A)	NM_152352	189.1	155.6	0.0471	0.77
KIF13B	kinesin family member 13B(KIF13B)	NM_015254	794.4	649.9	0.0472	0.75
MIR1253	microRNA 1253(MIR1253)	NR_031654	143.3	191.4	0.0472	1.17
STXBP5	syntaxin binding protein 5(STXBP5)	NM_139244	152.3	211.1	0.0473	1.23
KLHDC3	kelch domain containing 3(KLHDC3)	NM_057161	957.9	896.4	0.0474	0.87
TTR	transthyretin(TTR)	NM_000371	205.9	141	0.0474	0.59
		XR_017747	109.6	110.3	0.0474	0.92
		XR_017747	122.2	127.7	0.0474	0.92
		XR_037812	171.6	232.6	0.0474	1.2
		XR_038429	99.6	124.8	0.0474	1.13
CLDN3	claudin 3(CLDN3)	NM_001306	214.1	151.1	0.0476	0.67

OR2T12	olfactory receptor family 2 subfamily T member 12(OR2T12)	NM_001004692	167.6	232	0.0476	1.2
IFITM4P	interferon induced transmembrane protein 4 pseudogene(IFITM4P)	NR_001590	128.1	167.1	0.0477	1.13
GPD1L	glycerol-3-phosphate dehydrogenase 1-like(GPD1L)	NM_015141	758.3	659.4	0.0479	0.79
		XR_037672	131.4	130.6	0.0479	0.9
GGT6	gamma-glutamyltransferase 6(GGT6)	NM_153338	146.5	125.8	0.048	0.77
LINC01420	long intergenic non-protein coding RNA 1420(LINC01420)	NR_015367	1185.8	1017.2	0.048	0.8
		XR_037282	174.7	263.9	0.048	1.34
RIPK4	receptor interacting serine/threonine kinase 4(RIPK4)	NM_020639	129.6	128.8	0.0481	0.89

RPS3A	ribosomal protein S3A(RPS3A)	NM_001006	5938.6	8852.1	0.0482	1.18
RPS3A	ribosomal protein S3A(RPS3A)	NM_001006	6427	9708	0.0482	1.18
RPS3A	ribosomal protein S3A(RPS3A)	NM_001006	6930.3	9567.1	0.0482	1.18
MDM2	MDM2 proto-oncogene(MDM2)	NM_002392	146.5	194.2	0.0483	1.14
HSBP1	heat shock factor binding protein 1(HSBP1)	NM_001537	182.4	411.4	0.0485	1.9
		XM_930111	407.7	571.9	0.0485	1.31
		XM_940214	409	599.6	0.0485	1.37
AKT3	AKT serine/threonine kinase 3(AKT3)	NM_181690	117	155.4	0.0488	1.15
RPS21	ribosomal protein S21(RPS21)	NM_001024	129.8	165.5	0.0488	1.11
		XR_041286	1127.7	1954	0.0488	1.51
		XR_041286	3769.8	5828	0.0488	1.51
SMIM13	small integral membrane protein 13(SMIM13)	AJ420516	123	114.8	0.0489	0.86

ECEL1	endothelin converting enzyme like 1(ECEL1)	NM_004826	117.2	149.2	0.0491	1.12
		XM_0011125941	270.5	659.8	0.0491	2.22
		XM_0011125941	414.5	851	0.0491	2.22
		XM_929608	103.9	100	0.0491	0.88
FAM13B	family with sequence similarity 13 member B(FAM13B)	NM_016603	98.9	123.7	0.0492	1.13
HMBS	hydroxymethylbilane synthase(HMBS)	NM_000190	99.5	110.7	0.0492	0.81
HMBS	hydroxymethylbilane synthase(HMBS)	NM_000190	149.5	135.3	0.0492	0.81
		BQ007862	105.5	129.8	0.0492	1.09
CECR5	cat eye syndrome chromosome region, candidate 5(CECR5)	NM_017829	137.7	135.1	0.0494	0.88
LYPLAL1	lysophospholipase like 1(LYPLAL1)	NM_138794	125.1	132.7	0.0494	0.72

LYPLAL1	lysophospholipase like 1(LYPLAL1)	NM_138794	401.4	315	0.0494	0.72
		XM_932583	105.1	134.6	0.0494	1.14
EML1	echinoderm microtubule associated protein like 1(EML1)	NM_004434	145.4	142.5	0.0495	0.79
EML1	echinoderm microtubule associated protein like 1(EML1)	NM_004434	210.2	187	0.0495	0.79
ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4(ENTPD4)	NM_004901	150.7	196.6	0.0495	1.13
GADD45A	growth arrest and DNA damage inducible alpha(GADD45A)	NM_001924	1030.8	588.5	0.0495	0.51
GADD45A	growth arrest and DNA damage inducible alpha(GADD45A)	NM_001924	1193	939.9	0.0495	0.51
ALB	albumin(ALB)	NM_000477	1072.9	368.6	0.0497	0.31
ALB	albumin(ALB)	NM_000477	1474.5	558.4	0.0497	0.31

ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit(ATP5D)	NM_001687	244.3	225.6	0.0497	0.76			
ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit(ATP5D)	NM_001687	910.5	742.3	0.0497	0.76	NM_031012	19.39	0.85
MIR1185-1	microRNA 1185-1(MIR1185-1)	NR_031575	138.9	141.9	0.0497	0.91			
FGA	fibrinogen alpha chain(FGA)	NM_021871	187.3	127.9	0.0498	0.6			
ZC3H3	zinc finger CCCH-type containing 3(ZC3H3)	NM_015117	184.4	242.7	0.0499	1.18	NM_012904	10.16	55.22
PHF1	PHD finger protein 1(PHF1)	NM_024165	110.7	129.5	0.05	1.13			
PHF1	PHD finger protein 1(PHF1)	NM_024165	308.9	381.8	0.05	1.13			

Gene Symbol	**Gene Name**	**Accession No.**	**CON Chow M Mean**	**IUGR Chow M Mean**	**pval IUGR v CON M Chow**	**Ratio IUGR v CON M Chow**	**REFSEQ ID**	**NEPHRON (MEAN RPKM)**	**COLLECTING DUCT (MEAN RPKM)**
GTPBP6	GTP binding protein 6 (putative)(GTPBP6)	NM_012227	159.9	197	0.0000	1.41			

PDGFA	platelet derived growth factor subunit A(PDGFA)	NM_033023	123.1	163.8	0.0000	1.55			
		AW780096	106.2	112.4	0.0000	1.16			
		XM_927511	115.2	92.1	0.0000	0.85			
KDF1	keratinocyte differentiation factor 1(KDF1)	NM_152365	139	102.2	0.0000	0.8			
csnk1e	casein kinase 1 epsilon(CSNK1E)	NM_152221	127.6	189.3	0.0000	1.68			
csnk1e	casein kinase 1 epsilon(CSNK1E)	NM_152221	142.1	149.5	0.0000	1.68	NM_017193	356.13	8.18
RNA5S9	RNA, 5S ribosomal 9(RNA5S9)	NR_023371	156.7	218.1	0.0000	1.57	NM_017193	356.13	8.18
		XR_039453	110.5	109.9	0.0000	1.19	NM_017193	356.13	8.18
		XR_039453	196.8	203.3	0.0000	1.19			
		XM_931775	134.4	100.5	0.0000	0.81			
UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)(UPF3A)	NM_023011	231	347.5	0.0000	1.68			

MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like(MTHFD2L)	NM_001004346	95.7	108	0.0000	1.23
ZNF33B	zinc finger protein 33B(ZNF33B)	NM_006955	127.8	148.8	0.0000	1.35
		XM_942469	114.8	150.9	0.0000	1.5
		XM_942469	115.9	105	0.0000	1.5
FAM133B	family with sequence similarity 133 member B(FAM133B)	NM_152789	273.3	368.5	0.0000	1.5
CAPG	capping actin protein, gelsolin like(CAPG)	NM_001747	97.6	113.5	0.0000	1.28
MERTK	MER proto-oncogene, tyrosine kinase(MERTK)	NM_006343	113.3	127.8	0.0000	1.25
MERTK	MER proto-oncogene, tyrosine kinase(MERTK)	NM_006343	181.3	237.3	0.0000	1.25
TCL1B	T-cell leukemia/lymphoma 1B(TCL1B)	NM_004918	114	138.6	0.0000	1.39

ARID4B	AT-rich interaction domain 4B(ARID4B)	NM_016374	126.6	127.9	0.0000	2.14
ARID4B	AT-rich interaction domain 4B(ARID4B)	NM_016374	141.3	210.3	0.0000	2.14
ARID4B	AT-rich interaction domain 4B(ARID4B)	NM_016374	226.6	430.2	0.0000	2.14
THOC2	THO complex 2(THOC2)	NM_020449	245.8	402.9	0.0000	1.83
TDGP1	thymine-DNA glycosylase pseudogene 1(TDGP1)	NR_024382	94.7	112.1	0.0000	1.29
ZBTB43	zinc finger and BTB domain containing 43(ZBTB43)	NM_014007	116.3	139.1	0.0000	1.34
cep350	centrosomal protein 350(CEP350)	NM_014810	155.4	199.8	0.0000	1.45
KDM5A	lysine demethylase 5A(KDM5A)	NM_005056	144.1	241	0.0000	1.89

NUFIP2	NUFIP2, FMR1 interacting protein 2(NUFIP2)	NM_020772	111.9	158.4	0.0000	1.83
NUFIP2	NUFIP2, FMR1 interacting protein 2(NUFIP2)	NM_020772	211.3	341.6	0.0000	1.83
		XM_933083	143.5	101.3	0.0000	0.77
EXOC1	exocyst complex component 1(EXOC1)	NM_001024924	111.3	135	0.0000	1.38
TAOK1	TAO kinase 1(TAOK1)	NM_020791	96.6	114	0.0000	1.29
TDG	thymine DNA glycosylase(TDG)	NM_003211	133	190.1	0.0000	1.6
TDG	thymine DNA glycosylase(TDG)	NM_003211	280.2	326.3	0.0000	1.6
		BF107605	111.8	119.9	0.0000	1.21
ATXN3	ataxin 3(ATXN3)	NM_004993	105.1	116.8	0.0000	1.24
NUMBL	NUMB like, endocytic adaptor protein(NUMBL)	NM_004756	94.2	106	0.0000	1.24
RAD21	RAD21 cohesin complex component(RAD21)	NM_006265	294.9	498	0.0000	1.89

RAD21	RAD21 cohesin complex component(RAD21)	NM_006265	311.8	296.7	0.0000	1.89
RRBP1	ribosome binding protein 1(RRBP1)	NM_001042576	130.7	165.2	0.0000	1.44
RRBP1	ribosome binding protein 1(RRBP1)	NM_001042576	358.3	314.1	0.0000	1.44
VRK3	vaccinia related kinase 3(VRK3)	NM_001025778	106.9	96.8	0.0000	1.24
VRK3	vaccinia related kinase 3(VRK3)	NM_001025778	167.3	180.3	0.0000	1.24
WWOX	WW domain containing oxidoreductase(WWOX)	NM_130844	115.6	157.5	0.0000	1.53
PCBP2	poly(rC) binding protein 2(PCBP2)	NM_001098620	692.1	1075.5	0.0000	1.75
		NM_033531	98.3	152	0.0000	1.72
ANKRD17	ankyrin repeat domain 17(ANKRD17)	NM_032217	98.6	126	0.0000	1.43
RRAGB	Ras related GTP binding B(RRAGB)	NM_006064	124.9	110.8	0.0010	0.66
RRAGB	Ras related GTP binding B(RRAGB)	NM_006064	146.7	91.4	0.0010	0.66

ADAT1	adenosine deaminase, tRNA specific 1(ADAT1)	NM_012091	107.3	112.3	0.0010	1.15
TUBA3FP	tubulin alpha 3f pseudogene(TUBA3FP)	NR_003608	118.3	95.8	0.0010	0.86
ASAH1	N-acylsphingosine amidohydrolase 1(ASAH1)	NM_177924	120.5	96.2	0.0010	0.86
FRYL	FRY like transcription coactivator(FRYL)	NM_015030	101.3	99	0.0010	1.41
FRYL	FRY like transcription coactivator(FRYL)	NM_015030	115.5	105.1	0.0010	1.41
FRYL	FRY like transcription coactivator(FRYL)	NM_015030	187.9	237.9	0.0010	1.41
		XM_001131286	127.8	99.7	0.0010	0.83
RSPRY1	ring finger and SPRY domain containing 1(RSPRY1)	NM_133368	218.9	294.2	0.0010	1.5
		AW274669	124.3	94.1	0.0010	0.82

SUZ12	SUZ12 polycomb repressive complex 2 subunit(SUZ12)	NM_015355	297.5	493.9	0.0010	1.88			
		XR_039881	94.7	115.4	0.0010	1.33			
PHF7	PHD finger protein 7(PHF7)	NM_016483	116.6	96.1	0.0010	0.88	NM_053502	4.02	18.01
NPAT	nuclear protein, coactivator of histone transcription(NPAT)	NM_002519	92.4	103	0.0010	1.21	NM_053502	4.02	18.01
C1orf64	chromosome 1 open reading frame 64(C1orf64)	NM_178840	117.9	89.7	0.0010	0.81	NM_053502	4.02	18.01
FCGR1B	Fc fragment of IgG receptor Ib(FCGR1B)	NM_001017986	93.1	105.4	0.0010	1.23			
ABHD2	abhydrolase domain containing 2(ABHD2)	NM_152924	116.5	120.2	0.0010	1.23			
ABHD2	abhydrolase domain containing 2(ABHD2)	NM_152924	116.9	126.8	0.0010	1.23			

whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1(WHSC1L1)	NM_023034	96.6	112.4	0.0010	1.27			
SLC38A3	solute carrier family 38 member 3(SLC38A3)	NM_006841	210.4	114.2	0.0010	0.59			
CREB1	cAMP responsive element binding protein 1(CREB1)	AK126342	178	297.7	0.0010	1.89	NM_001009670	33.30	2.04
		NM_001001977	1360.1	813.4	0.0010	0.69			
RPRD2	regulation of nuclear pre-mRNA domain containing 2(RPRD2)	NM_015203	103.1	111.3	0.0010	1.18			
RPRD2	regulation of nuclear pre-mRNA domain containing 2(RPRD2)	NM_015203	194.2	177.9	0.0010	1.18			
		XR_040782	111.2	92.2	0.0010	0.89			
UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)(UPF2)	NM_015542	267.8	500.7	0.0010	2.13			
ZNF451	zinc finger protein 451(ZNF451)	NM_001031623	101.2	104.1	0.0010	1.37			

ZNF451	zinc finger protein 451(ZNF451)	NM_001031623	105.3	127.4	0.0010	1.37
CWC22	CWC22 spliceosome associated protein homolog(CWC22)	NM_020943	94.6	108.8	0.0010	1.26
PCBP2	poly(rC) binding protein 2(PCBP2)	NM_005016	1645.9	2165.2	0.0010	1.4
UBE2D2	ubiquitin conjugating enzyme E2 D2(UBE2D2)	NM_181838	93.5	103.9	0.0010	1.21
PSMD9	proteasome 26S subunit, non-ATPase 9(PSMD9)	NM_002813	141.1	103.9	0.0010	0.79
C21orf58	chromosome 21 open reading frame 58(C21orf58)	NM_058180	1075.2	1541.9	0.0010	1.64
HOOK3	hook microtubule tethering protein 3(HOOK3)	NM_032410	96.2	111.3	0.0010	1.26
POGZ	pogo transposable element with ZNF domain(POGZ)	NM_015100	112.2	139.6	0.0010	1.4

LSM8	LSM8 homolog, U6 small nuclear RNA associated(LSM8)	NM_016200	98.6	124.7	0.0010	1.4
C1orf115	chromosome 1 open reading frame 115(C1orf115)	NM_024709	249.6	110.1	0.0010	0.47
RBCK1	RANBP2-type and C3HC4-type zinc finger containing 1(RBCK1)	NM_006462	153	152.4	0.0010	1.13
MPHOSPH10	M-phase phosphoprotein 10(MPHOSPH10)	NM_005791	364.7	409.1	0.0010	1.27
ZNF689	zinc finger protein 689(ZNF689)	NM_138447	146.5	170.6	0.0010	1.34
CARS	cysteinyl-tRNA synthetase(CARS)	NM_001014438	146.1	224.4	0.0010	1.75
ATXN3	ataxin 3(ATXN3)	NM_030660	126.2	167.2	0.0010	1.49
GMCL1	germ cell-less, spermatogenesis associated 1(GMCL1)	NM_178439	99	95.1	0.0010	1.44

GMCL1	germ cell-less, spermatogenesis associated 1(GMCL1)	NM_178439	123	160.1	0.0010	1.44
VPS13C	vacuolar protein sorting 13 homolog C(VPS13C)	NM_018080	125	149.5	0.0010	1.36
RBBP6	RB binding protein 6, ubiquitin ligase(RBBP6)	NM_032626	144.7	204.2	0.0010	1.59
		XM_294209	92.7	103	0.0010	1.19
VCP	valosin containing protein(VCP)	NM_007126	504.6	324.9	0.0010	0.73
		XM_001725606	104.8	113.7	0.0010	1.2
RGPD5	RANBP2-like and GRIP domain containing 5(RGPD5)	NM_005054	85.4	101.5	0.0010	1.28
ELF2	E74 like ETS transcription factor 2(ELF2)	NM_006874	94.4	122.1	0.0010	1.45
ELF2	E74 like ETS transcription factor 2(ELF2)	NM_006874	146	149.3	0.0010	1.45
bbx	BBX, HMG-box containing(BBX)	NM_020235	236.9	373.6	0.0010	1.74

RUFY3	RUN and FYVE domain containing 3(RUFY3)	NM_014961	118.1	152.9	0.0010	1.43
		XM_001714086	94.7	117.5	0.0010	1.37
		XR_019071	332.4	502.8	0.0010	1.72
FOXO3	forkhead box O3(FOXO3)	NM_201559	197.9	362.9	0.0010	2.01
FOXO3	forkhead box O3(FOXO3)	NM_201559	273	307.7	0.0010	2.01
TIA1	TIA1 cytotoxic granule associated RNA binding protein(TIA1)	NM_022037	165.9	239	0.0010	1.6
UBC	ubiquitin C(UBC)	NM_021009	7920.3	5031	0.0020	0.66
UBC	ubiquitin C(UBC)	NM_021009	9534	7321.4	0.0020	0.66
XRCC5	X-ray repair cross complementing 5(XRCC5)	NM_021141	116.8	129.5	0.0020	1.27
		CD520639	103.8	109.2	0.0020	1.15
		DA877611	109.7	89.1	0.0020	0.86
CREBRF	CREB3 regulatory factor(CREBRF)	NM_153607	195.6	260.6	0.0020	1.45

CREBRF	CREB3 regulatory factor(CREBRF)	NM_153607	206.9	332	0.0020	1.45
BICD2	BICD cargo adaptor 2(BICD2)	NM_001003800	159.2	209.9	0.0020	1.5
MAD1L1	MAD1 mitotic arrest deficient like 1(MAD1L1)	NM_001013836	98.6	109	0.0020	1.2
MAD1L1	MAD1 mitotic arrest deficient like 1(MAD1L1)	NM_001013836	109.5	97.4	0.0020	1.2
OR6C74	olfactory receptor family 6 subfamily C member 74(OR6C74)	NM_001005490	117.6	92.6	0.0020	0.83
ZNF669	zinc finger protein 669(ZNF669)	NM_024804	229.4	271.1	0.0020	1.3
ZNF669	zinc finger protein 669(ZNF669)	NM_024804	490.1	450	0.0020	1.3
LRRC29	leucine rich repeat containing 29(LRRC29)	NM_001004055	215.6	135.7	0.0020	0.71
CDHR2	cadherin related family member 2(CDHR2)	NM_017675	140.3	106.7	0.0020	0.83
		XM_926303	117.5	95	0.0020	0.88

PCYT2	phosphate cytidylyltransferase 2, ethanolamine(PCYT2)	NM_002861	161.6	104.6	0.0020	0.71
		XM_942896	174.8	122.8	0.0020	0.79
CLK2P1	CDC like kinase 2, pseudogene 1(CLK2P1)	NR_002711	117.3	141.4	0.0020	1.35
C2orf78	chromosome 2 open reading frame 78(C2orf78)	NM_001080474	116.5	93.7	0.0020	0.84
PNLDC1	PARN like, ribonuclease domain containing 1(PNLDC1)	NM_173516	97.6	105.4	0.0020	1.19
AMMECR1L	AMMECR1 like(AMMECR1L)	NM_031445	134.5	164.7	0.0020	1.38
AGO2	argonaute 2, RISC catalytic component(AGO2)	NM_012154	221.4	378.9	0.0020	1.91
MYLK	myosin light chain kinase(MYLK)	NM_053026	142.6	161.7	0.0020	1.29
		XM_001726093	161.4	114.8	0.0020	0.79

SMG1P2	SMG1P2, nonsense mediated mRNA decay associated PI3K related kinase pseudogene 2(SMG1P2)	NR_002473	118.5	129.8	0.0020	1.22			
DENND1B	DENN domain containing 1B(DENND1B)	NM_019049	175.9	218.2	0.0020	1.46			
MSL3	male-specific lethal 3 homolog (Drosophila)(MSL3)	NM_078629	177.7	374.5	0.0020	2.39	NM_001107943	0.63	112.77
MSL3	male-specific lethal 3 homolog (Drosophila)(MSL3)	NM_078629	179.7	311	0.0020	2.39			
		XM_933942	144.2	111.9	0.0020	0.85			
CCNDBP1	cyclin D1 binding protein 1(CCNDBP1)	NM_037370	391.9	472.1	0.0020	1.39			
Snora2b	small nucleolar RNA, H/ACA box 2B(SNORA2B)	NR_002951	114.4	136	0.0020	1.36			
GSR	glutathione-disulfide reductase(GSR)	NM_000637	93.1	104.7	0.0020	1.22			

GSR	glutathione-disulfide reductase(GSR)	NM_000637	127.3	104.6	0.0020	1.22			
PLEKHG7	pleckstrin homology and RhoGEF domain containing G7(PLEKHG7)	NM_001004330	98.6	108.1	0.0020	1.2			
LYPD4	LY6/PLAUR domain containing 4(LYPD4)	NM_173506	135.8	106.4	0.0020	0.86			
VSIG8	V-set and immunoglobulin domain containing 8(VSIG8)	NM_001013661	86	100.1	0.0020	1.26			
KIF5A	kinesin family member 5A(KIF5A)	NM_004984	146.4	111.7	0.0020	0.84			
RABGAP1	RAB GTPase activating protein 1(RABGAP1)	NM_012197	309	385.1	0.0020	1.38			
PMS1	PMS1 homolog 1, mismatch repair system component(PMS1)	NM_000534	98.7	107	0.0020	1.18	NM_134372	22.51	0.03
		CD242195	119.9	94.6	0.0020	0.84			

ZRANB2	zinc finger RANBP2-type containing 2(ZRANB2)	NM_005455	117.1	118.4	0.0020	1.37
ZRANB2	zinc finger RANBP2-type containing 2(ZRANB2)	NM_005455	155.9	186.5	0.0020	1.37
		XR_038027	89.7	98.5	0.0020	1.19
		XR_038027	113.2	100.4	0.0020	1.19
ASXL2	additional sex combs like 2, transcriptional regulator(ASXL2)	NM_018263	130.2	206.1	0.0020	1.82
TTC14	tetratricopeptide repeat domain 14(TTC14)	NM_001042601	252.9	364.7	0.0020	1.62
STAU1	staufen double-stranded RNA binding protein 1(STAU1)	NM_017453	95.8	112.9	0.0020	1.31
		BM715751	123.2	96.7	0.0030	0.86
CCDC9	coiled-coil domain containing 9(CCDC9)	NM_015603	106.3	111.7	0.0030	1.16

RMND5B	required for meiotic nuclear division 5 homolog B(RMND5B)	NM_022762	120.5	133	0.0030	1.27
RRS1	ribosome biogenesis regulator homolog(RRS1)	NM_015169	119.4	131.8	0.0030	1.23
		XM_001126824	150.6	111.8	0.0030	0.82
MTERF1	mitochondrial transcription termination factor 1(MTERF1)	NM_006980	156.3	192.2	0.0030	1.41
TOX2	TOX high mobility group box family member 2(TOX2)	NM_001098796	95.6	102.3	0.0030	1.17
WRN	Werner syndrome RecQ like helicase(WRN)	NM_000553	119.9	136.4	0.0030	1.29
ARMCX6	armadillo repeat containing, X-linked 6(ARMCX6)	NM_019007	99	97.4	0.0030	1.3
ARMCX6	armadillo repeat containing, X-linked 6(ARMCX6)	NM_019007	115.1	132.9	0.0030	1.3

FAM98C	family with sequence similarity 98 member C(FAM98C)	NM_174905	153.5	177	0.0030	1.32			
ZSCAN9	zinc finger and SCAN domain containing 9(ZSCAN9)	NM_006299	93.8	113.4	0.0030	1.32			
SIRT5	sirtuin 5(SIRT5)	NM_031244	101.3	117.7	0.0030	1.28			
SIRT5	sirtuin 5(SIRT5)	NM_031244	107.1	102.1	0.0030	1.28			
MTF2	metal response element binding transcription factor 2(MTF2)	NM_007358	177.6	318	0.0030	2.02	NM_001031645	1.93	10.04
aste1	asteroid homolog 1 (Drosophila)(ASTE1)	NM_014065	90.3	102.8	0.0030	1.22			
ADGRF5	adhesion G protein-coupled receptor F5(ADGRF5)	NM_015234	1392.1	1820.8	0.0030	1.45			
		AK095804	139.3	101.1	0.0030	0.78			
TADA2A	transcriptional adaptor 2A(TADA2A)	NM_001488	101.5	107.8	0.0030	1.17			
		XM_930777	109.7	126.2	0.0030	1.29			

UGCG	UDP-glucose ceramide glucosyltransferase(UGCG)	NM_003358	265.4	517.2	0.0030	2.22			
C11orf84	chromosome 11 open reading frame 84(C11orf84)	NM_138471	99.7	107.1	0.0030	1.18			
		AA651832	100.5	106	0.0030	1.17			
RIMKLB	ribosomal modification protein rimK like family member B(RIMKLB)	NM_020734	106.4	116.8	0.0030	1.21			
		XR_038607	111.1	129.7	0.0030	1.32			
PSRC1	proline and serine rich coiled-coil 1(PSRC1)	NM_001032290	137.2	107.7	0.0030	0.86			
LILRA4	leukocyte immunoglobulin like receptor A4(LILRA4)	NM_012276	93.9	107	0.0030	1.24			
		XM_930350	108.5	121.4	0.0030	1.27			
		XM_928281	108.4	118.5	0.0030	1.2			
		XM_928619	177.5	132.5	0.0040	0.85	NM_144748	66.99	0.14

TRIM36	tripartite motif containing 36(TRIM36)	NM_001017397	109.7	87.1	0.0040	0.84			
IFITM4P	interferon induced transmembrane protein 4 pseudogene(IFITM4P)	NR_001590	143.1	107.8	0.0040	0.82			
LOC102724002	uncharacterized LOC102724002(LOC102724002)	AK025166	167	190.7	0.0040	1.31			
UBE2E3	ubiquitin conjugating enzyme E2 E3(UBE2E3)	NM_006357	127.3	102.7	0.0040	0.87			
UBE2E3	ubiquitin conjugating enzyme E2 E3(UBE2E3)	NM_006357	157.4	139.3	0.0040	0.87			
UBE2E3	ubiquitin conjugating enzyme E2 E3(UBE2E3)	NM_006357	431	339.9	0.0040	0.87			
		XR_015946	132.6	140.9	0.0040	1.21			
		XR_015946	228	225.6	0.0040	1.21	NM_001107793	77.29	6.85
LOC643923	uncharacterized LOC643923(LOC643923)	NM_001039772	94.1	107	0.0040	1.25	NM_001107793	77.29	6.85

CHRNA5	cholinergic receptor nicotinic alpha 5 subunit(CHRNA5)	NM_000745	897.2	1337	0.0040	1.64	NM_001107793	77.29	6.85
LRRK2	leucine rich repeat kinase 2(LRRK2)	NM_198578	99.3	104.1	0.0040	1.14			
DCAF16	DDB1 and CUL4 associated factor 16(DCAF16)	NM_017741	99.8	106.4	0.0040	1.15			
ZNF317	zinc finger protein 317(ZNF317)	NM_020933	127.1	143.5	0.0040	1.29			
DLGAP4	DLG associated protein 4(DLGAP4)	NM_183006	117.8	96.9	0.0040	0.89			
RPN2	ribophorin II(RPN2)	NM_002951	285.7	330.9	0.0040	1.29			
		XR_037397	93.1	104.6	0.0040	1.23			
		XM_372319	144.1	108.4	0.0040	0.82			
TTLL3	tubulin tyrosine ligase like 3(TTLL3)	NM_015644	126.8	102.6	0.0040	0.87			
TTLL3	tubulin tyrosine ligase like 3(TTLL3)	NM_015644	160.9	152.3	0.0040	0.87			
NEK8	NIMA related kinase 8(NEK8)	NM_178170	125.8	136.7	0.0040	1.25			

		XM_927957	130.6	98.5	0.0040	0.81
C9orf85	chromosome 9 open reading frame 85(C9orf85)	NM_182505	116.8	133.4	0.0040	1.27
TXLNGY	taxilin gamma pseudogene, Y-linked(TXLNGY)	NM_001005852	88.2	106.8	0.0040	1.32
ZNF148	zinc finger protein 148(ZNF148)	NM_021964	585.7	881.1	0.0040	1.69
RASAL2	RAS protein activator like 2(RASAL2)	NM_170692	92.3	104.5	0.0040	1.22
M6PR	mannose-6-phosphate receptor, cation dependent(M6PR)	NM_002355	675	1018	0.0040	1.64
WDFY3	WD repeat and FYVE domain containing 3(WDFY3)	NM_178583	113.6	92.1	0.0050	0.85
SCARNA18	small Cajal body-specific RNA 18(SCARNA18)	NR_003139	102.7	117.9	0.0050	1.29
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase type 1 beta(PIP5K1B)	NM_003558	99.6	114.7	0.0050	1.27

		XM_001720423	149.9	108	0.0050	0.81
SCML1	sex comb on midleg-like 1 (Drosophila)(SCML1)	NM_001037540	123.8	127.6	0.0050	1.21
SCML1	sex comb on midleg-like 1 (Drosophila)(SCML1)	NM_001037540	128.5	137.4	0.0050	1.21
		XR_017689	128.7	105.4	0.0050	0.89
		XR_038018	343.3	198.7	0.0050	0.66
TRIM52	tripartite motif containing 52(TRIM52)	NM_032765	109.9	143.1	0.0050	1.46
		XR_015455	131.6	112.3	0.0050	1.36
		XR_015455	134.9	157	0.0050	1.36
MAP3K7	mitogen-activated protein kinase kinase kinase 7(MAP3K7)	NM_145331	159.4	212.6	0.0050	1.49
		AB074162	112.2	132.5	0.0050	1.33
HJURP	Holliday junction recognition protein(HJURP)	NM_018410	93.4	103.8	0.0050	1.21

HNRNPA3P1	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1(HNRNPA3P1)	NR_002726	114.9	124	0.0050	1.21			
BAGE5	B melanoma antigen family member 5(BAGE5)	NM_182484	110.4	112.5	0.0050	1.13	NM_001009603	28.32	0.90
		XR_037956	121.3	93.8	0.0050	0.84			
SRP19	signal recognition particle 19(SRP19)	NM_003135	216.5	275.1	0.0050	1.4			
CHD2	chromodomain helicase DNA binding protein 2(CHD2)	NM_001042572	88.6	103	0.0050	1.27			
		AW297854	122.1	97.9	0.0050	0.86			
BCLAF1	BCL2 associated transcription factor 1(BCLAF1)	NM_001077440	107.8	132.4	0.0050	1.36			
BCLAF1	BCL2 associated transcription factor 1(BCLAF1)	NM_001077440	556.2	636.2	0.0050	1.36			
CBLL1	Cbl proto-oncogene like 1(CBLL1)	NM_024814	114	91.5	0.0050	0.86			
CBLL1	Cbl proto-oncogene like 1(CBLL1)	NM_024814	141.2	115.2	0.0050	0.86			

		XM_927142	102.6	112.5	0.0050	1.2
FBXO11	F-box protein 11(FBXO11)	NM_025133	351.7	374.5	0.0050	1.31
FBXO11	F-box protein 11(FBXO11)	NM_025133	514.1	596.4	0.0050	1.31
CDK11A	cyclin dependent kinase 11A(CDK11A)	NM_024011	112.4	131.7	0.0050	1.29
KAZN	kazrin, periplakin interacting protein(KAZN)	NM_001018000	128.2	152.1	0.0050	1.37
KAZN	kazrin, periplakin interacting protein(KAZN)	NM_001018000	212.7	253.4	0.0050	1.37
SF3B1	splicing factor 3b subunit 1(SF3B1)	NM_012433	114.4	148.3	0.0050	1.43
SF3B1	splicing factor 3b subunit 1(SF3B1)	NM_012433	542.8	636.6	0.0050	1.43
FAM122A	family with sequence similarity 122A(FAM122A)	NM_138333	118.4	96.9	0.0060	0.89
CPNE1	copine 1(CPNE1)	NM_003915	96.3	103.7	0.0060	1.17
		XM_929565	217.9	143.8	0.0060	0.76

PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1(PITPNC1)	NM_181671	142.3	159.1	0.0060	1.27
		BQ027703	100.5	105.4	0.0060	1.14
		BM668469	112.9	119.6	0.0060	1.19
mapk13	mitogen-activated protein kinase 13(MAPK13)	NM_002754	106.1	114.2	0.0060	1.19
SCLT1	sodium channel and clathrin linker 1(SCLT1)	NM_144643	88.3	102	0.0060	1.24
CRCP	CGRP receptor component(CRCP)	NM_014478	115.9	112.3	0.0060	1.46
CRCP	CGRP receptor component(CRCP)	NM_014478	2824.8	3977.5	0.0060	1.46
RBBP5	RB binding protein 5, histone lysine methyltransferase complex subunit(RBBP5)	NM_005057	114.2	114	0.0060	1.11
		XM_934567	123.1	126.1	0.0060	1.16
		NM_199345	148.2	185.7	0.0060	1.42
		BX105338	133	194.5	0.0060	1.65

FAM50A	family with sequence similarity 50 member A(FAM50A)	NM_004699	164.6	179.7	0.0060	1.26
		DB038929	143.4	110.9	0.0060	0.84
		XM_001134215	124.1	116	0.0060	1.44
		XM_001134215	216.9	275.7	0.0060	1.44
S100A13	S100 calcium binding protein A13(S100A13)	NM_001024211	122.2	128.7	0.0060	0.77
S100A13	S100 calcium binding protein A13(S100A13)	NM_001024211	170.6	116.5	0.0060	0.77
MTIF2	mitochondrial translational initiation factor 2(MTIF2)	NM_001005369	553.3	724.5	0.0060	1.44
MEIS3P1	Meis homeobox 3 pseudogene 1(MEIS3P1)	NR_002211	212.4	240.6	0.0060	1.27
		XM_001128983	102.6	111	0.0060	1.19
		XM_001713654	6200.5	5439.2	0.0060	0.85
ARHGEF7	Rho guanine nucleotide exchange factor 7(ARHGEF7)	NM_145735	86.5	108.6	0.0060	1.37

GCC1	GRIP and coiled-coil domain containing 1(GCC1)	NM_024523	193.4	216.1	0.0060	1.28
		XM_946257	101.3	107.6	0.0060	1.17
INTS2	integrator complex subunit 2(INTS2)	NM_020748	154.7	184.2	0.0060	1.36
UGGT1	UDP-glucose glycoprotein glucosyltransferase 1(UGGT1)	NM_020120	119.2	151.8	0.0060	1.44
		AI905886	121.5	95.1	0.0060	0.83
		AY475219	89.2	104.7	0.0060	1.27
		XM_933437	144.3	100.8	0.0060	0.75
PEX11B	peroxisomal biogenesis factor 11 beta(PEX11B)	NM_003846	506.9	289.2	0.0060	0.65
		XM_001131379	105.3	110.6	0.0060	1.15
RBM6	RNA binding motif protein 6(RBM6)	NM_005777	118.2	123.5	0.0060	1.18
NRDE2	NRDE-2, necessary for RNA interference, domain containing(NRDE2)	NM_017970	152.5	192.5	0.0060	1.44

		XM_932354	142.7	107	0.0060	0.83
		XM_001126418	114.3	117.8	0.0060	1.14
C1orf101	chromosome 1 open reading frame 101(C1orf101)	NM_173807	138.7	108	0.0060	0.85
MTMR14	myotubularin related protein 14(MTMR14)	NM_001077525	133.8	139.1	0.0060	1.25
MTMR14	myotubularin related protein 14(MTMR14)	NM_001077525	169.9	186.3	0.0060	1.25
DDIT4	DNA damage inducible transcript 4(DDIT4)	NM_019058	131.9	102.7	0.0060	0.86
MS4A6A	membrane spanning 4-domains A6A(MS4A6A)	NM_022349	98.3	104.3	0.0060	1.16
BAGE3	B melanoma antigen family member 3(BAGE3)	NM_182481	87.8	97.7	0.0060	1.19
RNF220	ring finger protein 220(RNF220)	NM_018150	208	238.3	0.0060	1.3

PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	90.1	94.4	0.0070	0.84
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	113.2	99.3	0.0070	0.84
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	130.2	101.7	0.0070	0.84
		AI911349	142.2	108.9	0.0070	0.82
SULT1A1	sulfotransferase family 1A member 1(SULT1A1)	NM_177530	2668.3	3612.2	0.0070	1.4
		XM_498969	203.5	118.8	0.0070	0.65
HCFC2	host cell factor C2(HCFC2)	NM_013320	110.7	116.6	0.0070	1.16
TMEM263	transmembrane protein 263(TMEM263)	NM_152261	93	101.2	0.0070	1.19
		XR_019471	956.6	1383.3	0.0070	1.57
WDR37	WD repeat domain 37(WDR37)	NM_014023	121.7	139.7	0.0070	1.29

WDR37	WD repeat domain 37(WDR37)	NM_014023	150.9	176.7	0.0070	1.29
AKAP10	A-kinase anchoring protein 10(AKAP10)	NM_007202	121.3	135.3	0.0070	1.26
		XM_001716137	99.1	104.8	0.0070	1.15
MACF1	microtubule-actin crosslinking factor 1(MACF1)	NM_012090	101.9	113.5	0.0070	1.23
MACF1	microtubule-actin crosslinking factor 1(MACF1)	NM_012090	486.3	494.9	0.0070	1.23
GSK3B	glycogen synthase kinase 3 beta(GSK3B)	NM_002093	234.2	260.7	0.0070	1.25
APH1A	aph-1 homolog A, gamma-secretase subunit(APH1A)	NM_001077628	213.3	181	0.0070	0.77
APH1A	aph-1 homolog A, gamma-secretase subunit(APH1A)	NM_001077628	275.7	186.2	0.0070	0.77
NACC2	NACC family member 2(NACC2)	AK094914	443.2	275.7	0.0070	0.69
MGA	MGA, MAX dimerization protein(MGA)	NM_001080541	102.8	104.7	0.0070	0.85

MGA	MGA, MAX dimerization protein(MGA)	NM_001080541	155.6	117.3	0.0070	0.85			
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	NM_003622	99.8	114.9	0.0070	1.25			
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	NM_003622	111	103	0.0070	1.25			
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	NM_003622	168.4	124	0.0070	1.25			
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	89.3	100	0.0070	1.21	NM_144744	0.11	40.01
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	102	94.7	0.0070	1.21			
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	102.6	101.7	0.0070	1.21			
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	102.6	105.3	0.0070	1.21			
		BQ447196	99.1	104.7	0.0070	1.15			
		AA430240	92.9	100.6	0.0070	1.16			
OR2G2	olfactory receptor family 2 subfamily G member 2(OR2G2)	NM_001001915	148.6	101	0.0070	0.74			
		XM_001723369	125.5	102.3	0.0070	0.88			
ZMYND11	zinc finger MYND-type containing 11(ZMYND11)	NM_006624	93.7	91.5	0.0070	1.3			

ZMYND11	zinc finger MYND-type containing 11(ZMYND11)	NM_006624	1043.1	1211.7	0.0070	1.3
		XR_039357	101	114.2	0.0070	1.24
		AK024852	109.8	145	0.0070	1.5
FXYD5	FXYD domain containing ion transport regulator 5(FXYD5)	NM_144779	103.4	180.9	0.0070	1.14
FXYD5	FXYD domain containing ion transport regulator 5(FXYD5)	NM_144779	109.4	113	0.0070	1.14
DUX4L1	double homeobox 4 like 1(DUX4L1)	NM_033178	113.3	97.3	0.0070	0.93
EIF5A	eukaryotic translation initiation factor 5A(EIF5A)	NM_001970	412.5	457.4	0.0070	1.26
sorbs1	sorbin and SH3 domain containing 1(SORBS1)	NM_001034954	101.8	108.2	0.0070	1.16
sorbs1	sorbin and SH3 domain containing 1(SORBS1)	NM_001034954	260.9	275.7	0.0070	1.16

SELENOP	selenoprotein P(SELENOP)	NM_005410	116.2	85.6	0.0070	0.79
CCL25	C-C motif chemokine ligand 25(CCL25)	NM_005624	152.6	112.7	0.0070	0.82
STX16	syntaxin 16(STX16)	NM_001001433	137.2	167	0.0070	1.39
STX16	syntaxin 16(STX16)	NM_001001433	288.6	381.4	0.0070	1.39
		XR_039439	110.9	86.2	0.0080	0.81
		XR_039439	649.4	557.2	0.0080	0.81
EXTL2	exostosin like glycosyltransferase 2(EXTL2)	NM_001033025	148.9	170.7	0.0080	1.29
ALX3	ALX homeobox 3(ALX3)	NM_006492	121.1	106.9	0.0080	0.85
ALX3	ALX homeobox 3(ALX3)	NM_006492	132.8	105.6	0.0080	0.85
MPPE1	metallophosphoesterase 1(MPPE1)	NM_023075	161	194.9	0.0080	1.38
MCM3AP	minichromosome maintenance complex component 3 associated protein(MCM3AP)	NM_003906	101.4	107.7	0.0080	1.18

OR2B11	olfactory receptor family 2 subfamily B member 11(OR2B11)	NM_001004492	131.4	101.4	0.0080	0.83
OCIAD2	OCIA domain containing 2(OCIAD2)	NM_152398	147.5	101.9	0.0080	0.74
spop	speckle type BTB/POZ protein(SPOP)	NM_001007230	556.6	727.7	0.0080	1.48
ADGRG2	adhesion G protein-coupled receptor G2(ADGRG2)	NM_001079859	96.3	103.4	0.0080	1.15
CYP11A1	cytochrome P450 family 11 subfamily A member 1(CYP11A1)	NM_000781	145.6	113.6	0.0080	0.86
		XM_937648	134.9	106.7	0.0080	0.85
ZC2HC1A	zinc finger C2HC-type containing 1A(ZC2HC1A)	NM_016010	101.2	106.2	0.0080	1.38
ZC2HC1A	zinc finger C2HC-type containing 1A(ZC2HC1A)	NM_016010	126.1	152	0.0080	1.38
TLR2	toll like receptor 2(TLR2)	NM_003264	98.5	127.1	0.0080	1.45
tcf20	transcription factor 20(TCF20)	NM_181492	107.8	101	0.0080	1.38

tcf20	transcription factor 20(TCF20)	NM_181492	242.8	304.4	0.0080	1.38
		XM_926130	110.9	141.1	0.0080	1.44
USP33	ubiquitin specific peptidase 33(USP33)	NM_015017	102.4	117.1	0.0080	1.27
ZNF565	zinc finger protein 565(ZNF565)	NM_152477	116.1	127.7	0.0080	1.23
ZNF565	zinc finger protein 565(ZNF565)	NM_152477	121	127.7	0.0080	1.23
POU2F1	POU class 2 homeobox 1(POU2F1)	NM_002697	98.3	114.2	0.0080	1.27
hist1h4c	histone cluster 1 H4 family member c(HIST1H4C)	NM_003542	397.6	1481.1	0.0080	3.75
CNNM3	cyclin and CBS domain divalent metal cation transport mediator 3(CNNM3)	NM_017623	108.2	93.2	0.0080	1.2
CNNM3	cyclin and CBS domain divalent metal cation transport mediator 3(CNNM3)	NM_017623	110.7	121.7	0.0080	1.2

FBXW2	F-box and WD repeat domain containing 2(FBXW2)	NM_012164	115.3	135.4	0.0080	1.34
PHF14	PHD finger protein 14(PHF14)	NM_014660	120.2	100.5	0.0080	0.91
FOXJ2	forkhead box J2(FOXJ2)	NM_018416	431.6	548	0.0080	1.47
or8g1	olfactory receptor family 8 subfamily G member 1 (gene/pseudogene)(OR8G1)	NM_001002905	111.3	90.1	0.0080	0.85
SKP2	S-phase kinase associated protein 2(SKP2)	NM_032637	104.4	113.8	0.0090	1.21
		XR_017962	118.5	98.1	0.0090	0.84
		XR_017962	129.4	99.9	0.0090	0.84
		XR_039678	126.8	92.9	0.0090	0.79
MAGEB1	MAGE family member B1(MAGEB1)	NM_002363	131.2	101.1	0.0090	0.84
FMC1	formation of mitochondrial complex V assembly factor 1 homolog(FMC1)	NM_197964	268.8	199.6	0.0090	1.43

FMC1	formation of mitochondrial complex V assembly factor 1 homolog(FMC1)	NM_197964	1082.9	1361.3	0.0090	1.43
FMC1	formation of mitochondrial complex V assembly factor 1 homolog(FMC1)	NM_197964	1369.2	870	0.0090	1.43
ERGIC1	endoplasmic reticulum-golgi intermediate compartment 1(ERGIC1)	NM_001031711	171.4	196.6	0.0090	1.31
LMBRD2	LMBR1 domain containing 2(LMBRD2)	NM_001007527	112.2	121.7	0.0090	1.19
BPIFA3	BPI fold containing family A member 3(BPIFA3)	NM_178466	92.5	98.6	0.0090	1.14
HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2(HLA-DQA2)	NM_020056	147.6	114.8	0.0090	0.86
ZBED5	zinc finger BED-type containing 5(ZBED5)	NM_021211	286.7	329.4	0.0090	1.55

ZBED5	zinc finger BED-type containing 5(ZBED5)	NM_021211	496.9	685.8	0.0090	1.55
CLPTM1L	CLPTM1 like(CLPTM1L)	NM_030782	222.8	269.7	0.0090	1.42
SMOC1	SPARC related modular calcium binding 1(SMOC1)	NM_001034852	114.4	101.6	0.0090	0.81
SMOC1	SPARC related modular calcium binding 1(SMOC1)	NM_001034852	118.7	90.2	0.0090	0.81
RPS26	ribosomal protein S26(RPS26)	NM_001029	89.2	93	0.0090	1.11
RPS26	ribosomal protein S26(RPS26)	NM_001029	1360.8	1438.4	0.0090	1.11
FDPS	farnesyl diphosphate synthase(FDPS)	NM_002004	142.8	160.3	0.0090	1.25
		NM_020231	221.5	330.2	0.0090	1.68
ZZEF1	zinc finger ZZ-type and EF-hand domain containing 1(ZZEF1)	NM_015113	210.3	255.3	0.0090	1.39
KLHL9	kelch like family member 9(KLHL9)	NM_018847	404.9	500.1	0.0090	1.39

C1orf137	chromosome 1 open reading frame 137(C1orf137)	NM_001013643	142.2	106.9	0.0090	0.83
UGDH	UDP-glucose 6-dehydrogenase(UGDH)	NM_003359	122.4	92.2	0.0090	0.81
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB(BDP1)	NM_018429	118.1	120.3	0.0090	1.14
GABBR1	gamma-aminobutyric acid type B receptor subunit 1(GABBR1)	NM_021905	100.3	104.8	0.0090	1.14
GABBR1	gamma-aminobutyric acid type B receptor subunit 1(GABBR1)	NM_021905	105.7	108.6	0.0090	1.14
		XR_038461	100	108.1	0.0090	1.17
ercc1	ERCC excision repair 1, endonuclease non-catalytic subunit(ERCC1)	NM_001983	108	100.1	0.0090	1.33

ercc1	ERCC excision repair 1, endonuclease non-catalytic subunit(ERCC1)	NM_001983	165.3	196.6	0.0090	1.33
ercc1	ERCC excision repair 1, endonuclease non-catalytic subunit(ERCC1)	NM_001983	177.3	179.5	0.0090	1.33
UBE2D3	ubiquitin conjugating enzyme E2 D3(UBE2D3)	NM_181890	1309.4	1623.6	0.0090	1.36
UBE2D3	ubiquitin conjugating enzyme E2 D3(UBE2D3)	NM_181890	1649.2	2032.9	0.0090	1.36
WDR20	WD repeat domain 20(WDR20)	NM_144574	124.1	97.5	0.0090	0.82
GRIA3	glutamate ionotropic receptor AMPA type subunit 3(GRIA3)	NM_181894	94.1	101	0.0090	1.16
		AW051978	132.7	106.3	0.0090	0.87
TMEM184C	transmembrane protein 184C(TMEM184C)	NM_018241	99.6	103.1	0.0100	1.11

TMEM184C	transmembrane protein 184C(TMEM184C)	NM_018241	289.7	256.8	0.0100	1.11
KEAP1	kelch like ECH associated protein 1(KEAP1)	NM_012289	211.3	176.5	0.0100	0.75
KEAP1	kelch like ECH associated protein 1(KEAP1)	NM_012289	311.4	210.9	0.0100	0.75
POMGNT2	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)(POMGNT2)	NM_032806	234.8	141.8	0.0100	0.68
		XM_929444	151.3	114.8	0.0100	0.85
RBM3	RNA binding motif (RNP1, RRM) protein 3(RBM3)	NM_001017430	105.3	112.6	0.0100	1.46
RBM3	RNA binding motif (RNP1, RRM) protein 3(RBM3)	NM_001017430	167.5	208.4	0.0100	1.46
BEND6	BEN domain containing 6(BEND6)	NM_152731	93.3	101.8	0.0100	1.19

BEND6	BEN domain containing 6(BEND6)	NM_152731	98.5	99	0.0100	1.19			
		XM_001714670	131.9	144.9	0.0100	1.25			
		XM_001126202	146.5	194.1	0.0100	1.51			
		XM_945223	118	95.1	0.0100	0.87			
trak1	trafficking kinesin protein 1(TRAK1)	NM_001042646	106.4	114.6	0.0100	1.18			
trak1	trafficking kinesin protein 1(TRAK1)	NM_001042646	160.3	131.9	0.0100	1.18			
TCEAL9	transcription elongation factor A like 9(TCEAL9)	NM_001006612	142.1	167.3	0.0100	1.39			
		XM_939730	126	98.3	0.0100	0.85			
SNHG3	small nucleolar RNA host gene 3(SNHG3)	NR_002909	120.3	96.7	0.0100	0.87	NM_017196	14.73	0.69
fsd1l	fibronectin type III and SPRY domain containing 1 like(FSD1L)	NM_207647	102.8	111.3	0.0100	1.18	NM_017196	14.73	0.69
fsd1l	fibronectin type III and SPRY domain containing 1 like(FSD1L)	NM_207647	126	108.7	0.0100	1.18	NM_017196	14.73	0.69

CGGBP1	CGG triplet repeat binding protein 1(CGGBP1)	NM_003663	599.8	867.6	0.0100	1.58			
		BX106221	124.5	102	0.0100	0.9			
		XM_945918	141	107.1	0.0100	0.83			
NUTF2	nuclear transport factor 2(NUTF2)	NM_005796	117.6	137.9	0.0100	1.31	NM_031356	5.43	24.53
		XM_001714845	110.4	92.4	0.0100	0.87	NM_031356	5.43	24.53
TARBP2	TARBP2, RISC loading complex RNA binding subunit(TARBP2)	NM_134323	100	107.1	0.0100	1.17			
FBXO2	F-box protein 2(FBXO2)	NM_012168	216.3	144	0.0100	0.75			
CYB561	cytochrome b561(CYB561)	NM_001017917	111.9	114.3	0.0100	1.14			
IFT88	intraflagellar transport 88(IFT88)	NM_175605	90.9	102.1	0.0100	1.21			
CARF	calcium responsive transcription factor(CARF)	NM_024744	103.2	106	0.0100	1.12			
CLIC5	chloride intracellular channel 5(CLIC5)	NM_016929	196.4	347.5	0.0100	2			
		AA705831	119.7	100.3	0.0100	0.89			

		XR_017601	136.4	109.8	0.0100	0.89			
		CN283269	135	110.1	0.0100	0.9			
		XM_942071	156.1	111.3	0.0110	0.79			
		XM_001726941	118.7	96.5	0.0110	0.88			
EFNA4	ephrin A4(EFNA4)	NM_182689	99.5	102.7	0.0110	1.13			
APOPT1	apoptogenic 1, mitochondrial(APOPT1)	NM_032374	1681.1	2076.8	0.0110	1.31			
		AI082160	151	116.3	0.0110	0.85			
		XM_001132307	119.6	95.6	0.0110	0.85	NM_017135	41.45	2.88
		XM_001713723	18151.9	14953.9	0.0110	0.81	NM_017135	41.45	2.88
RERE	arginine-glutamic acid dipeptide repeats(RERE)	NM_012102	293.4	307.3	0.0110	1.18	NM_017135	41.45	2.88
ADPRHL1	ADP-ribosylhydrolase like 1(ADPRHL1)	NM_138430	145.2	117.4	0.0110	0.89	NM_017135	41.45	2.88
VEZT	vezatin, adherens junctions transmembrane protein(VEZT)	NM_017599	194.2	251	0.0110	1.44			
BARD1	BRCA1 associated RING domain 1(BARD1)	NM_000465	98.6	130.8	0.0110	1.47			

MYO1C	myosin IC(MYO1C)	NM_033375	146.8	113.7	0.0110	0.86			
FBXW5	F-box and WD repeat domain containing 5(FBXW5)	NM_018998	95	101	0.0110	1.15			
AUP1	ancient ubiquitous protein 1(AUP1)	NM_181575	227.6	268.1	0.0110	1.31			
mri1	methylthioribose-1-phosphate isomerase 1(MRI1)	NM_032285	122.7	138.6	0.0110	1.28			
		BX108993	114.4	91.9	0.0110	0.84	NM_001033653	43.46	1.56
		BE465760	192.4	102	0.0110	0.54			
ZNF341	zinc finger protein 341(ZNF341)	NM_032819	94.6	106.8	0.0110	1.24			
RYBP	RING1 and YY1 binding protein(RYBP)	NM_012234	340.3	521.8	0.0110	1.73			
		NR_004402	108.4	114.4	0.0110	1.16			
LOC105376064	uncharacterized LOC105376064(LOC105376064)	AW205071	201.8	129.1	0.0110	0.73			
WDFY2	WD repeat and FYVE domain containing 2(WDFY2)	NM_052950	121.4	135.6	0.0110	1.25			

NDUFB11	NADH:ubiquinone oxidoreductase subunit B11(NDUFB11)	NM_019056	1103.5	755.4	0.0120	0.78
NEUROG3	neurogenin 3(NEUROG3)	NM_020999	174.3	121.5	0.0120	0.78
TNFSF14	tumor necrosis factor superfamily member 14(TNFSF14)	NM_003807	89	96.3	0.0120	1.15
SCYL1	SCY1 like pseudokinase 1(SCYL1)	NM_020680	172.9	156	0.0120	1.22
SCYL1	SCY1 like pseudokinase 1(SCYL1)	NM_020680	174.8	182.8	0.0120	1.22
KCNG2	potassium voltage-gated channel modifier subfamily G member 2(KCNG2)	NM_012283	95.5	100.2	0.0120	1.14
CNOT6L	CCR4-NOT transcription complex subunit 6 like(CNOT6L)	NM_144571	131.2	163.4	0.0120	1.37
CSF1	colony stimulating factor 1(CSF1)	NM_172212	113.9	93.2	0.0120	0.87
		XR_041749	223.6	118	0.0120	0.6

		BX102609	122.5	97.7	0.0120	0.87			
ASS1	argininosuccinate synthase 1(ASS1)	NM_000050	127.4	94	0.0120	0.81			
ASS1	argininosuccinate synthase 1(ASS1)	NM_000050	1505.7	823.6	0.0120	0.81			
PPARD	peroxisome proliferator activated receptor delta(PPARD)	NM_006238	94.5	98	0.0120	0.84			
PPARD	peroxisome proliferator activated receptor delta(PPARD)	NM_006238	129.7	102.3	0.0120	0.84			
PTPN9	protein tyrosine phosphatase, non-receptor type 9(PTPN9)	NM_002833	104	108	0.0120	1.13			
CEP164	centrosomal protein 164(CEP164)	NM_014956	133.7	141.7	0.0120	1.22	NM_134407	50.47	11.16
NIN	ninein(NIN)	NM_020921	118.1	136.9	0.0120	1.31			
F2R	coagulation factor II thrombin receptor(F2R)	NM_001992	16746	18218.7	0.0120	1.21			
ACADVL	acyl-CoA dehydrogenase, very long chain(ACADVL)	NM_001033859	174.1	121.1	0.0120	0.79			

RCN3	reticulocalbin 3(RCN3)	NM_020650	151.3	117.6	0.0120	0.86
RPUSD4	RNA pseudouridylate synthase domain containing 4(RPUSD4)	NM_032795	117.1	123.5	0.0120	1.19
		NR_024266	118.5	126.6	0.0120	1.2
		NM_138926	157.8	211.4	0.0120	1.48
PCIF1	PDX1 C-terminal inhibiting factor 1(PCIF1)	NM_022104	113.3	120.8	0.0120	1.21
ST5	suppression of tumorigenicity 5(ST5)	NM_139157	92.1	100.5	0.0120	1.17
ST5	suppression of tumorigenicity 5(ST5)	NM_139157	120.2	119.8	0.0120	1.17
NRXN2	neurexin 2(NRXN2)	NM_138734	127.5	128.6	0.0120	0.85
NRXN2	neurexin 2(NRXN2)	NM_138734	159.3	121.3	0.0120	0.85
HMGXB4	HMG-box containing 4(HMGXB4)	NM_005487	107.8	99.7	0.0120	1.17
HMGXB4	HMG-box containing 4(HMGXB4)	NM_005487	113.4	120.2	0.0120	1.17

		XM_942086	98.5	107.6	0.0120	1.18			
TIA1	TIA1 cytotoxic granule associated RNA binding protein(TIA1)	NM_022173	267.7	432.7	0.0120	1.82			
CDK5RAP2	CDK5 regulatory subunit associated protein 2(CDK5RAP2)	NM_001011649	122.1	150.1	0.0120	1.39	NM_001033706	2.42	10.86
TCOF1	treacle ribosome biogenesis factor 1(TCOF1)	NM_000356	145.9	109.5	0.0120	0.83			
RNU6-1	RNA, U6 small nuclear 1(RNU6-1)	NR_004394	1021.3	1283.5	0.0120	1.39			
SNX5	sorting nexin 5(SNX5)	NM_014426	165.7	204.2	0.0120	1.41			
LRP4	LDL receptor related protein 4(LRP4)	NM_002334	98.8	114.9	0.0120	1.28			
SLTM	SAFB like transcription modulator(SLTM)	NM_024755	110.5	132.4	0.0120	1.32			
SLTM	SAFB like transcription modulator(SLTM)	NM_024755	334.1	342.5	0.0120	1.32	NM_153300	0.14	61.17

SLC6A10P	solute carrier family 6 member 10, pseudogene(SLC6A10P)	NR_003083	184.2	120.9	0.0130	0.7			
DCAF13	DDB1 and CUL4 associated factor 13(DCAF13)	NM_015420	157.5	169.6	0.0130	1.23	NM_032416	108.51	1.87
FAM63A	family with sequence similarity 63 member A(FAM63A)	NM_018379	119.6	110	0.0130	1.41			
FAM63A	family with sequence similarity 63 member A(FAM63A)	NM_018379	539	672.1	0.0130	1.41			
		XM_001133026	591.5	817.8	0.0130	1.59			
		XM_001134374	115.9	94.1	0.0130	0.86			
		AI887987	94.6	100.2	0.0130	1.13			
rab41	RAB41, member RAS oncogene family(RAB41)	NM_001032726	159.4	118.4	0.0130	0.83			
CT45A6	cancer/testis antigen family 45 member A6(CT45A6)	NM_001017438	119.5	95.1	0.0130	0.87			

		XM_939521	103.3	105.4	0.0130	1.11			
RNF150	ring finger protein 150(RNF150)	NM_020724	104.9	151.1	0.0130	1.63			
KAZN	kazrin, periplakin interacting protein(KAZN)	NM_001017999	114.1	116.3	0.0130	1.12			
ACKR3	atypical chemokine receptor 3(ACKR3)	NM_001047841	152.2	225.8	0.0130	1.68			
BAIAP2	BAI1 associated protein 2(BAIAP2)	NM_006340	123.1	97	0.0130	0.86			
BAIAP2	BAI1 associated protein 2(BAIAP2)	NM_006340	183	133.2	0.0130	0.86	NM_001191088	10.07	0.03
		XM_001131851	121.6	131.7	0.0130	1.21	NM_001191088	10.07	0.03
ZAP70	zeta chain of T cell receptor associated protein kinase 70(ZAP70)	NM_001079	93.7	140	0.0130	0.83			
ZAP70	zeta chain of T cell receptor associated protein kinase 70(ZAP70)	NM_001079	157.2	117.9	0.0130	0.83			
		XR_038597	334.9	402.6	0.0130	1.39			

GABBR1	gamma-aminobutyric acid type B receptor subunit 1(GABBR1)	NM_021903	130.2	105.2	0.0130	0.88	NM_012496	1095.39	8.76
		XM_942516	110.1	91.9	0.0130	0.89			
ZNF787	zinc finger protein 787(ZNF787)	NM_001002836	160.4	166.5	0.0130	1.17			
		XR_016353	118.7	91.6	0.0130	0.83			
SRSF4	serine and arginine rich splicing factor 4(SRSF4)	NM_005626	813.3	1029.5	0.0130	1.4			
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	NM_001895	133.1	136.4	0.0130	0.78			
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	NM_001895	270	185.3	0.0130	0.78			
		XM_001723239	13523.8	15446.4	0.0130	1.22			
		XR_017532	190.2	214.7	0.0130	1.28			
		XM_935540	97.3	107	0.0130	1.18			

KCNH2	potassium voltage-gated channel subfamily H member 2(KCNH2)	NM_172056	108.7	111.7	0.0130	1.14
		BX107471	114.9	92.6	0.0130	0.86
FAM208A	family with sequence similarity 208 member A(FAM208A)	NM_015224	337	175.6	0.0140	0.61
LOC729609	uncharacterized LOC729609(LOC729609)	NR_024440	115.3	93.9	0.0140	0.88
RNF5	ring finger protein 5(RNF5)	NM_006913	537.7	347.2	0.0140	0.74
HS6ST2-AS1	HS6ST2 antisense RNA 1(HS6ST2-AS1)	BQ001311	115.6	95.2	0.0140	0.88
THOP1	thimet oligopeptidase 1(THOP1)	NM_003249	121.3	144.9	0.0140	1.34
		XM_942288	119.2	139	0.0140	1.31
		BQ188349	98.3	103.9	0.0140	1.14
OPN5	opsin 5(OPN5)	NM_001030051	174.7	120.6	0.0140	0.77
TLR9	toll like receptor 9(TLR9)	NM_017442	88.6	98.7	0.0140	1.19

REXO4	REX4 homolog, 3'-5' exonuclease(REXO4)	NM_020385	190.5	216.7	0.0140	1.31
TXNDC11	thioredoxin domain containing 11(TXNDC11)	NM_015914	101.5	112.8	0.0140	1.22
NGFR	nerve growth factor receptor(NGFR)	NM_002507	94.8	100.5	0.0140	1.13
TAF1C	TATA-box binding protein associated factor, RNA polymerase I subunit C(TAF1C)	NM_139353	143.4	156	0.0140	1.24
		XR_015650	118.6	129.5	0.0140	1.23
MCOLN1	mucolipin 1(MCOLN1)	NM_020533	103.6	141.9	0.0140	1.54
KHDRBS3	KH RNA binding domain containing, signal transduction associated 3(KHDRBS3)	NM_006558	123.7	131.3	0.0140	1.5

KHDRBS3	KH RNA binding domain containing, signal transduction associated 3(KHDRBS3)	NM_006558	208.7	278	0.0140	1.5
		AW044615	120.4	98.3	0.0140	0.88
HUS1	HUS1 checkpoint clamp component(HUS1)	NM_004507	120.9	97.1	0.0140	0.85
PSMD6-AS2	PSMD6 antisense RNA 2(PSMD6-AS2)	AK023371	107.5	109.9	0.0140	1.11
MRPL39	mitochondrial ribosomal protein L39(MRPL39)	NM_080794	106.8	121.7	0.0140	1.29
KRTAP12-4	keratin associated protein 12-4(KRTAP12-4)	NM_198698	122.6	97	0.0140	0.85
RBM26	RNA binding motif protein 26(RBM26)	NM_022118	144.5	170.5	0.0140	1.34
ATAD2B	ATPase family, AAA domain containing 2B(ATAD2B)	NM_017552	110.4	114.3	0.0140	1.16
EXOSC10	exosome component 10(EXOSC10)	NM_001001998	117.1	124.9	0.0140	1.2

EXOSC10	exosome component 10(EXOSC10)	NM_001001998	418.7	407.8	0.0140	1.2	NM_013059	21.02	0.11
SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1(SBDSP1)	NR_001588	279.4	179.6	0.0150	0.72			
SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1(SBDSP1)	NR_001588	299	214	0.0150	0.72			
		BQ185080	121.5	98.8	0.0150	0.87			
SEH1L	SEH1 like nucleoporin(SEH1L)	NM_001013437	137.3	156.3	0.0150	1.29			
SEH1L	SEH1 like nucleoporin(SEH1L)	NM_001013437	221.8	217.1	0.0150	1.29			
WDR35	WD repeat domain 35(WDR35)	NM_001006657	257.6	166	0.0150	0.73			
CCNI	cyclin I(CCNI)	NM_006835	3100.4	3698.5	0.0150	1.27			
		XM_927542	155.8	116.5	0.0150	0.83			
		XM_001721042	100.4	92.1	0.0150	0.85			
		XM_001721042	181.6	135.5	0.0150	0.85			

		XM_001725241	99.2	102.1	0.0150	1.12			
MAGEL2	MAGE family member L2(MAGEL2)	NM_019066	176.2	124.1	0.0150	0.79	NM_012816	19.78	2.28
		XR_001434	123.5	102.6	0.0150	0.89	NM_012816	19.78	2.28
DNAH6	dynein axonemal heavy chain 6(DNAH6)	NM_173645	166	185.3	0.0150	1.27			
RAD51C	RAD51 paralog C(RAD51C)	NM_002876	103.2	122.6	0.0150	1.32			
CSNK1A1	casein kinase 1 alpha 1(CSNK1A1)	NM_001892	195.1	256	0.0150	1.5			
SF3B1	splicing factor 3b subunit 1(SF3B1)	NM_001005526	96.4	105.3	0.0150	1.18			
CSTF3	cleavage stimulation factor subunit 3(CSTF3)	NM_001033506	112.2	124.4	0.0150	1.25			
PLA2G6	phospholipase A2 group VI(PLA2G6)	NM_001004426	182.4	129	0.0150	0.8			
ZNF462	zinc finger protein 462(ZNF462)	NM_021224	130.2	175.5	0.0150	1.5			
ZCCHC6	zinc finger CCHC-type containing 6(ZCCHC6)	NM_024617	142.7	332.1	0.0150	2.69			
		XM_936462	100.1	104.5	0.0150	1.13			

CLCN6	chloride voltage-gated channel 6(CLCN6)	NM_001286	152.7	151.3	0.0150	1.13			
ANKRD12	ankyrin repeat domain 12(ANKRD12)	NM_015208	122.6	140.8	0.0150	1.3			
RORA	RAR related orphan receptor A(RORA)	AK055969	117.3	134.3	0.0150	1.27			
PBXIP1	PBX homeobox interacting protein 1(PBXIP1)	NM_020524	161.6	122.6	0.0150	0.85			
nfic	nuclear factor I C(NFIC)	NM_005597	114.1	105.2	0.0150	0.83			
nfic	nuclear factor I C(NFIC)	NM_005597	115.2	89.5	0.0150	0.83			
DPT	dermatopontin(DPT)	NM_001937	670.8	373.6	0.0150	0.64			
LOC642947	uncharacterized LOC642947(LOC642947)	NM_001039895	11130.4	12980.5	0.0150	1.28			
FRA10AC1	FRA10A associated CGG repeat 1(FRA10AC1)	NM_203440	100.4	106	0.0150	1.14			
NXN	nucleoredoxin(NXN)	NM_022463	136.1	105.1	0.0150	0.84	NM_031544	4.79	38.59

SREK1	splicing regulatory glutamic acid and lysine rich protein 1(SREK1)	NM_139168	95.7	102.7	0.0150	1.17	NM_031544	4.79	38.59
		XM_001720144	97.4	102.9	0.0150	1.14			
KTI12	KTI12 chromatin associated homolog(KTI12)	NM_138417	138.8	107.1	0.0150	0.83			
		XM_944214	113.1	93.7	0.0150	0.89			
WDR19	WD repeat domain 19(WDR19)	NM_025132	146.6	167.2	0.0150	1.28			
PAPOLA	poly(A) polymerase alpha(PAPOLA)	NM_032632	661.5	930.2	0.0160	1.54			
RAB2B	RAB2B, member RAS oncogene family(RAB2B)	NM_032846	292.2	348.1	0.0160	1.33			
ITGA4	integrin subunit alpha 4(ITGA4)	NM_000885	89.1	98.8	0.0160	1.2			
		XM_928404	176.5	130.9	0.0160	0.84			
FLJ41327	FLJ41327 protein(FLJ41327)	NM_207485	98.4	101.4	0.0160	1.12			
ANKRD16	ankyrin repeat domain 16(ANKRD16)	NM_001009941	113.3	118.9	0.0160	1.2			

U2SURP	U2 snRNP associated SURP domain containing(U2SURP)	NM_001080415	243.1	272.7	0.0160	1.28
PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2(PFKFB2)	NM_001018053	124.3	100.1	0.0160	0.87
PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2(PFKFB2)	NM_001018053	126.5	114.8	0.0160	0.87
		XM_942545	96.5	103.1	0.0160	1.18
DZIP1	DAZ interacting zinc finger protein 1(DZIP1)	NM_198968	124.2	171.1	0.0160	1.54
TLE3	transducin like enhancer of split 3(TLE3)	NM_005078	96.4	104.6	0.0160	1.18
CYP2A13	cytochrome P450 family 2 subfamily A member 13(CYP2A13)	NM_000766	89	99.6	0.0160	1.2
CYP2A13	cytochrome P450 family 2 subfamily A member 13(CYP2A13)	NM_000766	111.3	100.3	0.0160	1.2

GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A(GRIN2A)	NM_000833	111.9	93.5	0.0160	0.88
SETX	senataxin(SETX)	NM_015046	104.1	123.3	0.0160	1.28
		AW975165	101.1	107.5	0.0160	1.14
		XM_001134195	121.6	99.8	0.0160	0.89
		XM_927996	114.5	95	0.0160	0.88
CAPRIN2	caprin family member 2(CAPRIN2)	NM_001002259	235.2	252.4	0.0160	1.23
		XM_001725231	115.2	92.7	0.0160	0.85
EPS8L3	EPS8 like 3(EPS8L3)	NM_024526	112	94.3	0.0160	0.9
LRRC15	leucine rich repeat containing 15(LRRC15)	NM_130830	105.1	110.5	0.0160	1.16
		XM_001721880	107.4	101.2	0.0160	1.15
		XM_001721880	175.1	177.7	0.0160	1.15
SCAF4	SR-related CTD associated factor 4(SCAF4)	NM_020706	183.1	219.9	0.0160	1.34
		XM_001715244	115.4	99	0.0160	0.91

UBE2Q2	ubiquitin conjugating enzyme E2 Q2(UBE2Q2)	NM_173469	105.9	114.7	0.0160	1.19
		XM_942049	126.3	98.4	0.0160	0.85
NCOR1P1	nuclear receptor corepressor 1 pseudogene 1(NCOR1P1)	NM_001039379	222.7	270.1	0.0160	1.35
BCL2	BCL2, apoptosis regulator(BCL2)	NM_000633	106.3	116.7	0.0170	1.23
BCL2	BCL2, apoptosis regulator(BCL2)	NM_000633	280.2	304.5	0.0170	1.23
GNB3	G protein subunit beta 3(GNB3)	NM_002075	142.1	105.4	0.0170	0.82
ALKBH5	alkB homolog 5, RNA demethylase(ALKBH5)	NM_017758	2465.6	1848.7	0.0170	0.83
CTGF	connective tissue growth factor(CTGF)	NM_001901	128	92.9	0.0170	0.79
TSSK1B	testis specific serine kinase 1B(TSSK1B)	NM_032028	102	107.2	0.0170	1.15
		BM671800	141.5	110.5	0.0170	0.85
HIC2	HIC ZBTB transcriptional repressor 2(HIC2)	NM_015094	145.2	158.9	0.0170	1.24

TNRC6A	trinucleotide repeat containing 6A(TNRC6A)	NM_014494	124.2	128.5	0.0170	1.15
TNRC6A	trinucleotide repeat containing 6A(TNRC6A)	NM_014494	138.8	134.2	0.0170	1.15
TNRC6A	trinucleotide repeat containing 6A(TNRC6A)	NM_014494	366.9	310.9	0.0170	1.15
CALCOCO1	calcium binding and coiled-coil domain 1(CALCOCO1)	NM_020898	209.2	148.7	0.0170	0.81
EXOSC9	exosome component 9(EXOSC9)	NM_001034194	170	169	0.0170	1.35
EXOSC9	exosome component 9(EXOSC9)	NM_001034194	170.9	205.6	0.0170	1.35
PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)(PTGIR)	NM_000960	131.9	101.3	0.0170	0.84
		XM_942713	95.4	101.9	0.0170	1.17
SNORA12	small nucleolar RNA, H/ACA box 12(SNORA12)	NR_002954	99.6	110.3	0.0170	1.19
TBC1D8	TBC1 domain family member 8(TBC1D8)	NM_007063	129.2	139.8	0.0170	1.23

NCOA5	nuclear receptor coactivator 5(NCOA5)	NM_020967	117.3	122.9	0.0170	1.17
MCM9	minichromosome maintenance 9 homologous recombination repair factor(MCM9)	NM_153255	108.4	127.1	0.0170	1.27
NDC1	NDC1 transmembrane nucleoporin(NDC1)	NM_018087	96	105.5	0.0170	1.2
CDK7	cyclin dependent kinase 7(CDK7)	NM_001799	180.2	223.1	0.0170	1.4
FA2H	fatty acid 2-hydroxylase(FA2H)	NM_024306	180	119.9	0.0170	0.75
MXRA7	matrix remodeling associated 7(MXRA7)	NM_001008528	106.5	111.3	0.0170	1.17
VPS39	VPS39, HOPS complex subunit(VPS39)	NM_015289	111.5	112.4	0.0170	1.12
WNK1	WNK lysine deficient protein kinase 1(WNK1)	NM_018979	154.4	142	0.0170	1.73
WNK1	WNK lysine deficient protein kinase 1(WNK1)	NM_018979	196.9	293.3	0.0170	1.73

EXOSC3	exosome component 3(EXOSC3)	NM_016042	141.8	168.3	0.0170	1.34
CNRIP1	cannabinoid receptor interacting protein 1(CNRIP1)	NM_001111101	96.3	102.1	0.0170	1.15
SGSH	N-sulfoglucosamine sulfohydrolase(SGSH)	NM_000199	364.2	245.8	0.0170	0.78
HAX1	HCLS1 associated protein X-1(HAX1)	NM_006118	120.3	122.7	0.0180	1.16
HAX1	HCLS1 associated protein X-1(HAX1)	NM_006118	310.8	288.5	0.0180	1.16
CD200R1	CD200 receptor 1(CD200R1)	NM_138806	95.7	102.4	0.0180	1.16
COQ10A	coenzyme Q10A(COQ10A)	NM_144576	331	176.8	0.0180	0.6
ZMYM5	zinc finger MYM-type containing 5(ZMYM5)	NM_001039650	113.5	118.2	0.0180	1.17
MBP	myelin basic protein(MBP)	NM_001025090	189.1	252.9	0.0180	1.48
NAG18	NAG18 mRNA(NAG18)	NR_002568	19695.2	16538.4	0.0180	0.81

RFC4	replication factor C subunit 4(RFC4)	NM_181573	95.2	113.1	0.0180	1.31
FAM160B2	family with sequence similarity 160 member B2(FAM160B2)	NM_022749	114.1	107.6	0.0180	1.15
FAM160B2	family with sequence similarity 160 member B2(FAM160B2)	NM_022749	124.6	128.4	0.0180	1.15
FAM131A	family with sequence similarity 131 member A(FAM131A)	NM_144635	220.5	155.3	0.0180	0.78
MRPL42	mitochondrial ribosomal protein L42(MRPL42)	NM_172177	100.1	107	0.0180	1.16
SLC45A4	solute carrier family 45 member 4(SLC45A4)	NM_001080431	104.9	86.9	0.0180	0.85
CES3	carboxylesterase 3(CES3)	NM_024922	120.8	98.3	0.0180	0.86
LINC00854	long intergenic non-protein coding RNA 854(LINC00854)	BC073918	122.7	97.5	0.0180	0.85

GPX5	glutathione peroxidase 5(GPX5)	NM_001509	124.2	91.8	0.0180	0.76
GPX5	glutathione peroxidase 5(GPX5)	NM_001509	135.3	95	0.0180	0.76
MCMDC2	minichromosome maintenance domain containing 2(MCMDC2)	NM_173518	109.1	103.5	0.0180	1.28
MCMDC2	minichromosome maintenance domain containing 2(MCMDC2)	NM_173518	3616.2	4452.2	0.0180	1.28
SELENOK	selenoprotein K(SELENOK)	NM_021237	119.7	97.3	0.0180	0.88
		NM_006674	130.6	133.4	0.0180	1.17
KCTD12	potassium channel tetramerization domain containing 12(KCTD12)	NM_138444	191.9	360.6	0.0180	2.1
		XR_038277	110.6	113.4	0.0180	1.14
		XM_0017223218	110.5	92.1	0.0180	0.88

NAA15	N(alpha)-acetyltransferase 15, NatA auxiliary subunit(NAA15)	NM_057175	102.9	104.5	0.0180	1.1			
		XR_015544	218.2	151.3	0.0180	0.79			
		XM_001722663	148.1	113.9	0.0180	0.86			
RND3	Rho family GTPase 3(RND3)	NM_005168	107.3	121.3	0.0180	1.27			
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3(AGPAT3)	NM_020132	153.7	118.1	0.0180	0.86			
SNORD33	small nucleolar RNA, C/D box 33(SNORD33)	NR_000020	113.1	123	0.0180	1.18			
ANKRD26	ankyrin repeat domain 26(ANKRD26)	NM_014915	131.5	146.1	0.0180	1.22			
KCTD17	potassium channel tetramerization domain containing 17(KCTD17)	NM_024681	103.4	112	0.0180	1.19	NM_031012	19.39	0.85
PPT1	palmitoyl-protein thioesterase 1(PPT1)	NM_000310	1353.3	1657.5	0.0180	1.32			

RPLP2	ribosomal protein lateral stalk subunit P2(RPLP2)	NM_001004	7146.7	9850.2	0.0190	1.43			
		XM_934553	112.5	93.5	0.0190	0.9	NM_012904	10.16	55.22
		XM_937753	156.6	119.7	0.0190	0.85			
FUT4	fucosyltransferase 4(FUT4)	NM_002033	89	97.5	0.0190	1.18			
Snora21	small nucleolar RNA, H/ACA box 21(SNORA21)	NR_002576	106.7	117.3	0.0190	1.23			
MOCS1	molybdenum cofactor synthesis 1(MOCS1)	NM_005943	221.3	150.3	0.0190	0.76			
TOP1P2	topoisomerase (DNA) I pseudogene 2(TOP1P2)	NR_001283	153.7	184.9	0.0190	1.36			
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta(YWHAB)	NM_139323	1349.8	1627.9	0.0190	1.31			
EIF4G3	eukaryotic translation initiation factor 4 gamma 3(EIF4G3)	NM_003760	200.8	256.1	0.0190	1.45			

CEACAM4	carcinoembryonic antigen related cell adhesion molecule 4(CEACAM4)	NM_001817	155.2	117.1	0.0190	0.84			
		XM_001133189	106.8	88.6	0.0190	0.87			
		XM_001133189	234	189.4	0.0190	0.87			
KLHL23	kelch like family member 23(KLHL23)	NM_144711	94.7	103.4	0.0190	1.18	NM_012823	17.52	0.04
AOC2	amine oxidase, copper containing 2(AOC2)	NM_001158	200.7	128.4	0.0190	0.73			
TSPEAR	thrombospondin type laminin G domain and EAR repeats(TSPEAR)	NM_144991	122.2	100.2	0.0190	0.88			
ADNP	activity dependent neuroprotector homeobox(ADNP)	NM_015339	115.9	124.2	0.0190	1.19			
		XM_929248	156.7	116.6	0.0190	0.83			
URI1	URI1, prefoldin like chaperone(URI1)	NM_134447	154.4	158.4	0.0190	1.45			

URI1	URI1, prefoldin like chaperone(URI1)	NM_134447	476.1	600.9	0.0190	1.45
DAZAP1	DAZ associated protein 1(DAZAP1)	NM_170711	154.8	168.1	0.0190	1.26
ZNF740	zinc finger protein 740(ZNF740)	NM_001004304	165.4	126	0.0190	0.86
CEP131	centrosomal protein 131(CEP131)	NM_014984	100.2	112.7	0.0190	1.25
TMEM9	transmembrane protein 9(TMEM9)	NM_016456	229.1	151.5	0.0190	0.74
ATXN10	ataxin 10(ATXN10)	NM_013236	174.8	128.1	0.0190	0.83
		XR_016385	204.3	102.5	0.0200	0.56
MRPL34	mitochondrial ribosomal protein L34(MRPL34)	NM_023937	324.5	240.3	0.0200	0.84
ZNF22	zinc finger protein 22(ZNF22)	NM_006963	246.9	364.2	0.0200	1.63
ZNF22	zinc finger protein 22(ZNF22)	NM_006963	353	311.8	0.0200	1.63
NSUN5	NOP2/Sun RNA methyltransferase family member 5(NSUN5)	NM_018044	92.7	99.7	0.0200	1.14

NSUN5	NOP2/Sun RNA methyltransferase family member 5(NSUN5)	NM_018044	136.7	130.9	0.0200	1.14
SLC17A5	solute carrier family 17 member 5(SLC17A5)	NM_012434	100.7	103.8	0.0200	1.12
USP16	ubiquitin specific peptidase 16(USP16)	NM_006447	292.9	275.6	0.0200	1.29
USP16	ubiquitin specific peptidase 16(USP16)	NM_006447	337.4	394.9	0.0200	1.29
		XM_929287	89.9	99.1	0.0200	1.16
DUSP18	dual specificity phosphatase 18(DUSP18)	NM_152511	103.2	111	0.0200	1.18
ZNF302	zinc finger protein 302(ZNF302)	NM_018443	136.8	155.1	0.0200	1.3
KRTAP10-1	keratin associated protein 10-1(KRTAP10-1)	NM_198691	106.4	87.3	0.0200	0.87
FAT1	FAT atypical cadherin 1(FAT1)	NM_005245	259.4	183.4	0.0200	0.64
FAT1	FAT atypical cadherin 1(FAT1)	NM_005245	291.5	168.2	0.0200	0.64
TMOD3	tropomodulin 3(TMOD3)	NM_014547	89.4	99	0.0200	1.18

TMOD3	tropomodulin 3(TMOD3)	NM_014547	161.7	183.8	0.0200	1.18
SERPINA11	serpin family A member 11(SERPINA11)	NM_001080451	123.9	97.9	0.0200	0.85
DLD	dihydrolipoamide dehydrogenase(DLD)	NM_000108	554.4	309.5	0.0200	0.62
		XR_038983	121.7	97.3	0.0200	0.86
ZNF426	zinc finger protein 426(ZNF426)	NM_024106	103.6	111.5	0.0200	1.17
USF1	upstream transcription factor 1(USF1)	NM_007122	114.7	163.8	0.0200	1.6
NALCN	sodium leak channel, non-selective(NALCN)	NM_052867	102.1	102.5	0.0200	1.1
FZD1	frizzled class receptor 1(FZD1)	NM_003505	117.6	119.8	0.0200	1.11
FZD1	frizzled class receptor 1(FZD1)	NM_003505	251.1	149.7	0.0200	1.11
SELENOH	selenoprotein H(SELENOH)	NM_170746	101.1	109.7	0.0200	1.19
ACKR3	atypical chemokine receptor 3(ACKR3)	NM_020311	289.6	535.3	0.0200	2.12

DHX15	DEAH-box helicase 15(DHX15)	NM_001358	230	241.5	0.0200	1.56
DHX15	DEAH-box helicase 15(DHX15)	NM_001358	752.7	1044.7	0.0200	1.56
		XM_940223	135	90.8	0.0200	0.75
BAIAP2L2	BAI1 associated protein 2 like 2(BAIAP2L2)	NM_025045	306.1	152.5	0.0200	0.56
CERS4	ceramide synthase 4(CERS4)	NM_024552	124.5	100.5	0.0200	0.85
CASKIN2	CASK interacting protein 2(CASKIN2)	NM_020753	105.8	107.8	0.0210	1.12
Snord96a	small nucleolar RNA, C/D box 96A(SNORD96A)	NR_002592	99.3	114.7	0.0210	1.27
CHMP2A	charged multivesicular body protein 2A(CHMP2A)	NM_198426	182.8	124.1	0.0210	0.76
		AV652851	115.8	150.5	0.0210	1.42
		XM_001715037	124	142.4	0.0210	1.29

MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type(MMAB)	NM_052845	152.9	117.8	0.0210	0.86			
MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type(MMAB)	NM_052845	221.6	166	0.0210	0.86			
FBRS	fibrosin(FBRS)	NM_001105079	188.8	217.5	0.0210	1.33			
PTGER4	prostaglandin E receptor 4(PTGER4)	NM_000958	442.3	547.7	0.0210	1.41	NM_017170	13.37	0.05
HMGB1P1	high mobility group box 1 pseudogene 1(HMGB1P1)	NM_001008735	215.7	378.6	0.0210	2.01			
HMGB1P1	high mobility group box 1 pseudogene 1(HMGB1P1)	NM_001008735	264.9	352.8	0.0210	2.01			
MRPS35	mitochondrial ribosomal protein S35(MRPS35)	NM_021821	214.1	143.6	0.0210	0.74			
RNVU1-18	RNA, variant U1 small nuclear 18(RNVU1-18)	NR_004400	170	208.3	0.0210	1.38			

ING3	inhibitor of growth family member 3(ING3)	NM_198267	108.3	122.6	0.0210	1.24			
RNU1-3	RNA, U1 small nuclear 3(RNU1-3)	NR_004408	157.3	196.5	0.0210	1.4			
C9ORF24	chromosome 9 open reading frame 24(C9orf24)	NM_147169	131.7	105.7	0.0210	0.87			
KCNH6	potassium voltage-gated channel subfamily H member 6(KCNH6)	NM_030779	12897.2	14787	0.0210	1.29	NM_001106492	2.61	10.85
		XM_942932	125.1	98.5	0.0210	0.85	NM_001106492	2.61	10.85
		XM_927702	112.2	93	0.0210	0.88			
		NM_001013840	122.3	123.3	0.0210	1.14			
		NM_001013840	130.5	108.1	0.0210	1.14			
FLII	FLII, actin remodeling protein(FLII)	NM_002018	165.1	179.2	0.0210	1.24			
SYNJ1	synaptojanin 1(SYNJ1)	NM_203446	199.5	234.2	0.0210	1.33			

b4galnt4	beta-1,4-N-acetyl-galactosaminyltransferase 4(B4GALNT4)	NM_178537	89.4	99.2	0.0210	1.19
TRMT10A	tRNA methyltransferase 10A(TRMT10A)	NM_152292	95	101	0.0210	1.15
GAPT	GRB2 binding adaptor protein, transmembrane(GAPT)	NM_152687	112.4	107.4	0.0210	0.79
GAPT	GRB2 binding adaptor protein, transmembrane(GAPT)	NM_152687	154.8	109.6	0.0210	0.79
OR52E5	olfactory receptor family 52 subfamily E member 5(OR52E5)	NM_001005166	106.9	85.8	0.0210	0.84
ACY3	aminoacylase 3(ACY3)	NM_080658	147.2	108.7	0.0210	0.81
SLC35E1	solute carrier family 35 member E1(SLC35E1)	NM_024881	109.2	105.9	0.0210	1.07
SLC35E1	solute carrier family 35 member E1(SLC35E1)	NM_024881	1302.4	1529.4	0.0210	1.07
		AI349750	87	96.5	0.0210	1.18

CTDSP1	CTD small phosphatase 1(CTDSP1)	NM_021198	113.3	90.5	0.0210	0.83			
CTDSP1	CTD small phosphatase 1(CTDSP1)	NM_021198	310.6	287.9	0.0210	0.83			
CEP85L	centrosomal protein 85 like(CEP85L)	NM_001042475	107.7	125	0.0210	1.29			
PYM1	PYM homolog 1, exon junction complex associated factor(PYM1)	NM_032345	107.5	121.7	0.0210	1.26			
BLMH	bleomycin hydrolase(BLMH)	NM_000386	127.3	147.7	0.0210	1.32	NM_001270681	26.79	0.09
SAMD1	sterile alpha motif domain containing 1(SAMD1)	NM_138352	109	118.2	0.0210	1.2			
RAD54L2	RAD54-like 2 (S. cerevisiae)(RAD54L2)	DB305811	125.1	103	0.0210	0.88			
		NM_015106	116.7	128	0.0210	1.24			
		XM_001717507	150.8	111.1	0.0210	0.82			
rn7sk	RNA, 7SK small nuclear(RN7SK)	NR_001445	279	410.6	0.0210	1.64			
KDM2B	lysine demethylase 2B(KDM2B)	NM_001005366	279.2	159.7	0.0210	0.66			

ACTR5	ARP5 actin-related protein 5 homolog(ACTR5)	NM_024855	125.2	130.7	0.0220	1.19	NM_019373	263.23	1.01
		AA744250	147	153.4	0.0220	1.2			
FAM156A	family with sequence similarity 156 member A(FAM156A)	NM_014138	278.8	299.8	0.0220	1.23			
NKTR	natural killer cell triggering receptor(NKTR)	NM_005385	168.2	216.3	0.0220	1.44			
MITD1	microtubule interacting and trafficking domain containing 1(MITD1)	NM_138798	146.5	173.7	0.0220	1.34			
GRK4	G protein-coupled receptor kinase 4(GRK4)	NM_001004056	119.5	164.7	0.0220	1.54			
ANKRD6	ankyrin repeat domain 6(ANKRD6)	NM_014942	102.3	104.5	0.0220	1.12			
STX11	syntaxin 11(STX11)	NM_003764	104.9	159.5	0.0220	1.71			
CCDC130	coiled-coil domain containing 130(CCDC130)	NM_030818	407.7	487.2	0.0220	1.38			

BRD3	bromodomain containing 3(BRD3)	NM_007371	227.9	287.9	0.0220	1.46			
RBMS1	RNA binding motif single stranded interacting protein 1(RBMS1)	NM_002897	134.1	162	0.0220	1.66			
RBMS1	RNA binding motif single stranded interacting protein 1(RBMS1)	NM_002897	293.1	431.7	0.0220	1.66			
RBMS1	RNA binding motif single stranded interacting protein 1(RBMS1)	NM_002897	337.9	419.5	0.0220	1.66	NM_012778	744.78	0.71
ZMYND12	zinc finger MYND-type containing 12(ZMYND12)	NM_032257	198.3	130.4	0.0220	0.73	NM_012778	744.78	0.71
		BX101207	106.6	112.6	0.0220	1.18			
TTC14	tetratricopeptide repeat domain 14(TTC14)	NM_133462	297	398.9	0.0220	1.52			
AKAP13	A-kinase anchoring protein 13(AKAP13)	NM_006738	144.6	168.4	0.0220	1.32	NM_012909	6.73	5427.66

GNAQ	G protein subunit alpha q(GNAQ)	NM_002072	128.9	101.4	0.0220	0.86	NM_022181	0.40	160.77
		XM_001724189	130.5	148.3	0.0220	1.26	NM_019157	14.48	0.05
SOX17	SRY-box 17(SOX17)	NM_022454	98.6	119.6	0.0220	1.34			
SNORD16	small nucleolar RNA, C/D box 16(SNORD16)	NR_002440	112.6	132.5	0.0220	1.3			
LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1(LRRCC1)	NM_033402	122.6	101.1	0.0220	1.3			
LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1(LRRCC1)	NM_033402	127.3	153.5	0.0220	1.3			
RNU4-1	RNA, U4 small nuclear 1(RNU4-1)	NR_003925	111.3	120.7	0.0220	1.21			
slc26a6	solute carrier family 26 member 6(SLC26A6)	NM_001040454	107.9	88.9	0.0220	0.87			
tmem187	transmembrane protein 187(TMEM187)	NM_003492	102.1	113	0.0220	1.2			

FEN1	flap structure-specific endonuclease 1(FEN1)	NM_004111	99.3	109.8	0.0220	1.21
FEN1	flap structure-specific endonuclease 1(FEN1)	NM_004111	131.7	154.5	0.0220	1.21
YY1	YY1 transcription factor(YY1)	NM_003403	276.4	282.3	0.0220	1.58
YY1	YY1 transcription factor(YY1)	NM_003403	728.1	1066.2	0.0220	1.58
SNRPB2	small nuclear ribonucleoprotein polypeptide B2(SNRPB2)	NM_003092	216.6	153.9	0.0230	0.81
LIG3	DNA ligase 3(LIG3)	NM_002311	98.5	106	0.0230	1.16
		XM_937260	104.3	109	0.0230	1.15
NPIPB15	nuclear pore complex interacting protein family member B15(NPIPB15)	NM_001018059	118.4	98.7	0.0230	0.89

YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon(YWHAE)	NM_006761	109	115.5	0.0230	1.18			
B3GAT1	beta-1,3-glucuronyltransferase 1(B3GAT1)	NM_054025	171.9	123.6	0.0230	0.82			
PIWIL4	piwi like RNA-mediated gene silencing 4(PIWIL4)	NM_152431	87.6	97.7	0.0230	1.2			
STX18	syntaxin 18(STX18)	NM_016930	113.5	96.4	0.0230	0.9			
		BF509118	115.1	123.4	0.0230	1.2			
C3orf62	chromosome 3 open reading frame 62(C3orf62)	NM_198562	105.3	110.3	0.0230	1.15			
NDUFAF7	NADH:ubiquinone oxidoreductase complex assembly factor 7(NDUFAF7)	NM_144736	122.7	114.2	0.0230	1.36			
NDUFAF7	NADH:ubiquinone oxidoreductase complex assembly factor 7(NDUFAF7)	NM_144736	296.5	349.9	0.0230	1.36	NM_019168	8.26	61.49

ZNF263	zinc finger protein 263(ZNF263)	NM_005741	160.8	181.7	0.0230	1.29
		XR_040873	110.8	93.1	0.0230	0.88
RNF115	ring finger protein 115(RNF115)	NM_014455	126.8	145.2	0.0230	1.55
RNF115	ring finger protein 115(RNF115)	NM_014455	462.1	652.9	0.0230	1.55
RUFY3	RUN and FYVE domain containing 3(RUFY3)	NM_001037442	104	106.6	0.0230	1.13
RUFY3	RUN and FYVE domain containing 3(RUFY3)	NM_001037442	349.3	389.7	0.0230	1.13
PICALM	phosphatidylinositol binding clathrin assembly protein(PICALM)	NM_007166	121.6	97.9	0.0230	0.84
PICALM	phosphatidylinositol binding clathrin assembly protein(PICALM)	NM_007166	866.6	648.3	0.0230	0.84
		BX111977	120.5	101.4	0.0240	0.91
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	166.4	156.6	0.0240	1.21

MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	182.9	195.8	0.0240	1.21
C11orf57	chromosome 11 open reading frame 57(C11orf57)	NM_018195	191.7	142.5	0.0240	0.84
ARF1	ADP ribosylation factor 1(ARF1)	NM_001024227	1348.5	902.1	0.0240	0.76
		XM_939026	127.1	102.8	0.0240	0.88
VPS37D	VPS37D, ESCRT-I subunit(VPS37D)	NM_001077621	567.1	324.4	0.0240	0.65
GPATCH4	G-patch domain containing 4(GPATCH4)	NM_182679	97.6	98	0.0240	0.89
GPATCH4	G-patch domain containing 4(GPATCH4)	NM_182679	117.7	97.8	0.0240	0.89
ZNF366	zinc finger protein 366(ZNF366)	NM_152625	114.4	122.4	0.0240	1.19
SPDYE8P	speedy/RINGO cell cycle regulator family member E8, pseudogene(SPDYE8P)	NR_003664	157.4	106.3	0.0240	0.75

SPDYE8P	speedy/RINGO cell cycle regulator family member E8, pseudogene(SPDYE8P)	NR_003664	11806.9	13009	0.0240	0.75
SCP2	sterol carrier protein 2(SCP2)	NM_001007098	286	178.5	0.0240	0.73
nthl1	nth like DNA glycosylase 1(NTHL1)	NM_002528	119.6	131.8	0.0240	1.24
ZBTB8A	zinc finger and BTB domain containing 8A(ZBTB8A)	NM_001040441	102.8	114.1	0.0240	1.21
MATR3	matrin 3(MATR3)	NM_199189	97.7	91.5	0.0240	1.15
MATR3	matrin 3(MATR3)	NM_199189	100.8	107.2	0.0240	1.15
MATR3	matrin 3(MATR3)	NM_199189	1659.9	2099.5	0.0240	1.15
BRPF1	bromodomain and PHD finger containing 1(BRPF1)	NM_004634	432.9	664.6	0.0240	1.72
TLDC1	TBC/LysM-associated domain containing 1(TLDC1)	NM_020947	99.8	102.9	0.0240	1.12

SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily c member 2(SMARCC2)	NM_139067	248.7	301.3	0.0240	1.35
		XR_018904	123.1	133.3	0.0240	1.22
ZNF676	zinc finger protein 676(ZNF676)	NM_001001411	102.6	106.4	0.0240	1.14
		XM_001724301	101.8	105.2	0.0240	1.13
GLMN	glomulin, FKBP associated protein(GLMN)	NM_053274	222.4	274.3	0.0240	1.4
		XM_001724735	153.2	167.9	0.0240	1.25
DDX19B	DEAD-box helicase 19B(DDX19B)	NM_001014449	124	132.7	0.0240	1.19
		XM_927306	111.3	93.2	0.0240	0.86
PRR19	proline rich 19(PRR19)	NM_199285	131.5	107.1	0.0240	0.88

CMTM3	CKLF like MARVEL transmembrane domain containing 3(CMTM3)	NM_181553	186.3	132	0.0240	0.81
UBE2O	ubiquitin conjugating enzyme E2 O(UBE2O)	NM_022066	133.9	143.6	0.0240	1.19
		XM_939186	159	190.9	0.0240	1.38
ANAPC11	anaphase promoting complex subunit 11(ANAPC11)	NM_001002246	106.2	112.6	0.0240	1.17
ANAPC11	anaphase promoting complex subunit 11(ANAPC11)	NM_001002246	414	382.8	0.0240	1.17
AGXT	alanine-glyoxylate aminotransferase(AGXT)	NM_000030	1763.1	657.1	0.0240	0.42
PHF20L1	PHD finger protein 20-like 1(PHF20L1)	NM_198513	97.4	107.4	0.0240	1.19
NSA2	NSA2, ribosome biogenesis homolog(NSA2)	NM_014886	1103.8	1275	0.0240	1.26

NSA2	NSA2, ribosome biogenesis homolog(NSA2)	NM_014886	1434.7	1488	0.0240	1.26			
RAP2B	RAP2B, member of RAS oncogene family(RAP2B)	NM_002886	227.5	151	0.0250	0.75			
or1l4	olfactory receptor family 1 subfamily L member 4(OR1L4)	NM_001005235	103.7	95.1	0.0250	0.88			
or1l4	olfactory receptor family 1 subfamily L member 4(OR1L4)	NM_001005235	144.4	115.3	0.0250	0.88	NM_001106061	2.22	12.22
NOC3L	NOC3 like DNA replication regulator(NOC3L)	NM_022451	160.2	214.1	0.0250	1.53			
HEATR6	HEAT repeat containing 6(HEATR6)	NM_022070	154.9	206.3	0.0250	1.47			
EP400	E1A binding protein p400(EP400)	NM_015409	131.6	145.5	0.0250	1.24			
KIAA0430	KIAA0430(KIAA0430)	NM_014647	369.1	401.5	0.0250	1.25			
SNORA14B	small nucleolar RNA, H/ACA box 14B(SNORA14B)	NR_002956	106.5	108.6	0.0250	1.11			

NUB1	negative regulator of ubiquitin like proteins 1(NUB1)	NM_016118	128.1	103	0.0250	0.88
NUB1	negative regulator of ubiquitin like proteins 1(NUB1)	NM_016118	364.7	343.6	0.0250	0.88
		XM_926147	99	105.4	0.0250	1.15
ATOH8	atonal bHLH transcription factor 8(ATOH8)	NM_032827	99.4	117.3	0.0250	1.32
mthfd2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase(MTHFD2)	NM_006636	89	98	0.0250	1.19
CEPT1	choline/ethanolamine phosphotransferase 1(CEPT1)	NM_006090	332.9	524.5	0.0250	1.81
TRIM9	tripartite motif containing 9(TRIM9)	NM_015163	122.3	98.1	0.0250	0.87
		XR_039516	112.6	92.6	0.0250	0.88

		XR_039516	184.9	188.3	0.0250	0.88
USP19	ubiquitin specific peptidase 19(USP19)	NM_006677	107.6	113.3	0.0250	1.16
PLAGL1	PLAG1 like zinc finger 1(PLAGL1)	NM_001080952	113.4	119.2	0.0250	1.18
SFSWAP	splicing factor SWAP homolog(SFSWAP)	NM_004592	143.9	155.8	0.0250	1.22
NUDT6	nudix hydrolase 6(NUDT6)	NM_007083	115.7	102.6	0.0250	0.79
NUDT6	nudix hydrolase 6(NUDT6)	NM_007083	132.2	110.8	0.0250	0.79
NUDT6	nudix hydrolase 6(NUDT6)	NM_007083	172	122.8	0.0250	0.79
GJC2	gap junction protein gamma 2(GJC2)	NM_020435	189.5	133.9	0.0250	0.79
		XR_017492	128.7	162.5	0.0250	1.46
		XR_017492	153.4	141.9	0.0250	1.46
		XR_017492	1141.3	1826.9	0.0250	1.46
UBAP2L	ubiquitin associated protein 2 like(UBAP2L)	NM_014847	224	284.6	0.0250	1.42

TSC1	tuberous sclerosis 1(TSC1)	NM_000368	127.4	116.9	0.0250	1.19
TSC1	tuberous sclerosis 1(TSC1)	NM_000368	177.3	183.4	0.0250	1.19
TSC1	tuberous sclerosis 1(TSC1)	NM_000368	444.8	471.5	0.0250	1.19
AP2A2	adaptor related protein complex 2 alpha 2 subunit(AP2A2)	NM_012305	128.7	100.4	0.0250	0.85
PIH1D1	PIH1 domain containing 1(PIH1D1)	NM_017916	186.1	209.3	0.0260	1.27
FAM32A	family with sequence similarity 32 member A(FAM32A)	NM_014077	132.7	153.7	0.0260	1.31
SNORA70C	small nucleolar RNA, H/ACA box 70C(SNORA70C)	NR_003708	127	129.6	0.0260	1.13
		XR_037303	112.5	92.1	0.0260	0.86
P2RY6	pyrimidinergic receptor P2Y6(P2RY6)	NM_176796	93.7	109.9	0.0260	1.29
HPN	hepsin(HPN)	NM_002151	329.3	231.5	0.0260	0.53
HPN	hepsin(HPN)	NM_002151	739.4	351.3	0.0260	0.53

CASP2	caspase 2(CASP2)	NM_032983	106.4	120.7	0.0260	1.26
PPP1R12B	protein phosphatase 1 regulatory subunit 12B(PPP1R12B)	NM_032103	94	98.1	0.0260	1.12
PPP1R12B	protein phosphatase 1 regulatory subunit 12B(PPP1R12B)	NM_032103	101.4	103.6	0.0260	1.12
RAB20	RAB20, member RAS oncogene family(RAB20)	NM_017817	102.9	105.4	0.0260	1.13
UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI(UQCR11)	NM_006830	126.6	102.6	0.0260	0.88
pik3r6	phosphoinositide-3-kinase regulatory subunit 6(PIK3R6)	NM_001010855	148.7	110.2	0.0260	0.83
RAD52	RAD52 homolog, DNA repair protein(RAD52)	NM_134424	108.8	92.2	0.0260	0.88

SC5D	sterol-C5-desaturase(SC5D)	NM_006918	532.6	324.3	0.0260	0.69			
		XM_938671	117.4	122.6	0.0260	1.16			
		XM_936333	109.8	113.2	0.0260	1.14			
RAE1	ribonucleic acid export 1(RAE1)	NM_003610	128.1	100.3	0.0260	0.86			
RAE1	ribonucleic acid export 1(RAE1)	NM_003610	281.3	269.9	0.0260	0.86			
		XM_001720371	96.9	103.9	0.0260	1.17			
		XM_001715936	103.4	109.1	0.0260	1.15			
STT3B	STT3B, catalytic subunit of the oligosaccharyltransferase complex(STT3B)	NM_178862	163.6	188.3	0.0260	1.28			
		XM_938093	97.3	110	0.0260	1.23			
		XM_938093	150.6	186	0.0260	1.23			
		XM_933275	119.4	98.7	0.0260	0.9			
SMYD5	SMYD family member 5(SMYD5)	NM_006062	194.1	143.4	0.0260	0.84			
		XM_931329	116.3	95.5	0.0260	0.87	NM_001014273	3.32	15.01

CCNY	cyclin Y(CCNY)	NM_145012	202.3	272.5	0.0260	1.45	NM_001014273	3.32	15.01
NICN1	nicolin 1(NICN1)	NM_032316	103.3	107	0.0260	1.13	NM_001014273	3.32	15.01
LCOR	ligand dependent nuclear receptor corepressor(LCOR)	NM_032440	125.2	111.6	0.0260	1.28			
LCOR	ligand dependent nuclear receptor corepressor(LCOR)	NM_032440	139.9	164.1	0.0260	1.28			
aire	autoimmune regulator(AIRE)	NM_000658	101.8	106.7	0.0260	1.16			
SLC13A2	solute carrier family 13 member 2(SLC13A2)	NM_003984	281.3	166.8	0.0260	0.68			
SCNM1	sodium channel modifier 1(SCNM1)	NM_024041	113	110.4	0.0260	1.18			
SCNM1	sodium channel modifier 1(SCNM1)	NM_024041	138.3	145.4	0.0260	1.18			
ZNF786	zinc finger protein 786(ZNF786)	NM_152411	966.8	1160.6	0.0270	1.39			
NFASC	neurofascin(NFASC)	NM_001005387	114.6	98.2	0.0270	0.92			
		XM_001132115	157.4	100.9	0.0270	0.71			

TARBP1	TAR (HIV-1) RNA binding protein 1(TARBP1)	NM_005646	113.6	122.8	0.0270	1.22
		XR_017629	115.4	126.5	0.0270	1.23
CPNE6	copine 6(CPNE6)	NM_006032	260.4	119.5	0.0270	0.53
MIR488	microRNA 488(MIR488)	NR_030163	117.2	99.1	0.0270	0.91
METTL15	methyltransferase like 15(METTL15)	NM_152636	107.7	111.2	0.0270	1.13
DDX52	DExD-box helicase 52(DDX52)	NM_007010	294.2	333.2	0.0270	1.27
TANGO2	transport and golgi organization 2 homolog(TANGO2)	NM_152906	113.2	138.2	0.0270	1.37
		XM_001725354	119.8	95.8	0.0270	0.87
MNT	MAX network transcriptional repressor(MNT)	NM_020310	152	167.2	0.0270	1.23
ZNF274	zinc finger protein 274(ZNF274)	NM_016324	126.2	99.8	0.0270	0.86
GON4L	gon-4 like(GON4L)	NM_001037533	277.2	349.3	0.0270	1.49
		XR_038286	110.5	87.6	0.0270	0.83

CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1(CHCHD1)	NM_203298	111.9	115.8	0.0270	1.15
TUBB3	tubulin beta 3 class III(TUBB3)	NM_006086	144.5	111.1	0.0270	0.85
RNASEH1	ribonuclease H1(RNASEH1)	NM_002936	114.7	123.8	0.0270	1.22
		NM_183041	112.9	94.4	0.0270	0.89
		XM_498608	115.6	95.9	0.0270	0.9
TSPAN31	tetraspanin 31(TSPAN31)	NM_005981	261.6	280.4	0.0270	1.22
TRAF7	TNF receptor associated factor 7(TRAF7)	NM_032271	132.5	127.3	0.0270	0.85
TRAF7	TNF receptor associated factor 7(TRAF7)	NM_032271	141.6	109	0.0270	0.85
		XR_016218	303.5	114.4	0.0280	0.43
		XM_944104	172.2	99.2	0.0280	0.65
		XM_944104	2909.6	2692.8	0.0280	0.65
ODF3L2	outer dense fiber of sperm tails 3 like 2(ODF3L2)	NM_182577	137.8	111.1	0.0280	0.89

ACYP2	acylphosphatase 2(ACYP2)	NM_138448	183	134.3	0.0280	0.83
ACYP2	acylphosphatase 2(ACYP2)	NM_138448	255.9	167.5	0.0280	0.83
ZNF304	zinc finger protein 304(ZNF304)	NM_020657	105.8	107.2	0.0280	1.12
SERF1B	small EDRK-rich factor 1B(SERF1B)	NM_022978	111.8	88	0.0280	0.84
ARID4A	AT-rich interaction domain 4A(ARID4A)	NM_023001	101.7	106.8	0.0280	1.15
plxdc2	plexin domain containing 2(PLXDC2)	NM_032812	118.9	137.3	0.0280	1.28
RALGDS	ral guanine nucleotide dissociation stimulator(RALGDS)	NM_006266	252.8	476.7	0.0280	2.11
LILRB5	leukocyte immunoglobulin like receptor B5(LILRB5)	NM_006840	108.6	111.5	0.0280	1.1
		XM_932143	190.8	215.8	0.0280	1.27
		XR_015609	111.5	95.8	0.0280	0.92
		XM_001718130	127.1	100.9	0.0280	0.87

f8a1	coagulation factor VIII-associated 1(F8A1)	NM_012151	233.4	159.3	0.0280	0.78
RARRES1	retinoic acid receptor responder 1(RARRES1)	NM_206963	92.6	104.2	0.0280	1.23
HOXC13	homeobox C13(HOXC13)	NM_017410	116.4	92.7	0.0280	0.84
MOSPD2	motile sperm domain containing 2(MOSPD2)	NM_152581	122.9	101.6	0.0280	1.25
MOSPD2	motile sperm domain containing 2(MOSPD2)	NM_152581	151.1	169.8	0.0280	1.25
UBE2Z	ubiquitin conjugating enzyme E2 Z(UBE2Z)	NM_023079	116.7	129	0.0280	1.24
AJAP1	adherens junctions associated protein 1(AJAP1)	NM_001042478	103.6	117.8	0.0280	1.26
		XR_037881	112.8	93.1	0.0280	0.86
		XR_037881	835.7	882.2	0.0280	0.86

CDKN2AIPNL	CDKN2A interacting protein N-terminal like(CDKN2AIPNL)	NM_080656	9284.9	11373	0.0280	1.34
		XM_927976	84.7	96.2	0.0280	1.2
SLC35D1	solute carrier family 35 member D1(SLC35D1)	NM_015139	113	96.2	0.0280	0.91
ALS2CL	ALS2 C-terminal like(ALS2CL)	NM_182775	122.6	124.5	0.0290	1.14
CRCP	CGRP receptor component(CRCP)	NM_001040648	119.4	122.8	0.0290	1.16
SLCO1A2	solute carrier organic anion transporter family member 1A2(SLCO1A2)	NM_134431	325.3	184	0.0290	0.66
FLT4	fms related tyrosine kinase 4(FLT4)	NM_002020	124.4	100.7	0.0290	0.89
		XM_944907	341.4	451.1	0.0290	1.53
SPIN4	spindlin family member 4(SPIN4)	NM_001012968	105.1	111	0.0290	1.17

Snord89	small nucleolar RNA, C/D box 89(SNORD89)	NR_003070	381.2	655.7	0.0290	1.88
		AL110176	107.3	108.5	0.0290	1.11
		XM_001715878	125.7	101.3	0.0290	0.88
H1FOO	H1 histone family member O, oocyte specific(H1FOO)	NM_153833	111.7	95.5	0.0290	0.9
PSMC3IP	PSMC3 interacting protein(PSMC3IP)	NM_013290	118.1	96.7	0.0290	0.87
ARSB	arylsulfatase B(ARSB)	NM_000046	124.2	102.4	0.0290	0.9
ARSB	arylsulfatase B(ARSB)	NM_000046	149.8	126.1	0.0290	0.9
ARSG	arylsulfatase G(ARSG)	NM_014960	195.9	145.7	0.0290	0.84
SNAPIN	SNAP associated protein(SNAPIN)	NM_012437	112.2	118.8	0.0290	1.16
HSPA9	heat shock protein family A (Hsp70) member 9(HSPA9)	NM_004134	758.7	422.6	0.0290	0.63
RNVU1-7	RNA, variant U1 small nuclear 7(RNVU1-7)	NR_004426	156.7	187.9	0.0290	1.35

LCAT	lecithin-cholesterol acyltransferase(LCAT)	NM_000229	250	312.9	0.0290	1.44
UBXN7	UBX domain protein 7(UBXN7)	NM_015562	91.5	100.5	0.0290	1.19
DNAAF5	dynein axonemal assembly factor 5(DNAAF5)	NM_017802	88.2	107.2	0.0290	1.33
FAM63B	family with sequence similarity 63 member B(FAM63B)	NM_001040450	115.2	139.8	0.0290	1.34
		XM_930835	202.8	145.5	0.0290	0.82
NR6A1	nuclear receptor subfamily 6 group A member 1(NR6A1)	NM_001489	109.4	93.9	0.0290	0.9
SNX22	sorting nexin 22(SNX22)	NM_024798	133.3	101.7	0.0290	0.82
STRN3	striatin 3(STRN3)	NM_014574	311.9	385.9	0.0290	1.39
		XM_925901	99.2	102.1	0.0290	1.11
ENY2	ENY2, transcription and export complex 2 subunit(ENY2)	NM_020189	972.6	641.6	0.0290	0.73

OR2B2	olfactory receptor family 2 subfamily B member 2(OR2B2)	NM_033057	129.6	101.4	0.0290	0.82			
CACTIN	cactin, spliceosome C complex subunit(CACTIN)	NM_001080543	114.2	113.2	0.0300	1.1			
		XR_017883	222.1	139.3	0.0300	0.72			
MED1	mediator complex subunit 1(MED1)	NM_004774	146.2	158.8	0.0300	1.22			
MED1	mediator complex subunit 1(MED1)	NM_004774	251.7	199.4	0.0300	1.22			
		XM_933621	127.6	103.3	0.0300	0.88			
SPC25	SPC25, NDC80 kinetochore complex component(SPC25)	NM_020675	90.4	97.5	0.0300	1.16			
HOXA6	homeobox A6(HOXA6)	NM_024014	472.9	282.8	0.0300	0.7	NM_145089	67.02	12.33
ACBD3	acyl-CoA binding domain containing 3(ACBD3)	NM_022735	286.2	184.8	0.0300	0.72	NM_013157	76.74	0.47
MT2A	metallothionein 2A(MT2A)	NM_005953	1687.2	603.4	0.0300	0.42	NM_013157	76.74	0.47

BVES	blood vessel epicardial substance(BVES)	NM_147147	124.8	105	0.0300	0.92	NM_013157	76.74	0.47
FANCG	Fanconi anemia complementation group G(FANCG)	NM_004629	133.6	164.5	0.0300	1.38			
KRTAP12-3	keratin associated protein 12-3(KRTAP12-3)	NM_198697	104.4	106.2	0.0300	1.11			
ZFPM2	zinc finger protein, FOG family member 2(ZFPM2)	NM_012082	94.3	105.6	0.0300	1.22			
PTPRB	protein tyrosine phosphatase, receptor type B(PTPRB)	NM_002837	151.1	197.8	0.0300	1.48			
UCKL1	uridine-cytidine kinase 1 like 1(UCKL1)	NM_017859	413.3	491.9	0.0300	1.36			
WHAMM	WAS protein homolog associated with actin, golgi membranes and microtubules(WHAMM)	NM_001080435	137.2	145.8	0.0300	1.2			

FAM110B	family with sequence similarity 110 member B(FAM110B)	NM_147189	156.1	198.6	0.0300	1.45
		XM_928195	95.5	108.2	0.0300	1.24
BBS2	Bardet-Biedl syndrome 2(BBS2)	NM_031885	468.1	314.5	0.0300	0.74
BBS2	Bardet-Biedl syndrome 2(BBS2)	NM_031885	712.8	548.9	0.0300	0.74
PSAT1	phosphoserine aminotransferase 1(PSAT1)	NM_021154	136.1	140.6	0.0300	1.2
BAZ1A	bromodomain adjacent to zinc finger domain 1A(BAZ1A)	NM_013448	95.7	113.1	0.0300	1.3
		CN304251	97.8	103.2	0.0300	1.14
c19orf60	chromosome 19 open reading frame 60(C19orf60)	NM_001100419	682.4	483	0.0300	0.8
SUMO2	small ubiquitin-like modifier 2(SUMO2)	NM_001005849	399.9	512.5	0.0300	1.47
SUMO2	small ubiquitin-like modifier 2(SUMO2)	NM_001005849	697.5	875.6	0.0300	1.47

qsox1	quiescin sulfhydryl oxidase 1(QSOX1)	NM_001004128	202.9	241.6	0.0300	1.33
		XR_039017	104.9	128.7	0.0300	1.36
HDLBP	high density lipoprotein binding protein(HDLBP)	NM_203346	132.5	102.2	0.0300	0.84
RNF138	ring finger protein 138(RNF138)	NM_016271	107.4	91.2	0.0300	0.88
csnk1g3	casein kinase 1 gamma 3(CSNK1G3)	NM_001031812	125.5	132.2	0.0310	1.17
C1orf87	chromosome 1 open reading frame 87(C1orf87)	NM_152377	94.1	91.7	0.0310	1.11
C1orf87	chromosome 1 open reading frame 87(C1orf87)	NM_152377	104.5	105.8	0.0310	1.11
CRISP2	cysteine rich secretory protein 2(CRISP2)	NM_003296	558.3	262.7	0.0310	0.56
		AW085986	224.5	145.6	0.0310	0.73
ESYT2	extended synaptotagmin 2(ESYT2)	NM_020728	135.9	99.6	0.0310	0.79

		XM_928722	125.3	104.5	0.0310	0.92
LOC284933	uncharacterized LOC284933(LOC284933)	BC048428	110.5	94.7	0.0310	0.9
MOK	MOK protein kinase(MOK)	NM_014226	97.2	108	0.0310	1.21
CDK5R1	cyclin dependent kinase 5 regulatory subunit 1(CDK5R1)	NM_003885	81.6	95.8	0.0310	1.26
CDK5R1	cyclin dependent kinase 5 regulatory subunit 1(CDK5R1)	NM_003885	145.7	154.1	0.0310	1.26
ACTRT1	actin related protein T1(ACTRT1)	NM_138289	211.4	138.1	0.0310	0.73
SIRT6	sirtuin 6(SIRT6)	NM_016539	142.2	105.3	0.0310	0.82
C6orf47	chromosome 6 open reading frame 47(C6orf47)	NM_021184	149.3	172.3	0.0310	1.31
TONSL	tonsoku-like, DNA repair protein(TONSL)	NM_013432	197.9	143.4	0.0310	0.82

GDF11	growth differentiation factor 11(GDF11)	AK091091	122.1	142.5	0.0310	1.3			
CLUAP1	clusterin associated protein 1(CLUAP1)	NM_024793	111.7	106.1	0.0310	1.13			
CLUAP1	clusterin associated protein 1(CLUAP1)	NM_024793	129.3	119.1	0.0310	1.13			
CLUAP1	clusterin associated protein 1(CLUAP1)	NM_024793	16683.3	17456.7	0.0310	1.13	NM_134394	3.46	15.03
NAV3	neuron navigator 3(NAV3)	NM_014903	99.5	128.2	0.0310	1.43			
LPP	LIM domain containing preferred translocation partner in lipoma(LPP)	NM_005578	500.5	621.5	0.0310	1.39			
C1orf52	chromosome 1 open reading frame 52(C1orf52)	NM_198077	251.3	309.2	0.0310	1.37			
TAF6	TATA-box binding protein associated factor 6(TAF6)	NM_005641	119.5	99.8	0.0310	0.91			

TP53BP2	tumor protein p53 binding protein 2(TP53BP2)	NM_001031685	104.8	106.5	0.0310	1.12
TSHZ3	teashirt zinc finger homeobox 3(TSHZ3)	NM_020856	110.8	141.1	0.0310	1.41
PHIP	pleckstrin homology domain interacting protein(PHIP)	BX537762	108.4	135.4	0.0310	1.39
		XR_037871	101.6	112.9	0.0310	1.21
		XM_929738	318.1	390.1	0.0310	1.36
		XM_001721243	92.6	98	0.0310	1.14
		XM_001717548	89.2	97.8	0.0310	1.17
		XR_038911	114.5	91.2	0.0310	0.86
KMT2C	lysine methyltransferase 2C(KMT2C)	NM_170606	133.5	147.2	0.0320	0.8
KMT2C	lysine methyltransferase 2C(KMT2C)	NM_170606	156	111.9	0.0320	0.8
TRAP1	TNF receptor associated protein 1(TRAP1)	NM_016292	127.9	104	0.0320	0.89

AIM1L	absent in melanoma 1-like(AIM1L)	NM_017977	125.2	101.7	0.0320	0.89
NRCAM	neuronal cell adhesion molecule(NRCAM)	NM_005010	107.2	117.5	0.0320	1.2
NRCAM	neuronal cell adhesion molecule(NRCAM)	NM_005010	145.4	187.6	0.0320	1.2
		XR_017484	292	115.3	0.0320	0.46
TUBB2B	tubulin beta 2B class IIb(TUBB2B)	NM_178012	100.2	116.1	0.0320	1.28
SEPT1	septin 1(SEPT1)	NM_052838	82.4	99.8	0.0320	1.3
MED16	mediator complex subunit 16(MED16)	NM_005481	111.7	111.1	0.0320	1.11
MED16	mediator complex subunit 16(MED16)	NM_005481	128.8	116.1	0.0320	1.11
OSBP2	oxysterol binding protein 2(OSBP2)	NM_030758	117.1	121.8	0.0320	1.17
SP140	SP140 nuclear body protein(SP140)	NM_007237	193.9	125.1	0.0320	0.73

ACADVL	acyl-CoA dehydrogenase, very long chain(ACADVL)	NM_000018	443.6	256.4	0.0320	0.67
USP3	ubiquitin specific peptidase 3(USP3)	NM_006537	116.8	95.9	0.0320	0.88
		XR_038054	316.2	119.3	0.0320	0.44
		XM_941155	557.1	931	0.0320	1.94
		XM_941155	4625	5065	0.0320	1.94
USF1	upstream transcription factor 1(USF1)	NM_207005	146.7	215.1	0.0320	1.61
FAM78A	family with sequence similarity 78 member A(FAM78A)	NM_033387	124.2	97.4	0.0320	0.84
		XM_938838	191.4	135.8	0.0320	0.81
		XR_037962	112.9	120.3	0.0320	1.17
TLE4	transducin like enhancer of split 4(TLE4)	NM_007005	103.7	114.3	0.0320	1.2
TLE4	transducin like enhancer of split 4(TLE4)	NM_007005	153.9	211.2	0.0320	1.2

		AA883754	111.4	93	0.0320	0.88
		XR_019076	93.7	96	0.0320	1.1
ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6(ENPP6)	NM_153343	106.5	87.9	0.0320	0.87
RPL6	ribosomal protein L6(RPL6)	NM_001024662	114.1	131.7	0.0320	1.32
RPL6	ribosomal protein L6(RPL6)	NM_001024662	1707.2	1910.7	0.0320	1.32
RPL6	ribosomal protein L6(RPL6)	NM_001024662	2873.7	3047.8	0.0320	1.32
		AW593356	116.2	96.3	0.0320	0.88
DNASE1L1	deoxyribonuclease 1 like 1(DNASE1L1)	NM_006730	107.8	110.5	0.0320	1.12
LOC100190986	uncharacterized LOC100190986(LOC100190986)	NR_024456	118.9	97.7	0.0320	0.9
ZNF606	zinc finger protein 606(ZNF606)	NM_025027	121.2	125	0.0320	1.13
		XM_940806	112.5	93.1	0.0320	0.88
ACD	adrenocortical dysplasia homolog(ACD)	NM_022914	145.9	145.9	0.0330	1.13
CEBPZ	CCAAT/enhancer binding protein zeta(CEBPZ)	NM_005760	424.8	463.6	0.0330	1.23

CPM	carboxypeptidase M(CPM)	NM_001005502	104.8	108.6	0.0330	1.15
CPM	carboxypeptidase M(CPM)	NM_001005502	109.2	102.9	0.0330	1.15
HAT1	histone acetyltransferase 1(HAT1)	NM_003642	134.1	121.8	0.0330	1.24
HAT1	histone acetyltransferase 1(HAT1)	NM_003642	172.6	188.1	0.0330	1.24
TINF2	TERF1 interacting nuclear factor 2(TINF2)	NM_012461	152.6	157.5	0.0330	1.18
MFHAS1	malignant fibrous histiocytoma amplified sequence 1(MFHAS1)	NM_004225	137.7	174.5	0.0330	1.38
ETNK2	ethanolamine kinase 2(ETNK2)	NM_018208	218.3	134.7	0.0330	0.69
PDPK1	3-phosphoinositide dependent protein kinase 1(PDPK1)	NM_031268	105.6	89.3	0.0330	0.9
PDPK1	3-phosphoinositide dependent protein kinase 1(PDPK1)	NM_031268	472.1	387.7	0.0330	0.9

slx4ip	SLX4 interacting protein(SLX4IP)	NM_001009608	112.8	113.6	0.0330	1.11
pnkd	paroxysmal nonkinesigenic dyskinesia(PNKD)	NM_022572	158.3	119.9	0.0330	0.84
pnkd	paroxysmal nonkinesigenic dyskinesia(PNKD)	NM_022572	163.9	136.1	0.0330	0.84
TMEM80	transmembrane protein 80(TMEM80)	NM_174940	206.1	135.9	0.0330	0.76
BUB1	BUB1 mitotic checkpoint serine/threonine kinase(BUB1)	NM_004336	80.2	101.5	0.0330	1.38
CACNA2D4	calcium voltage-gated channel auxiliary subunit alpha2delta 4(CACNA2D4)	NM_001005737	123	102.4	0.0330	0.91
CASP10	caspase 10(CASP10)	NM_001230	91.1	99.1	0.0330	1.15
		BX117604	117.2	96.6	0.0330	0.86
RAB27B	RAB27B, member RAS oncogene family(RAB27B)	AF131784	127.3	147.8	0.0330	1.31
		XR_015468	108.4	89.4	0.0330	0.85

TMIGD1	transmembrane and immunoglobulin domain containing 1(TMIGD1)	NM_206832	133.2	94.7	0.0330	0.76
SOCS4	suppressor of cytokine signaling 4(SOCS4)	NM_199421	102.4	117.8	0.0330	1.29
LCA5L	LCA5L, lebercilin like(LCA5L)	NM_152505	131.2	104.9	0.0330	0.88
SPTBN4	spectrin beta, non-erythrocytic 4(SPTBN4)	NM_020971	110	92.4	0.0330	0.86
ZBTB16	zinc finger and BTB domain containing 16(ZBTB16)	NM_006006	90.5	107.4	0.0330	1.28
ZBTB16	zinc finger and BTB domain containing 16(ZBTB16)	NM_006006	172.1	263	0.0330	1.28
NRSN2	neurensin 2(NRSN2)	NM_024958	196.8	140.5	0.0330	0.81
VNN2	vanin 2(VNN2)	NM_004665	103.2	108	0.0330	1.17
STRN	striatin(STRN)	NM_003162	160	118.2	0.0330	0.83
		XM_001716173	134.1	99.2	0.0330	0.77

FHIT	fragile histidine triad(FHIT)	NM_002012	111.6	94.4	0.0330	0.89			
SHISA4	shisa family member 4(SHISA4)	NM_198149	106.5	91.8	0.0340	0.91			
TSPYL4	TSPY like 4(TSPYL4)	NM_021648	145.1	109.3	0.0340	0.83			
APOOL	apolipoprotein O like(APOOL)	NM_198450	189.3	206.1	0.0340	1.24			
HDGF	hepatoma-derived growth factor(HDGF)	NM_004494	358.3	234.1	0.0340	0.77			
CALHM2	calcium homeostasis modulator 2(CALHM2)	NM_015916	100.3	105.4	0.0340	1.13			
LRR1	leucine rich repeat protein 1(LRR1)	NM_203467	92.4	110.1	0.0340	1.3			
FANCE	Fanconi anemia complementation group E(FANCE)	NM_021922	162.8	217.7	0.0340	1.53			
		XR_015615	170.5	108.4	0.0340	0.71			
TLR10	toll like receptor 10(TLR10)	NM_030956	95.8	118.8	0.0340	1.36			
TLR8	toll like receptor 8(TLR8)	NM_016610	91	110.7	0.0340	1.33			
WDR73	WD repeat domain 73(WDR73)	NM_032856	114.2	130.2	0.0340	1.23	NM_001011972	5.50	125.06

		XM_944290	333.5	163.5	0.0340	0.57			
CKAP2L	cytoskeleton associated protein 2 like(CKAP2L)	NM_152515	104.3	115	0.0340	1.21			
QRICH1	glutamine rich 1(QRICH1)	NM_017730	156.8	180.2	0.0340	1.3			
PCDH17	protocadherin 17(PCDH17)	NM_014459	158.6	577.3	0.0340	3.92			
		BU561024	124.9	102.1	0.0340	0.87	NM_001107867	13.22	158.63
CLCF1	cardiotrophin-like cytokine factor 1(CLCF1)	NM_013246	212.3	141.9	0.0340	0.75			
SYNE1	spectrin repeat containing nuclear envelope protein 1(SYNE1)	NM_033071	123.7	86.7	0.0340	0.75			
CLOCK	clock circadian regulator(CLOCK)	NM_004898	267.2	163.1	0.0340	0.71			
PRKDC	protein kinase, DNA-activated, catalytic polypeptide(PRKDC)	NM_001081640	485.4	581.2	0.0340	1.38	NM_001014199	0.43	104.20
TUBB4A	tubulin beta 4A class IVa(TUBB4A)	NM_006087	171.7	128.1	0.0340	0.84			

POM121C	POM121 transmembrane nucleoporin C(POM121C)	NM_001099415	111.7	119.3	0.0340	1.19	NM_198745	128.13	517.66
DUS3L	dihydrouridine synthase 3 like(DUS3L)	NM_020175	137	153.6	0.0340	1.26	NM_198745	128.13	517.66
		XM_927468	104.4	106	0.0340	1.1			
		XM_496054	95.6	101.7	0.0340	1.14			
TTPAL	alpha tocopherol transfer protein like(TTPAL)	NM_024331	138.7	154.6	0.0340	1.27			
		CK299443	149.4	117.2	0.0340	0.88	NM_001105991	1.24	549.69
CCT8L1P	chaperonin containing TCP1 subunit 8 like 1, pseudogene(CCT8L1P)	NM_001029866	104.4	105.4	0.0340	1.1	NM_001105991	1.24	549.69
RBM10	RNA binding motif protein 10(RBM10)	NM_152856	283.8	311.5	0.0350	1.25	NM_001013929	4.59	30.85
YIF1B	Yip1 interacting factor homolog B, membrane trafficking protein(YIF1B)	NM_033557	106.6	107.7	0.0350	1.11	NM_001013929	4.59	30.85
		XM_001723141	695.1	854.9	0.0350	1.35			

		XR_037908	112.4	93.7	0.0350	0.89
PCDHGC4	protocadherin gamma subfamily C, 4(PCDHGC4)	NM_032406	120.7	98.4	0.0350	0.88
KLHL36	kelch like family member 36(KLHL36)	NM_024731	151.1	120.3	0.0350	0.87
		XM_0011130428	130.9	105.5	0.0350	0.89
TAGLN	transgelin(TAGLN)	NM_0011001522	126.5	104.2	0.0350	0.89
C15orf56	chromosome 15 open reading frame 56(C15orf56)	NM_0011039905	118.4	97.5	0.0350	0.89
RBMXL2	RNA binding motif protein, X-linked like 2(RBMXL2)	NM_014469	106.8	88.7	0.0350	0.87
SEC31A	SEC31 homolog A, COPII coat complex component(SEC31A)	NM_014933	115.5	110.1	0.0350	1.37
SEC31A	SEC31 homolog A, COPII coat complex component(SEC31A)	NM_014933	207.9	230.8	0.0350	1.37

SEC31A	SEC31 homolog A, COPII coat complex component(SEC31A)	NM_014933	462.7	564.9	0.0350	1.37
MYCBP2	MYC binding protein 2, E3 ubiquitin protein ligase(MYCBP2)	NM_015057	224.3	362.9	0.0350	1.82
GSTA3	glutathione S-transferase alpha 3(GSTA3)	NM_000847	89	95.1	0.0350	1.15
		AI627272	113	113.4	0.0350	1.11
		BX092585	112.7	94.3	0.0350	0.87
SCFD2	sec1 family domain containing 2(SCFD2)	NM_152540	105.5	117.9	0.0350	1.22
CD27-AS1	CD27 antisense RNA 1(CD27-AS1)	NR_015382	107.9	116.6	0.0350	1.18
ATRX	ATRX, chromatin remodeler(ATRX)	NM_000489	102.8	113	0.0350	1.2
RWDD1	RWD domain containing 1(RWDD1)	NM_001007464	605	699.3	0.0350	1.29
		XM_930558	131	104.6	0.0350	0.88
AOAH	acyloxyacyl hydrolase(AOAH)	NM_001637	87.8	95.9	0.0350	1.16

SRPK2	SRSF protein kinase 2(SRPK2)	NM_182692	105.6	109.9	0.0350	1.14
CTDP1	CTD phosphatase subunit 1(CTDP1)	NM_004715	103.6	101.4	0.0350	0.86
CTDP1	CTD phosphatase subunit 1(CTDP1)	NM_004715	122	96.1	0.0350	0.86
		XM_941100	95	109.4	0.0350	1.26
NOTUM	NOTUM, palmitoleoyl-protein carboxylesterase(NOTUM)	NM_178493	112.2	96.9	0.0360	0.92
DTD2	D-tyrosyl-tRNA deacylase 2 (putative)(DTD2)	NM_080664	105.6	111.8	0.0360	1.16
USP33	ubiquitin specific peptidase 33(USP33)	NM_201624	95.5	100.8	0.0360	1.13
		BX641358	100.2	104	0.0360	1.13
		XM_001720809	113.1	91.1	0.0360	0.85
DUSP23	dual specificity phosphatase 23(DUSP23)	NM_017823	361.1	247.6	0.0360	0.77

RITA1	RBPJ interacting and tubulin associated 1(RITA1)	NM_032848	157.2	120.9	0.0360	0.85
LOC613206	myeloproliferative disease associated tumor antigen 5(LOC613206)	NM_001033016	113.9	92.9	0.0360	0.87
DLGAP4	DLG associated protein 4(DLGAP4)	NM_001042486	176.7	189.6	0.0360	1.21
TRIM47	tripartite motif containing 47(TRIM47)	NM_033452	104.5	105.6	0.0360	1.1
SELENOS	selenoprotein S(SELENOS)	NM_018445	167.6	206.1	0.0360	1.38
SELENOS	selenoprotein S(SELENOS)	NM_018445	911.9	899.4	0.0360	1.38
UGT1A6	UDP glucuronosyltransferase family 1 member A6(UGT1A6)	NM_001072	146.1	107.1	0.0360	0.69
UGT1A6	UDP glucuronosyltransferase family 1 member A6(UGT1A6)	NM_001072	161.1	106.8	0.0360	0.69

AP1B1	adaptor related protein complex 1 beta 1 subunit(AP1B1)	NM_145730	192.3	242.6	0.0360	1.43			
METTL21B	methyltransferase like 21B(METTL21B)	NM_015433	698.4	358.2	0.0360	0.57			
MIR561	microRNA 561(MIR561)	NR_030287	104	108.4	0.0360	1.15			
		BQ028043	119.2	98	0.0360	0.87			
		BQ021435	121.2	100.1	0.0360	0.89	NM_019136	6.29	354.89
		XM_944418	93.7	100	0.0360	1.15			
KIF20A	kinesin family member 20A(KIF20A)	NM_005733	95.5	103.7	0.0360	1.17			
ASB3	ankyrin repeat and SOCS box containing 3(ASB3)	NM_145863	100.7	106.7	0.0360	1.15			
AAED1	AhpC/TSA antioxidant enzyme domain containing 1(AAED1)	NM_153698	124.3	134.3	0.0360	1.21			
CLEC2D	C-type lectin domain family 2 member D(CLEC2D)	NM_013269	118	102	0.0360	1.3			

CLEC2D	C-type lectin domain family 2 member D(CLEC2D)	NM_013269	2236.2	2836.9	0.0360	1.3
		XM_938002	100.5	105.8	0.0360	1.12
NKRF	NFKB repressing factor(NKRF)	NM_017544	132.2	141	0.0360	1.2
FAM3D	family with sequence similarity 3 member D(FAM3D)	NM_138805	125.4	98.5	0.0360	0.87
FAM162B	family with sequence similarity 162 member B(FAM162B)	NM_001085480	107.3	114.9	0.0360	1.19
C8orf82	chromosome 8 open reading frame 82(C8orf82)	NM_001001795	107.7	107.7	0.0360	1.1
OR5P3	olfactory receptor family 5 subfamily P member 3(OR5P3)	NM_153445	127.9	106.9	0.0360	0.91
STOX2	storkhead box 2(STOX2)	NM_020225	141.9	197.9	0.0360	1.58
		CR748464	97.2	100	0.0370	1.11
		XM_001125808	124.7	134	0.0370	1.19

DDX39B	DExD-box helicase 39B(DDX39B)	NM_080598	770.4	967	0.0370	1.42
ITGB4	integrin subunit beta 4(ITGB4)	NM_001005619	103.6	97.8	0.0370	1.12
ITGB4	integrin subunit beta 4(ITGB4)	NM_001005619	105.4	108.2	0.0370	1.12
TBX3	T-box 3(TBX3)	NM_005996	111.7	114.8	0.0370	1.13
KLC4	kinesin light chain 4(KLC4)	NM_201521	107.2	87.8	0.0370	0.87
DNMT3A	DNA methyltransferase 3 alpha(DNMT3A)	NM_175630	94.8	100.2	0.0370	1.15
		AA383317	114.3	95.5	0.0370	0.89
		XM_001717251	88.9	98.2	0.0370	1.18
		XM_928923	233.6	146.9	0.0370	0.72
HEATR4	HEAT repeat containing 4(HEATR4)	NM_203309	115.3	95.7	0.0370	0.89
MEF2C	myocyte enhancer factor 2C(MEF2C)	NM_002397	107.2	199.8	0.0370	2.08
ZNF75A	zinc finger protein 75a(ZNF75A)	NM_153028	97.5	103	0.0370	1.14
ANKRD49	ankyrin repeat domain 49(ANKRD49)	NM_017704	168.1	179.1	0.0370	1.19

TOX4	TOX high mobility group box family member 4(TOX4)	NM_014828	104.8	109.5	0.0370	1.13
COL11A1	collagen type XI alpha 1 chain(COL11A1)	NM_080629	129.7	96.4	0.0370	0.82
CNST	consortin, connexin sorting protein(CNST)	NM_152609	259.4	427.8	0.0370	1.86
		XM_940361	103.5	106.4	0.0370	1.13
PLEC	plectin(PLEC)	NM_201380	130.1	102.7	0.0370	0.87
GLIPR2	GLI pathogenesis related 2(GLIPR2)	NM_022343	99.5	115.4	0.0380	1.29
DEFB123	defensin beta 123(DEFB123)	NM_153324	395	184.7	0.0380	0.55
		XM_938495	132.5	106.1	0.0380	0.87
OGDH	oxoglutarate dehydrogenase(OGDH)	NM_001003941	98.9	103.2	0.0380	1.12
BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1(BPNT1)	NM_006085	116.7	128.3	0.0380	1.2

CTR9	CTR9 homolog, Paf1/RNA polymerase II complex component(CTR9)	NM_014633	118	94.8	0.0380	0.87
RANBP17	RAN binding protein 17(RANBP17)	NM_022897	164.1	119.8	0.0380	0.78
U2AF2	U2 small nuclear RNA auxiliary factor 2(U2AF2)	NM_007279	103.3	109.6	0.0380	1.16
U2AF2	U2 small nuclear RNA auxiliary factor 2(U2AF2)	NM_007279	663.9	593.8	0.0380	1.16
		XM_941035	116.1	94	0.0380	0.88
		XM_001724530	116.3	97.3	0.0380	0.9
SNORD56	small nucleolar RNA, C/D box 56(SNORD56)	NR_002739	105.8	120.7	0.0380	1.26
RPL13	ribosomal protein L13(RPL13)	NM_033251	110.1	124.2	0.0380	1.25
HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	103	98.1	0.0380	0.89

HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	112.7	94.6	0.0380	0.89
HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	137.8	117.2	0.0380	0.89
HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	150.8	123.4	0.0380	0.89
DSP	desmoplakin(DSP)	NM_001008844	183.9	173.5	0.0380	0.8
DSP	desmoplakin(DSP)	NM_001008844	190.6	134.1	0.0380	0.8
EIF6	eukaryotic translation initiation factor 6(EIF6)	NM_181469	1332.8	937.9	0.0380	0.79
BCAP29	B-cell receptor associated protein 29(BCAP29)	NM_001008405	178.4	216.6	0.0380	1.33
RABGGTA	Rab geranylgeranyltransferase alpha subunit(RABGGTA)	NM_004581	99.8	104.8	0.0380	1.14
KIAA1191	KIAA1191(KIAA1191)	NM_001079685	109.4	91.3	0.0380	0.88

DECR1	2,4-dienoyl-CoA reductase 1, mitochondrial(DECR1)	NM_001359	1053.4	548	0.0380	0.6			
LGALS2	galectin 2(LGALS2)	NM_006498	1166.8	439.6	0.0380	0.41			
bag4	BCL2 associated athanogene 4(BAG4)	NM_004874	143.4	152.1	0.0390	1.19	NM_139082	11.11	0.48
RACK1	receptor for activated C kinase 1(RACK1)	NM_006098	1619.3	1944.8	0.0390	1.3			
ACBD5	acyl-CoA binding domain containing 5(ACBD5)	NM_145698	106.6	107.3	0.0390	1.11			
TEDDM1	transmembrane epididymal protein 1(TEDDM1)	NM_172000	188.6	132.9	0.0390	0.81			
HAND1	heart and neural crest derivatives expressed 1(HAND1)	NM_004821	92.7	98	0.0390	1.13			
ASB16-AS1	ASB16 antisense RNA 1(ASB16-AS1)	NM_178542	153	115.6	0.0390	0.84			
CDC14A	cell division cycle 14A(CDC14A)	NM_003672	124	128	0.0390	1.14			

GDAP2	ganglioside induced differentiation associated protein 2(GDAP2)	NM_017686	193	201	0.0390	1.19
		CD516455	117	97.1	0.0390	0.89
ZDHHC4	zinc finger DHHC-type containing 4(ZDHHC4)	NM_018106	200.7	149	0.0390	0.83
EEF2	eukaryotic translation elongation factor 2(EEF2)	NM_001961	172.4	112.2	0.0390	0.74
CER1	cerberus 1, DAN family BMP antagonist(CER1)	NM_005454	147.2	114.8	0.0390	0.86
		BF054947	116.6	99.1	0.0390	0.92
		XR_015400	208.9	238.3	0.0390	1.29
TMEM8B	transmembrane protein 8B(TMEM8B)	NM_016446	98.6	102.4	0.0390	1.13
		NM_001009937	171.7	127.3	0.0390	0.82
		XM_0017155992	147.3	111.7	0.0390	0.86
RYK	receptor-like tyrosine kinase(RYK)	NM_001005861	121.1	109.5	0.0390	1.37

RYK	receptor-like tyrosine kinase(RYK)	NM_001005861	217.5	269	0.0390	1.37
ZNF607	zinc finger protein 607(ZNF607)	NM_032689	97.8	107	0.0390	1.19
ZNF607	zinc finger protein 607(ZNF607)	NM_032689	101.9	92.3	0.0390	1.19
		XM_931025	118.9	123.8	0.0390	1.17
RNF181	ring finger protein 181(RNF181)	NM_016494	550.9	360.6	0.0390	0.74
adck5	aarF domain containing kinase 5(ADCK5)	NM_174922	139.7	146.4	0.0390	1.16
		XM_933681	143.3	111.4	0.0390	0.85
		XR_039005	156.7	110.3	0.0390	0.78
DYRK1B	dual specificity tyrosine phosphorylation regulated kinase 1B(DYRK1B)	NM_006484	177.2	130.8	0.0390	0.82
HELQ	helicase, POLQ-like(HELQ)	NM_133636	164.1	191.9	0.0390	1.3
SYT7	synaptotagmin 7(SYT7)	NM_004200	117.2	139.6	0.0390	1.35
		XM_942604	98.7	102.3	0.0390	1.12
		XM_001717551	101.5	103.1	0.0390	1.09

NEDD4	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase(NEDD4)	NM_006154	95.9	106.7	0.0390	1.21
NEDD4	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase(NEDD4)	NM_006154	202.6	173.9	0.0390	1.21
		XR_017364	236.8	139.8	0.0390	0.65
HSD17B7P2	hydroxysteroid 17-beta dehydrogenase 7 pseudogene 2(HSD17B7P2)	NR_003086	98.5	99.7	0.0390	1.09
MEF2A	myocyte enhancer factor 2A(MEF2A)	NM_005587	97.5	93.3	0.0390	1.3
MEF2A	myocyte enhancer factor 2A(MEF2A)	NM_005587	104	122.2	0.0390	1.3
KATNA1	katanin catalytic subunit A1(KATNA1)	NM_007044	190.6	226.5	0.0390	1.32

FAM26D	family with sequence similarity 26 member D(FAM26D)	NM_153036	106.6	92.8	0.0400	0.92			
FAM26D	family with sequence similarity 26 member D(FAM26D)	NM_153036	121.7	103.4	0.0400	0.92			
		XM_929427	156.5	119.7	0.0400	0.86	NM_017253	1.16	16.79
ELP5	elongator acetyltransferase complex subunit 5(ELP5)	NM_203413	132.5	137.6	0.0400	1.19			
ELP5	elongator acetyltransferase complex subunit 5(ELP5)	NM_203413	247.8	200.5	0.0400	1.19			
HCCS	holocytochrome c synthase(HCCS)	NM_005333	109.1	100.7	0.0400	0.66			
HCCS	holocytochrome c synthase(HCCS)	NM_005333	302	166.4	0.0400	0.66			
PTPN23	protein tyrosine phosphatase, non-receptor type 23(PTPN23)	NM_015466	101.1	106.7	0.0400	1.16			
RBM39	RNA binding motif protein 39(RBM39)	NM_184237	103.9	114.3	0.0400	1.22			

HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1(HMGCS1)	NM_002130	599.5	385	0.0400	0.73
SOX21	SRY-box 21(SOX21)	NM_007084	111.9	88.8	0.0400	0.85
SRPK1	SRSF protein kinase 1(SRPK1)	NM_003137	110.4	89.9	0.0400	0.87
SUCLG2	succinate-CoA ligase GDP-forming beta subunit(SUCLG2)	NM_003848	157.2	106.9	0.0400	0.76
		XM_379270	119.7	93.6	0.0400	0.82
		XM_938817	116.7	98.7	0.0400	0.92
STAMBPL1	STAM binding protein like 1(STAMBPL1)	NM_020799	121.7	178.1	0.0400	1.67
H3F3AP4	H3 histone, family 3A, pseudogene 4(H3F3AP4)	NR_002315	468.8	162.3	0.0400	0.41
H3F3AP4	H3 histone, family 3A, pseudogene 4(H3F3AP4)	NR_002315	2589.7	2420.9	0.0400	0.41
LIMS1	LIM zinc finger domain containing 1(LIMS1)	NM_004987	96.9	88.8	0.0400	1.15

LIMS1	LIM zinc finger domain containing 1(LIMS1)	NM_004987	136	138.6	0.0400	1.15
PRSS3P2	protease, serine 3 pseudogene 2(PRSS3P2)	NR_001296	95.5	100.1	0.0400	1.12
PYGL	phosphorylase, glycogen, liver(PYGL)	NM_002863	149.1	113.9	0.0400	0.83
CYP2S1	cytochrome P450 family 2 subfamily S member 1(CYP2S1)	NM_030622	134.6	108.5	0.0400	0.89
S100A10	S100 calcium binding protein A10(S100A10)	NM_002966	128.4	98.1	0.0400	0.82
S100A10	S100 calcium binding protein A10(S100A10)	NM_002966	679.2	583.1	0.0400	0.82
ZNHIT1	zinc finger HIT-type containing 1(ZNHIT1)	NM_006349	1690.2	1015	0.0400	0.68
		XM_928726	147	114.2	0.0400	0.86
DFNA5	DFNA5, deafness associated tumor suppressor(DFNA5)	NM_004403	238.1	143.6	0.0400	0.65
		XM_942417	112.2	94.9	0.0400	0.89

USP1	ubiquitin specific peptidase 1(USP1)	NM_003368	93.7	107.1	0.0400	1.24
		BU182441	133	107.6	0.0400	0.88
		XM_936375	90.7	96.5	0.0400	1.14
CNOT3	CCR4-NOT transcription complex subunit 3(CNOT3)	NM_014516	102.1	107.7	0.0400	1.15
ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	NM_020038	108.7	109.2	0.0410	1.09
		XM_931381	336.9	181.6	0.0410	0.62
KRTAP13-4	keratin associated protein 13-4(KRTAP13-4)	NM_181600	132.8	104.3	0.0410	0.86
SLC25A48	solute carrier family 25 member 48(SLC25A48)	NM_145282	182.4	137.1	0.0410	0.85
PRAM1	PML-RARA regulated adaptor molecule 1(PRAM1)	NM_032152	117.5	101.1	0.0410	0.92
BIRC2	baculoviral IAP repeat containing 2(BIRC2)	NM_001166	128.7	131.1	0.0410	1.3

BIRC2	baculoviral IAP repeat containing 2(BIRC2)	NM_001166	171.2	202.2	0.0410	1.3
		BU734093	136.2	141.7	0.0410	1.18
		XM_001719745	104.4	123.6	0.0410	1.29
FKRP	fukutin related protein(FKRP)	NM_024301	111.4	118.1	0.0410	1.17
MAP2K2	mitogen-activated protein kinase kinase 2(MAP2K2)	NM_030662	118.9	93	0.0410	0.85
BCOR	BCL6 corepressor(BCOR)	NM_017745	215.9	250.5	0.0410	1.3
JADE1	jade family PHD finger 1(JADE1)	NM_199320	202.2	150.5	0.0410	0.83
NFAT5	nuclear factor of activated T-cells 5(NFAT5)	NM_173215	101.4	108	0.0410	1.16
ASUN	asunder, spermatogenesis regulator(ASUN)	NM_018164	103.3	108.8	0.0410	1.18
ASUN	asunder, spermatogenesis regulator(ASUN)	NM_018164	133.4	139.3	0.0410	1.18
MKNK2	MAP kinase interacting serine/threonine kinase 2(MKNK2)	NM_199054	352.4	221.1	0.0410	0.73
		CB048233	94.5	101.6	0.0410	1.16

TMED9	transmembrane p24 trafficking protein 9(TMED9)	NM_017510	262.4	187.4	0.0410	0.8
CNIH2	cornichon family AMPA receptor auxiliary protein 2(CNIH2)	NM_182553	111.8	103.9	0.0410	0.83
CNIH2	cornichon family AMPA receptor auxiliary protein 2(CNIH2)	NM_182553	136.5	102.3	0.0410	0.83
CNIH2	cornichon family AMPA receptor auxiliary protein 2(CNIH2)	NM_182553	164.8	133.1	0.0410	0.83
GPR180	G protein-coupled receptor 180(GPR180)	NM_180989	122.3	130.2	0.0410	1.22
		BU685158	98.4	101	0.0410	1.12
PRICKLE1	prickle planar cell polarity protein 1(PRICKLE1)	NM_153026	126.2	161.6	0.0410	1.43
		XM_943683	118.6	98.8	0.0410	0.9
SSR1	signal sequence receptor subunit 1(SSR1)	NM_003144	443	498.9	0.0410	1.26
NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147133	121.5	125.1	0.0410	1.16

NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147133	181.8	136.2	0.0410	1.16
MT1E	metallothionein 1E(MT1E)	NM_175617	130.8	103.5	0.0410	0.41
MT1E	metallothionein 1E(MT1E)	NM_175617	5309.7	1957.7	0.0410	0.41
NEMF	nuclear export mediator factor(NEMF)	NM_004713	205.5	245.1	0.0410	1.32
POTEH	POTE ankyrin domain family member H(POTEH)	NM_001004053	103.1	112	0.0410	1.18
		XR_040084	95.9	100	0.0410	1.13
MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2)	NM_016431	143	124	0.0410	0.88
MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2)	NM_016431	146.3	115.8	0.0410	0.88
		XR_038700	115.6	89.3	0.0420	0.84

RAPGEF1	Rap guanine nucleotide exchange factor 1(RAPGEF1)	NM_005312	144.9	115	0.0420	0.89			
STK10	serine/threonine kinase 10(STK10)	NM_005990	211.8	147.7	0.0420	0.8	NM_019368	2.87	13.68
		XM_001725448	135	109.8	0.0420	0.88			
PSENEN	presenilin enhancer gamma-secretase subunit(PSENEN)	NM_172341	269.7	198.5	0.0420	0.85			
UIMC1	ubiquitin interaction motif containing 1(UIMC1)	NM_016290	199.8	249.3	0.0420	1.4			
		XM_001128559	118.5	89.6	0.0420	0.81			
KMT2E	lysine methyltransferase 2E(KMT2E)	NM_182931	144.7	190.2	0.0420	1.49			
KMT2E	lysine methyltransferase 2E(KMT2E)	NM_182931	171	135.3	0.0420	1.49			
OGDH	oxoglutarate dehydrogenase(OGDH)	NM_002541	333.9	208.1	0.0420	0.71	NM_001037554	15.49	101.99

B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2(B3GALNT2)	NM_152490	118.6	137	0.0420	1.29			
DCTD	dCMP deaminase(DCTD)	NM_001921	142.3	148.9	0.0420	1.15			
HLA-DPB1	major histocompatibility complex, class II, DP beta 1(HLA-DPB1)	NM_002121	116.5	95.9	0.0420	0.89	NM_017087	51.82	0.25
		XM_933749	123.3	101.2	0.0420	0.9			
NDUFA10	NADH:ubiquinone oxidoreductase subunit A10(NDUFA10)	NM_004544	102.4	96.8	0.0420	0.79			
NDUFA10	NADH:ubiquinone oxidoreductase subunit A10(NDUFA10)	NM_004544	118.1	88.1	0.0420	0.79			
OR2A5	olfactory receptor family 2 subfamily A member 5(OR2A5)	NM_012365	111.1	91.7	0.0420	0.88			
		XM_001720686	194.7	126	0.0420	0.73			
GLTSCR1L	GLTSCR1 like(GLTSCR1L)	NM_015349	150.6	208.6	0.0420	1.5			

TM7SF3	transmembrane 7 superfamily member 3(TM7SF3)	NM_016551	189.5	131.8	0.0420	0.8
PXMP4	peroxisomal membrane protein 4(PXMP4)	NM_183397	129.5	133.2	0.0420	1.15
		XR_039263	114.9	115.4	0.0420	1.13
SNORD113-1	small nucleolar RNA, C/D box 113-1(SNORD113-1)	NR_003229	101.4	107.8	0.0420	1.17
CBX5	chromobox 5(CBX5)	NM_012117	110.4	144.6	0.0420	1.48
ALPK3	alpha kinase 3(ALPK3)	NM_020778	179.2	129.7	0.0420	0.83
FARP1	FERM, ARH/RhoGEF and pleckstrin domain protein 1(FARP1)	NM_005766	144	112.7	0.0420	0.86
		XM_945430	110.6	120.5	0.0420	1.22
		BE673312	167.8	97.6	0.0420	0.66
ZEB1-AS1	ZEB1 antisense RNA 1(ZEB1-AS1)	AK026657	112.3	91.7	0.0420	0.87
FBXO28	F-box protein 28(FBXO28)	NM_015176	118.8	135.7	0.0420	1.25

CAPN5	calpain 5(CAPN5)	NM_004055	399.8	209.9	0.0430	0.61
ARHGAP26	Rho GTPase activating protein 26(ARHGAP26)	NM_015071	116.5	95.1	0.0430	0.88
NSUN4	NOP2/Sun RNA methyltransferase family member 4(NSUN4)	NM_199044	99.7	104.7	0.0430	1.14
ATRAID	all-trans retinoic acid induced differentiation factor(ATRAID)	NM_080592	831.4	584.6	0.0430	0.62
ATRAID	all-trans retinoic acid induced differentiation factor(ATRAID)	NM_080592	1464.5	799.2	0.0430	0.62
		XR_017229	353.9	188	0.0430	0.61
		DA453004	144	110.2	0.0430	0.86
NPIPB13	nuclear pore complex interacting protein family, member B13(NPIPB13)	NR_002555	209	141	0.0430	0.78
		XM_001723520	111.9	112.7	0.0430	1.11
		AI633632	156.9	120.5	0.0430	0.86
MT1X	metallothionein 1X(MT1X)	NM_005952	6772.5	2570	0.0430	0.44

		XR_038314	3375.1	4770.6	0.0430	1.35	NM_001025767	5.06	85.80
SMC4	structural maintenance of chromosomes 4(SMC4)	NM_001002800	86.2	102.3	0.0430	1.29			
RAD54L	RAD54-like (S. cerevisiae)(RAD54L)	NM_003579	95.5	104.6	0.0430	1.2	NM_001037349	4.94	35.26
ARL5B	ADP ribosylation factor like GTPase 5B(ARL5B)	NM_178815	92.4	98.2	0.0430	1.13	NM_001037349	4.94	35.26
CYP8B1	cytochrome P450 family 8 subfamily B member 1(CYP8B1)	NM_004391	254.8	153.8	0.0430	0.67			
		XM_926112	143.2	161.8	0.0430	1.27			
PSME1	proteasome activator subunit 1(PSME1)	NM_176783	113.7	112	0.0430	1.1			
MDC1	mediator of DNA damage checkpoint 1(MDC1)	NM_014641	249.2	300.8	0.0430	1.34			
		BF194881	131.1	107.8	0.0430	0.87			
SCRIB	scribbled planar cell polarity protein(SCRIB)	NM_182706	110.8	113.3	0.0430	1.14			

TMEM128	transmembrane protein 128(TMEM128)	NM_032927	119	100	0.0430	0.91			
		XR_038706	316.4	360.2	0.0430	1.3			
SON	SON DNA binding protein(SON)	NM_138927	119.6	122.1	0.0430	1.13			
SON	SON DNA binding protein(SON)	NM_138927	171.9	176	0.0430	1.13	NM_001107368	10.94	1.12
SON	SON DNA binding protein(SON)	NM_138927	1267.9	1422.7	0.0430	1.13			
ZNF471	zinc finger protein 471(ZNF471)	NM_020813	100	113.7	0.0430	1.23			
ZNF471	zinc finger protein 471(ZNF471)	NM_020813	135.5	131.7	0.0430	1.23			
IPO11	importin 11(IPO11)	NM_016338	227.6	242.9	0.0430	1.22			
		XM_001132362	108.5	91.4	0.0430	0.89			
BIRC5	baculoviral IAP repeat containing 5(BIRC5)	NM_001168	94.2	113.8	0.0440	1.31			
LSM1	LSM1 homolog, mRNA degradation associated(LSM1)	NM_014462	354.8	371	0.0440	1.17			

CSNK2B	casein kinase 2 beta(CSNK2B)	NM_001320	465.5	332.4	0.0440	0.82
		BF375676	104.8	114.8	0.0440	1.2
JAG1	jagged 1(JAG1)	NM_000214	132.6	132.6	0.0440	1.14
DUSP27	dual specificity phosphatase 27 (putative)(DUSP27)	NM_001080426	107.7	111.5	0.0440	1.13
TSPAN17	tetraspanin 17(TSPAN17)	NM_012171	158.7	169.5	0.0440	1.24
SLC30A7	solute carrier family 30 member 7(SLC30A7)	NM_133496	346.9	431.7	0.0440	1.43
SP140	SP140 nuclear body protein(SP140)	NM_001005176	81.4	99.1	0.0440	1.32
		DB344577	136	106.1	0.0440	0.86
		XM_001126647	112.3	123.9	0.0440	1.24
		XM_001126647	118.3	108.3	0.0440	1.24
FER1L5	fer-1 like family member 5(FER1L5)	NM_001077400	167.4	127.7	0.0440	0.87
FER1L5	fer-1 like family member 5(FER1L5)	NM_001077400	249.8	184.4	0.0440	0.87
RWDD2A	RWD domain containing 2A(RWDD2A)	AJ420581	228.2	154.5	0.0440	0.78

ZNF2	zinc finger protein 2(ZNF2)	NM_021088	102.5	105.9	0.0440	1.12			
NQO1	NAD(P)H quinone dehydrogenase 1(NQO1)	NM_000903	141.9	100.9	0.0440	0.79			
NQO1	NAD(P)H quinone dehydrogenase 1(NQO1)	NM_000903	3501.7	2236.7	0.0440	0.79	NM_017312	61.39	265.99
		BG911604	126.8	99.5	0.0440	0.84			
LRCH3	leucine rich repeats and calponin homology domain containing 3(LRCH3)	NM_032773	144.3	174.9	0.0440	1.35			
PDE11A	phosphodiesterase 11A(PDE11A)	NM_016953	110.6	91.2	0.0440	0.87			
SRSF5	serine and arginine rich splicing factor 5(SRSF5)	NM_006925	1451.3	1528.5	0.0440	1.28			
SRSF5	serine and arginine rich splicing factor 5(SRSF5)	NM_006925	1464.5	1688	0.0440	1.28			
MGAM	maltase-glucoamylase(MGAM)	NM_004668	117.3	91.8	0.0440	0.84			

IL2RG	interleukin 2 receptor subunit gamma(IL2RG)	NM_000206	94.1	107.7	0.0440	1.26
		XM_0017244244	116.4	117.2	0.0440	1.14
FAM120A	family with sequence similarity 120A(FAM120A)	NM_014612	1682.3	1799.4	0.0440	1.19
ZNF524	zinc finger protein 524(ZNF524)	NM_153219	151.3	160.5	0.0440	1.2
MARS	methionyl-tRNA synthetase(MARS)	NM_004990	95	96.4	0.0440	1.08
MT1IP	metallothionein 1I, pseudogene(MT1IP)	NM_175621	1855.3	667.1	0.0440	0.42
ZC3H3	zinc finger CCCH-type containing 3(ZC3H3)	NM_015117	177.4	182.4	0.0450	1.18
TTC31	tetratricopeptide repeat domain 31(TTC31)	NM_022492	209.4	235.6	0.0450	1.27
		XM_0017233153	123.9	88.5	0.0450	0.78
WDR4	WD repeat domain 4(WDR4)	NM_033661	98	100.8	0.0450	1.1
DERL2	derlin 2(DERL2)	AK092218	142.3	112.5	0.0450	0.86
		AW136029	148.4	115.2	0.0450	0.87

dhx37	DEAH-box helicase 37(DHX37)	NM_032656	166.2	201.6	0.0450	1.39
st6gal1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	NM_003032	104.6	109.5	0.0450	0.78
st6gal1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	NM_003032	167.9	116.2	0.0450	0.78
		XM_930029	348.7	229	0.0450	0.75
		XM_942439	189.3	140	0.0450	0.84
ak5	adenylate kinase 5(AK5)	NM_012093	124.3	95.3	0.0450	0.84
		NR_002214	147.6	110.4	0.0450	0.83
AMPD3	adenosine monophosphate deaminase 3(AMPD3)	NM_000480	137.6	111.8	0.0450	0.89
		XM_937706	375.2	242.9	0.0450	0.74
SF3A3	splicing factor 3a subunit 3(SF3A3)	NM_006802	817.1	906.7	0.0450	1.26
		XM_935575	104.3	112	0.0450	1.2

EIF2B4	eukaryotic translation initiation factor 2B subunit delta(EIF2B4)	NM_172195	106.5	106.4	0.0450	1.1
YTHDC1	YTH domain containing 1(YTHDC1)	NM_001031732	103.1	102.1	0.0450	1.31
YTHDC1	YTH domain containing 1(YTHDC1)	NM_001031732	104	123.2	0.0450	1.31
YTHDC1	YTH domain containing 1(YTHDC1)	NM_001031732	729.1	833.2	0.0450	1.31
TEX10	testis expressed 10(TEX10)	NM_017746	125.4	145.9	0.0450	1.33
MTNR1B	melatonin receptor 1B(MTNR1B)	NM_005959	95.3	102.3	0.0450	1.15
PLIN5	perilipin 5(PLIN5)	NM_001013706	372.8	494.9	0.0450	1.54
SDHAF1	succinate dehydrogenase complex assembly factor 1(SDHAF1)	NM_001042631	114.9	119.6	0.0460	1.16
PI15	peptidase inhibitor 15(PI15)	NM_015886	95.2	98.4	0.0460	1.11
PI15	peptidase inhibitor 15(PI15)	NM_015886	136.8	117	0.0460	1.11

POU2F2	POU class 2 homeobox 2(POU2F2)	NM_002698	91.4	104.4	0.0460	1.25	NM_001107453	3.00	15.94
KLHL7	kelch like family member 7(KLHL7)	NM_001031710	112.5	115.2	0.0460	1.11			
ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1(ARAP1)	NM_001040118	108.1	117.7	0.0460	1.21			
ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1(ARAP1)	NM_001040118	114.3	118.6	0.0460	1.21			
		XM_001721348	107	115.9	0.0460	1.2			
SOX30	SRY-box 30(SOX30)	NM_178424	203.1	134.7	0.0460	0.76			
PDX1	pancreatic and duodenal homeobox 1(PDX1)	NM_000209	150.3	121.4	0.0460	0.9			
RWDD2B	RWD domain containing 2B(RWDD2B)	NM_016940	299.1	185.6	0.0460	0.72			
		XM_942399	98.4	103.1	0.0460	1.15			
IL17C	interleukin 17C(IL17C)	NM_013278	230.6	155.9	0.0460	0.78			

MAP1LC3A	microtubule associated protein 1 light chain 3 alpha(MAP1LC3A)	NM_181509	774.1	844.6	0.0460	1.23
ZNF816	zinc finger protein 816(ZNF816)	NM_001031665	107.7	111.6	0.0460	1.14
		XM_001717865	116.1	99.2	0.0460	0.93
TAGLN3	transgelin 3(TAGLN3)	NM_001008273	116.1	97.4	0.0460	0.91
acap3	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3(ACAP3)	NM_030649	92.1	98.2	0.0460	1.14
SNHG11	small nucleolar RNA host gene 11(SNHG11)	NR_003239	383.3	257.4	0.0460	0.78
MAMSTR	MEF2 activating motif and SAP domain containing transcriptional regulator(MAMSTR)	NM_182574	156.7	115.6	0.0460	0.83
ITM2B	integral membrane protein 2B(ITM2B)	NM_021999	120.8	84.1	0.0460	0.75

ITM2B	integral membrane protein 2B(ITM2B)	NM_021999	4258	3405.8	0.0460	0.75
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1(ENTPD1)	NM_001098175	106.3	127.1	0.0460	1.35
GEM	GTP binding protein overexpressed in skeletal muscle(GEM)	NM_181702	138.5	166.6	0.0460	1.36
GEM	GTP binding protein overexpressed in skeletal muscle(GEM)	NM_181702	154.3	177	0.0460	1.36
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	119.7	111.3	0.0460	0.9
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	133.1	108.1	0.0460	0.9
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	401.5	351.6	0.0460	0.9
C19orf47	chromosome 19 open reading frame 47(C19orf47)	NM_178830	153.4	119.6	0.0470	0.86

MRPS11	mitochondrial ribosomal protein S11(MRPS11)	NM_176805	249.3	172.2	0.0470	0.77			
MRPS11	mitochondrial ribosomal protein S11(MRPS11)	NM_176805	457.1	374.9	0.0470	0.77			
		XM_001132864	120.5	96	0.0470	0.86			
		XM_930715	127.4	101.4	0.0470	0.87			
SEPT2	septin 2(SEPT2)	NM_004404	1066.6	1278	0.0470	1.32			
		XM_001715568	126.2	122.7	0.0470	1.1			
FAM86JP	family with sequence similarity 86, member A pseudogene(FAM86JP)	NR_024250	101.6	104.8	0.0470	1.14	NM_030848	56.65	0.04
CYTH3	cytohesin 3(CYTH3)	NM_004227	311	125	0.0470	0.47			
ttc32	tetratricopeptide repeat domain 32(TTC32)	NM_001008237	181.9	199.3	0.0470	1.23			
ttc32	tetratricopeptide repeat domain 32(TTC32)	NM_001008237	221.6	195.1	0.0470	1.23			
CHKA	choline kinase alpha(CHKA)	NM_212469	203.1	232.7	0.0470	1.31			

HNRNPM	heterogeneous nuclear ribonucleoprotein M(HNRNPM)	NM_031203	242.8	324.1	0.0470	1.49
ABR	active BCR-related(ABR)	NM_001092	319.5	373.5	0.0470	1.33
HOXA7	homeobox A7(HOXA7)	NM_006896	175.5	129.8	0.0470	0.83
EXOC3L1	exocyst complex component 3 like 1(EXOC3L1)	NM_178516	102.5	113	0.0470	1.21
NDUFAF3	NADH:ubiquinone oxidoreductase complex assembly factor 3(NDUFAF3)	NM_199074	122.9	98.9	0.0470	0.89
clstn3	calsyntenin 3(CLSTN3)	NM_014718	120.6	100.9	0.0470	0.9
EDNRA	endothelin receptor type A(EDNRA)	NM_001957	85.7	93.3	0.0470	1.16
		XM_001716912	90.4	96.6	0.0470	1.14
PHYKPL	5-phosphohydroxy-L-lysine phospho-lyase(PHYKPL)	NM_153373	218.2	147.5	0.0470	0.78
		XM_929696	104.1	96.7	0.0470	0.77
		XM_929696	157.3	108	0.0470	0.77

		XM_001128702	147.2	114.5	0.0470	0.87			
ZMYM6	zinc finger MYM-type containing 6(ZMYM6)	NM_007167	124.4	143.4	0.0470	1.29			
		DB369246	111.4	112.2	0.0470	1.11			
FBXO38	F-box protein 38(FBXO38)	NM_030793	165.1	176.1	0.0470	1.21	NM_017258	66.46	359.19
FBXO38	F-box protein 38(FBXO38)	NM_030793	181.3	177.5	0.0470	1.21			
		XM_001125904	126.9	135.8	0.0470	1.22			
ZXDB	zinc finger, X-linked, duplicated B(ZXDB)	NM_007157	174.1	132.8	0.0470	0.87			
zbtb18	zinc finger and BTB domain containing 18(ZBTB18)	NM_205768	289.4	185.5	0.0470	0.75			
		XM_936103	141.5	158.8	0.0470	1.28			
WDR27	WD repeat domain 27(WDR27)	NM_182552	210.5	153.9	0.0470	0.83			
SNX29P2	sorting nexin 29 pseudogene 2(SNX29P2)	NR_002939	401.9	263.8	0.0470	1.89			
SNX29P2	sorting nexin 29 pseudogene 2(SNX29P2)	NR_002939	800.3	1275	0.0470	1.89			

nomo1	NODAL modulator 1(NOMO1)	NM_014287	284.9	183.8	0.0470	0.76
ANAPC11	anaphase promoting complex subunit 11(ANAPC11)	NM_001002244	173.5	128.4	0.0470	0.84
RNF135	ring finger protein 135(RNF135)	NM_197939	121.6	131.1	0.0470	1.23
		XM_001124651	129	104.1	0.0480	0.88
BPTF	bromodomain PHD finger transcription factor(BPTF)	NM_182641	167.9	123.3	0.0480	0.83
TENM2	teneurin transmembrane protein 2(TENM2)	NM_001080428	109.5	108.7	0.0480	1.09
CTPS1	CTP synthase 1(CTPS1)	NM_001905	110.3	148.1	0.0480	1.52
MEIOB	meiosis specific with OB domains(MEIOB)	NM_152764	118.1	96	0.0480	0.85
USP49	ubiquitin specific peptidase 49(USP49)	NM_018561	1581.2	2265.6	0.0480	1.52
PARP8	poly(ADP-ribose) polymerase family member 8(PARP8)	NM_024615	103.5	123.3	0.0480	1.32

eif2ak2	eukaryotic translation initiation factor 2 alpha kinase 2(EIF2AK2)	NM_002759	110.9	121.9	0.0480	1.22
ZNF394	zinc finger protein 394(ZNF394)	NM_032164	1982.7	2445.7	0.0480	1.31
		BG201242	103.3	105.5	0.0480	1.11
EXTL1	exostosin like glycosyltransferase 1(EXTL1)	NM_004455	116	115.9	0.0480	1.12
RAB3C	RAB3C, member RAS oncogene family(RAB3C)	NM_138453	100.1	86.4	0.0480	0.88
RLF	rearranged L-myc fusion(RLF)	NM_012421	142.3	157.2	0.0480	1.24
		XM_001720625	3030	4299.8	0.0480	1.35
		XM_934672	106.9	104.5	0.0480	1.06
RPF2	ribosome production factor 2 homolog(RPF2)	NM_032194	158	171.6	0.0480	1.24
		NR_003253	168	128.1	0.0480	0.86
FSIP1	fibrous sheath interacting protein 1(FSIP1)	NM_152597	135.3	106.7	0.0480	0.87
		XM_940764	106.1	88.3	0.0480	0.86

ZNF622	zinc finger protein 622(ZNF622)	NM_033414	410.6	325.4	0.0490	0.89
CHRNA6	cholinergic receptor nicotinic alpha 6 subunit(CHRNA6)	NM_004198	101.6	106.8	0.0490	1.13
ZBTB32	zinc finger and BTB domain containing 32(ZBTB32)	NM_014383	89.9	98.5	0.0490	1.17
CBFB	core-binding factor beta subunit(CBFB)	NM_001755	100.2	106.6	0.0490	1.15
PCDHB16	protocadherin beta 16(PCDHB16)	NM_020957	116	93.9	0.0490	0.85
NLGN4X	neuroligin 4, X-linked(NLGN4X)	NM_020742	85.6	97.6	0.0490	1.22
COL20A1	collagen type XX alpha 1 chain(COL20A1)	NM_020882	381.6	203.5	0.0490	0.63
PIAS4	protein inhibitor of activated STAT 4(PIAS4)	NM_015897	467.2	510.9	0.0490	1.24
NOP56	NOP56 ribonucleoprotein(NOP56)	NM_006392	112	111.6	0.0490	1.73
NOP56	NOP56 ribonucleoprotein(NOP56)	NM_006392	343.3	532.7	0.0490	1.73

		XR_042317	119.9	119.6	0.0490	1.13
FBXO4	F-box protein 4(FBXO4)	NM_033484	90.8	99.3	0.0490	1.18
Krtap5-1	keratin associated protein 5-1(KRTAP5-1)	NM_001005922	118.6	100.6	0.0490	0.93
ITGA2	integrin subunit alpha 2(ITGA2)	NM_002203	99.4	104.4	0.0490	1.13
CPVL	carboxypeptidase, vitellogenic like(CPVL)	NM_019029	90.5	133.4	0.0490	1.64
XCL1	X-C motif chemokine ligand 1(XCL1)	NM_002995	106.1	90.2	0.0490	0.9
GUCA1A	guanylate cyclase activator 1A(GUCA1A)	NM_000409	129.1	105.2	0.0490	0.87
TSC22D2	TSC22 domain family member 2(TSC22D2)	NM_014779	198.9	208	0.0490	1.35
TSC22D2	TSC22 domain family member 2(TSC22D2)	NM_014779	406.5	483.1	0.0490	1.35
		XR_039891	102	101.8	0.0490	1.08
KRTAP10-8	keratin associated protein 10-8(KRTAP10-8)	NM_198695	100.4	100.9	0.0490	1.1

CCDC90B	coiled-coil domain containing 90B(CCDC90B)	NM_021825	101.4	105.8	0.0490	1.13
DNAJB14	DnaJ heat shock protein family (Hsp40) member B14(DNAJB14)	NM_001031723	98.2	117.2	0.0490	1.2
DNAJB14	DnaJ heat shock protein family (Hsp40) member B14(DNAJB14)	NM_001031723	110.8	121.7	0.0490	1.2
		XM_943600	89.2	97.3	0.0490	1.17
SPRED1	sprouty related EVH1 domain containing 1(SPRED1)	NM_152594	371.3	439	0.0490	1.31
UPK3BL	uroplakin 3B-like(UPK3BL)	NM_001114403	116.8	91.8	0.0490	0.85
ZNF830	zinc finger protein 830(ZNF830)	NM_052857	134.4	143.2	0.0490	1.19
STAMBP	STAM binding protein(STAMBP)	NM_006463	126.4	132	0.0490	1.19
STAMBP	STAM binding protein(STAMBP)	NM_006463	148.9	122.4	0.0490	1.19
ALAD	aminolevulinate dehydratase(ALAD)	NM_001003945	114.6	103.1	0.0500	0.69

ALAD	aminolevulinate dehydratase(ALAD)	NM_001003945	370.1	223	0.0500	0.69
		XR_040201	173.3	114.2	0.0500	0.75
CELF1	CUGBP, Elav-like family member 1(CELF1)	NM_198700	141.3	151.3	0.0500	1.19
ZNF621	zinc finger protein 621(ZNF621)	NM_001098414	109.6	116.4	0.0500	1.19
CHM	CHM, Rab escort protein 1(CHM)	NM_000390	118	122.3	0.0500	1.17
BTLA	B and T lymphocyte associated(BTLA)	NM_181780	86.4	103	0.0500	1.29
BTLA	B and T lymphocyte associated(BTLA)	NM_181780	121.9	140.4	0.0500	1.29
		AA421413	154	118.7	0.0500	0.87
		XM_927848	123	101.2	0.0500	0.9
RAB30	RAB30, member RAS oncogene family(RAB30)	NM_014488	115.6	252.8	0.0500	2.42
MT1A	metallothionein 1A(MT1A)	NM_005946	11240.4	4350.9	0.0500	0.45
RPL36	ribosomal protein L36(RPL36)	NM_015414	95.5	101.3	0.0500	1.14
FLJ35816	FLJ35816 protein(FLJ35816)	NM_207489	169.5	121.2	0.0500	0.8

TXLNG	taxilin gamma(TXLNG)	NM_018360	211.3	232.1	0.0500	1.23
mocs2	molybdenum cofactor synthesis 2(MOCS2)	NM_176806	148.7	104.2	0.0500	0.75
		XM_940734	160.2	110.1	0.0500	0.77
CYP17A1	cytochrome P450 family 17 subfamily A member 1(CYP17A1)	NM_000102	151.7	113.4	0.0500	0.84
GPKOW	G-patch domain and KOW motifs(GPKOW)	NM_015698	122.3	130.7	0.0500	1.21
PURB	purine rich element binding protein B(PURB)	NM_033224	536.6	636	0.0500	1.35
BRSK1	BR serine/threonine kinase 1(BRSK1)	NM_032430	146.6	154.8	0.0500	1.22
CCNT2	cyclin T2(CCNT2)	NM_001241	101.4	109.2	0.0500	1.17
MVP	major vault protein(MVP)	NM_005115	200.5	210.9	0.0500	1.2
DGKQ	diacylglycerol kinase theta(DGKQ)	NM_001347	104.3	110.5	0.0500	1.16
		XM_940726	110.2	91.5	0.0500	0.88

		XM_940726	136.9	109.4	0.0500	0.88
HM13	histocompatibility minor 13(HM13)	NM_178580	132.4	107.8	0.0500	0.87
HM13	histocompatibility minor 13(HM13)	NM_178580	175	143.4	0.0500	0.87
TNPO3	transportin 3(TNPO3)	NM_012470	279.4	297.4	0.0500	1.2
AGFG1	ArfGAP with FG repeats 1(AGFG1)	NM_004504	160.9	183.1	0.0500	1.28
NRAS	neuroblastoma RAS viral oncogene homolog(NRAS)	NM_002524	109	114.3	0.0500	1.15

Supplementary Table 2: Pathways

	-log(p-value)	Ratio	End of Pathway	Direction
Female IUGR Chow versus Female CON Chow				
Oxidative Phosphorylation	**4.330**	**0.092**	**Y**	**D**
Cell Cycle Control of Chromosomal Replication	**4.030**	**0.125**	**Y**	**U**
LXR/RXR Activation	**3.260**	**0.074**	**y**	**D**
Mitochondrial Function	**2.760**	**0.059**	**Y**	**D**
Sirtuin Signaling Pathway	4.820	0.062	N	
FXR/RXR Activation	4.500	0.087	N	
Iron homeostasis signaling pathway	3.500	0.073	N	
EIF2 Signaling	3.300	0.057	N	
Polyamine Regulation in Colon Cancer	3.130	0.182	N	
Extrinsic Prothrombin Activation Pathway	2.490	0.188	N	
Clathrin-mediated Endocytosis Signaling	2.140	0.048	N	

Male IUGR Chow versus Male CON Chow

IGF-1 Signaling	**3.540**	**0.133**	**Y**	**D**
PI3K/AKT Signaling	**3.390**	**0.124**	**Y**	**D**
DNA Double-Strand Break Repair by Non-Homologous End Joining	**2.460**	**0.286**	**Y**	**U**
Role of BRCA1 in DNA Damage Response	**2.350**	**0.125**	**Y**	**U**
Toll-like Receptor Signaling	**2.010**	**0.118**	**Y**	**U**
PTEN Signaling	4.150	0.138	N	
Amyloid Processing	3.920	0.196	N	
Phosphatidylethanolamine Biosynthesis II	3.280	0.444	N	
p53 Signaling	3.030	0.124	N	
ERK5 Signaling	2.830	0.145	N	
PDGF Signaling	2.640	0.122	N	
14-3-3-mediated Signaling	2.600	0.108	N	
Protein Ubiquitination Pathway	2.590	0.089	N	
FAK Signaling	2.320	0.112	N	

p70S6K Signaling	2.170	0.100	N	
Endometrial Cancer Signaling	2.170	0.125	N	
IL-2 Signaling	2.170	0.125	N	
Integrin Signaling	2.040	0.086	N	
Insulin Receptor Signaling	1.990	0.095	N	

Female CON HFCS Diet versus Chow Diet

Hepatic Fibrosis / Hepatic Stellate Cell Activation	**2.59**	**0.0374**	**Y**	**U**
Acute Phase Response Signaling	**2.09**	**0.0341**	**Y**	**D**
LXR/RXR Activation	6.47	0.0826	N	
FXR/RXR Activation	5.35	0.0714	N	
GP6 Signaling Pathway	5.13	0.0672	N	
Atherosclerosis Signaling	4.42	0.063	N	
Intrinsic Prothrombin Activation Pathway	4.25	0.119	N	
Apelin Liver Signaling Pathway	2.68	0.115	N	

Female IUGR HFCS Diet versus Chow Diet

EIF2 Signaling	**13**	**0.115**	**Y**	**D**
mTOR Signaling	**8.86**	**0.0971**	**Y**	**D**
Regulation of eIF4 and p70S6K Signaling	**8.09**	**0.104**	**Y**	**D**
PI3K/AKT Signaling	**3.19**	**0.0692**	**Y**	**D**
p70S6K Signaling	**2.41**	**0.058**	**Y**	**D**
Gap Junction Signaling	**2.4**	**0.0498**	**Y**	**D**
PTEN Signaling	**2.11**	**0.0565**	**Y**	**D**
Adrenomedullin signaling pathway	2.94	0.055	N	
D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis	2.86	0.148	N	
ERK5 Signaling	2.73	0.0845	N	
DNA damage-induced 14-3-3σ Signaling	2.33	0.158	N	
AMPK Signaling	2.19	0.0463	N	
RhoA Signaling	2.11	0.0565	N	
Endocannabinoid Developing Neuron Pathway	2.06	0.0551	N	
Male CON HFCS Diet versus Chow Diet				
Integrin Signaling	**3.63**	**0.0731**	**Y**	**U**
Actin Cytoskeleton Signaling	**3.33**	**0.0687**	**Y**	**U**
PTEN Signaling	**2.79**	**0.0806**	**Y**	**U**

Cholesterol Biosynthesis I	**2.37**	**0.231**	**Y**	**U**
Cholesterol Biosynthesis II (via 24,25-dihydrolanosterol)	**2.37**	**0.231**	**Y**	**U**
Cholesterol Biosynthesis III (via Desmosterol)	**2.37**	**0.231**	**Y**	**U**
ILK Signaling	**2.22**	**0.0609**	**Y**	**U**
FAK Signaling	**2.19**	**0.0762**	**Y**	**U**
Amyloid Processing	2.68	0.118	N	
Cellular Effects of Sildenafil (Viagra)	2.62	0.0763	N	
NRF2-mediated Oxidative Stress Response	2.6	0.065	N	
Adrenomedullin signaling pathway	2.6	0.065	N	
Germ Cell-Sertoli Cell Junction Signaling	2.55	0.067	N	
Corticotropin Releasing Hormone Signaling	2.43	0.0719	N	
RAR Activation	2.34	0.0632	N	
Serotonin Receptor Signaling	2.29	0.116	N	
Melanocyte Development and Pigmentation Signaling	2.24	0.0777	N	
Wnt/β-catenin Signaling	2.23	0.064	N	

IL-8 Signaling	2.12	0.0591	N	
Molecular Mechanisms of Cancer	2.07	0.0482	N	
p53 Signaling	2.05	0.0721	N	
IGF-1 Signaling	2.05	0.0721	N	
Regulation of Actin-based Motility by Rho	2.02	0.0778	N	
Male IUGR HFCS Diet versus Chow Diet				
Mitochondrial Function	**2.44**	**0.076**	**Y**	**U**
Assembly of RNA Polymerase I Complex	**2.23**	**0.25**	**Y**	**D**
RAR Activation	2.46	0.0737	N	
Protein Ubiquitination Pathway	2.25	0.0642	N	
CDK5 Signaling	2.17	0.0857	N	

Supplementary Table 2: Pathways

	Molecules
Female IUGR Chow versus Female CON Chow	
Oxidative Phosphorylation	**SDHA,ATP5PF,NDUFB11,ATP5F1D,NDUFA11,UQCRFS1,NDUFB8,COX7A1,NDUFA1,COX4I1**
Cell Cycle Control of Chromosomal Replication	**CDK12,CDK18,CDC45,CDC6,RPA1,MCM7,ORC1**
LXR/RXR Activation	**APOE,HPX,TTR,ALB,SREBF1,APOA2,GC,FGA,PON3**
Mitochondrial Function	**SDHA,ATP5PF,NDUFB11,ATP5F1D,NDUFA11,UQCRFS1,NDUFB8,COX7A1,NDUFA1,COX4I1**
Sirtuin Signaling Pathway	ATP5PF,PPARA,SDHA,SLC25A4,ATP5F1D,TIMM9,ATG4B,GLUD1,NDUFB8,TIMM23,NDUFA1,PFKM,NDUFB11,GADD45A,SREBF1,NDUFA11,UQCRFS1,GOT2
FXR/RXR Activation	PPARA,APOE,HPX,TTR,ALB,SREBF1,APOA2,AKT3,GC,FGA,PON3
Iron homeostasis signaling pathway	ATP6V1E1,HAMP,HPX,PDGFA,ATP6V0D1,CIAO2B,CIAO2A,ATP6V0E1,PDGFB,SKP2
EIF2 Signaling	RPS6,RPL32,RPL14,RPS15,EIF1,RPS3A,SREBF1,RPLP2,AKT3,RPS21,PPP1CA,RPL36,EIF3M
Polyamine Regulation in Colon Cancer	PSMF1,MXD1,PSMB11,ODC1
Extrinsic Prothrombin Activation Pathway	SERPINC1,FGA,FGG
Clathrin-mediated Endocytosis Signaling	APOE,AP2M1,ALB,ACTR3,FGF18,PDGFA,APOA2,MDM2,UBC,PDGFB

Male IUGR Chow versus Male CON Chow	
IGF-1 Signaling	**RAP2B,NEDD4,CSNK2A1,NRAS,CTGF,MAP2K2,YWHAE,YWHAB,PIK3R1,FOXO3,PIK3R6,PDPK1,SOCS4,CSNK2B,TLR9**
PI3K/AKT Signaling	**RAP2B,TSC1,NRAS,YWHAE,YWHAB,PIK3R1,ITGA2,PDPK1,BCL2,SYNJ1,MAP2K2,LIMS1,FOXO3,INPP5K,GSK3B,ITGA4**
DNA Double-Strand Break Repair by Non-Homologous End Joining	**PRKDC,WRN,XRCC5,LIG3**
Role of BRCA1 in DNA Damage Response	**FANCE,PBRM1,BRD7,POU2F1,RFC4,FANCG,BARD1,MDC1,UIMC1,SMARCC2**
Toll-like Receptor Signaling	**TLR2,TLR10,TICAM1,TLR8,MAP3K7,EIF2AK2,MAPK13,TLR9,UBC**
PTEN Signaling	RAP2B,CSNK2A1,NRAS,PIK3R1,ITGA2,FLT4,PDPK1,BCL2,SYNJ1,MAP2K2,SIRT6,NGFR,FOXO3,GSK3B,CSNK2B,INPP5K,ITGA4
Amyloid Processing	CSNK1E,CAPN5,CSNK2A1,PSENEN,APH1A,CSNK1A1,GSK3B,CSNK2B,MAPK13,CDK5R1
Phosphatidylethanolamine Biosynthesis II	ETNK2,CEPT1,PCYT2,CHKA
p53 Signaling	PRKDC,MED1,PLAGL1,PIK3R1,TNFRSF10B,TLR9,BIRC5,TP53BP2,BCL2,CASP6,PIK3R6,ADGRB1,GSK3B,PML
ERK5 Signaling	RAP2B,NRAS,YWHAE,YWHAB,CREB1,FOXO3,GNAQ,MEF2A,MEF2C,WNK1
PDGF Signaling	RAP2B,CSNK2A1,NRAS,MAP2K2,SYNJ1,PDGFA,PIK3R1,PIK3R6,EIF2AK2,CSNK2B,INPP5K,TLR9
14-3-3-mediated Signaling	RAP2B,TSC1,TUBB3,NRAS,YWHAE,YWHAB,PIK3R1,NOTUM,TLR9,TUBB2B,SRPK2,MAP2K2,PIK3R6,TUBB4A,GSK3B
Protein Ubiquitination Pathway	NEDD4,PSMD9,HSPA9,TRAP1,UBE2Z,FBXW7,USP19,USP1,THOP1,UBE2O,DNAJB14,USP33,SKP2,USP3,PSME1,UBE2D2,USP16,UBE2E3,ANAPC11,UBC,USP49,UBE2D3,UBE2Q2,BIRC2
FAK Signaling	CAPN5,RAP2B,NRAS,ARHGAP26,MAP2K2,ARHGEF7,PIK3R1,ITGA2,PIK3R6,PDPK1,TLR9,ITGA4

p70S6K Signaling	RAP2B,IL2RG,NRAS,YWHAE,F2R,YWHAB,EEF2,PIK3R1,NOTUM,GNAQ,PDPK1,TLR9,MAP2K2,PIK3R6
Endometrial Cancer Signaling	RAP2B,NRAS,MAP2K2,PIK3R1,FOXO3,PIK3R6,PDPK1,GSK3B,TLR9
IL-2 Signaling	RAP2B,CSNK2A1,IL2RG,NRAS,MAP2K2,PIK3R1,PIK3R6,CSNK2B,TLR9
Integrin Signaling	RAP2B,CAPN5,RAPGEF1,ARHGAP26,NRAS,ARF1,ARHGEF7,PIK3R1,ITGA2,MYLK,TLR9,PPP1R12B,MAP2K2,RND3,LIMS1,PIK3R6,GSK3B,ITGB4,ITGA4
Insulin Receptor Signaling	RAP2B,RAPGEF1,TSC1,NRAS,EIF2B4,PIK3R1,PDPK1,TLR9,SYNJ1,MAP2K2,FOXO3,PIK3R6,INPP5K,GSK3B
Female CON HFCS Diet versus Chow Diet	
Hepatic Fibrosis / Hepatic Stellate Cell Activation	**COL1A2,COL5A1,COL1A1,COL6A2,COL6A3,COL6A5,COL3A1**
Acute Phase Response Signaling	**HAMP,HPX,ALB,ORM1,FGB,FGG**
LXR/RXR Activation	SCD,HPX,ALB,ORM1,CD36,FASN,PCYOX1,PLTP,GC,PON3
FXR/RXR Activation	PPARG,HPX,ALB,ORM1,FASN,PCYOX1,PLTP,GC,PON3
GP6 Signaling Pathway	COL1A2,COL5A1,COL1A1,COL6A3,COL6A2,FGB,COL6A5,FGG,COL3A1
Atherosclerosis Signaling	COL1A2,COL1A1,ALB,PLA2G2E,ORM1,CD36,PCYOX1,COL3A1
Intrinsic Prothrombin Activation Pathway	COL1A2,COL1A1,FGB,FGG,COL3A1
Apelin Liver Signaling Pathway	COL1A2,COL1A1,COL3A1
Female IUGR HFCS Diet versus Chow Diet	

EIF2 Signaling	**EIF2B4,RPS3A,PDPK1,RPL7A,RPS4X,RPL7,BCL2,RPS7,PPP1CC,AKT1,EIF4G2,AKT3,RPL36,RPL36AL,ACTB,RPS8,RPS10,RPL23,RPS21,RPL10A,EIF3M,RPS15,RPS27A,RPS15A,RPL6,RPS14**
mTOR Signaling	**RHEB,RPS3A,STK11,RPS8,RPS10,PDPK1,RPS21,RPS4X,EIF3M,RPS7,RPS15,AKT1,EIF4G2,PTPA,AKT3,RPS27A,RPS15A,GNB1L,EIF4B,RPS14**
Regulation of eIF4 and p70S6K Signaling	**EIF2B4,RPS3A,RPS8,RPS10,PDPK1,RPS21,RPS4X,EIF3M,RPS7,RPS15,AKT1,EIF4G2,PTPA,AKT3,RPS27A,RPS15A,RPS14**
PI3K/AKT Signaling	**RHEB,AKT1,YWHAH,PTPA,AKT3,PDPK1,HSP90AA1,JAK3,BCL2**
p70S6K Signaling	**PLCD1,AKT1,YWHAH,PTPA,EEF2,PDPK1,AKT3,PLCD4**
Gap Junction Signaling	**PLCD1,TUBA1A,AKT1,SP3,ACTB,CSNK1G3,AKT3,MAPK7,PLCD4,MAP2K5**
PTEN Signaling	**AKT1,YWHAH,FLT4,AKT3,PDPK1,FASLG,BCL2**
Adrenomedullin signaling pathway	PLCD1,CRCP,IL18,AKT1,MAX,AKT3,MAPK7,PLCD4,RAMP2,MAP2K5,BCL2
D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis	PLCD1,PIP4K2B,PLCD4,PI4KA
ERK5 Signaling	IL6ST,AKT1,YWHAH,CREB1,MAPK7,MAP2K5
DNA damage-induced 14-3-3σ Signaling	AKT1,RAD9A,AKT3
AMPK Signaling	AKT1,PTPA,EEF2,ACTB,STK11,CREB1,AKT3,PDPK1,SMARCD1,GNB1L
RhoA Signaling	NGEF,ACTR3,ACTB,BAIAP2,PIP4K2B,ARHGAP1,PI4KA
Endocannabinoid Developing Neuron Pathway	AKT1,CREB1,AKT3,MAPK7,GNG5,GNB1L,MAP2K5
Male CON HFCS Diet versus Chow Diet	
Integrin Signaling	**ITGB1,ARHGAP26,MPRIP,ILK,MYLK,CRK,RAC3,MYL9,PTK2,CAPNS1,MAP2K2,RHOT1,TSPAN1,FGFR4,PFN2,VCL**
Actin Cytoskeleton Signaling	**PTK2,MYL9,ITGB1,MYH10,MPRIP,MAP2K2,F2R,PDGFA,FGFR4,FGF12,PFN2,MYLK,CRK,VCL,RAC3,FGF13**
PTEN Signaling	**ITGB1,PTK2,CSNK2A1,SHARPIN,MAP2K2,FGFR4,FLT4,FOXO3,ILK,RAC3**

Cholesterol Biosynthesis I	**SQLE,DHCR7,MSMO1**
Cholesterol Biosynthesis II (via 24,25-dihydrolanosterol)	**SQLE,DHCR7,MSMO1**
Cholesterol Biosynthesis III (via Desmosterol)	**SQLE,DHCR7,MSMO1**
ILK Signaling	**ITGB1,MYL9,PTK2,FOS,MYH10,RHOT1,FGFR4,PPP2R2B,ILK,VCL,PTGS2,HIF1A**
FAK Signaling	**ITGB1,PTK2,ARHGAP26,CAPNS1,MAP2K2,FGFR4,CRK,VCL**
Amyloid Processing	CSNK1E,CSNK2A1,CAPNS1,PRKAR2A,APP,PSEN1
Cellular Effects of Sildenafil (Viagra)	MYL9,CALM1 (includes others),MYH10,ADCY9,MPRIP,ADCY6,PRKAR2A,MYLK,KCNH2,GUCY1B1
NRF2-mediated Oxidative Stress Response	FOS,AKR7A3,MAP2K2,FGFR4,GSTM4,SLC35A2,JUND,DNAJC10,DNAJB6,UBE2E3,JUNB,FKBP5,ABCC4
Adrenomedullin signaling pathway	PTK2,ADCY9,FOS,CALM1 (includes others),MAP2K2,FGFR4,ADCY6,PRKAR2A,MYLK,CFH,HIF1A,KCNH2,GUCY1B1
Germ Cell-Sertoli Cell Junction Signaling	ITGB1,PTK2,TUBB6,MAP2K2,RHOT1,FGFR4,ILK,TUBB4A,VCL,RAC3,MAP3K3,CTNND1
Corticotropin Releasing Hormone Signaling	FOS,CALM1 (includes others),ADCY9,MAP2K2,ADCY6,PRKAR2A,JUND,PTGS2,CACNA2D4,GUCY1B1
RAR Activation	FOS,ADCY9,ADH7,LRAT,CSNK2A1,RARB,ADCY6,PRKAR2A,PML,STAT5B,RBP1,PRMT1
Serotonin Receptor Signaling	ADCY9,HTR2B,SMOX,HTR3A,ADCY6
Melanocyte Development and Pigmentation Signaling	KITLG,ADCY9,MAP2K2,FGFR4,RPS6KA3,ADCY6,PRKAR2A,CRK
Wnt/β-catenin Signaling	CSNK1E,SOX4,CSNK2A1,APPL2,DKK3,CSNK1G3,MARK2,PPP2R2B,RARB,ILK,FZD1

IL-8 Signaling	RAB11FIP2,MYL9,PTK2,FOS,ANGPT2,NAPEPLD,MAP2K2,RHOT1,FGFR4,FLT4,PTGS2,RAC3
Molecular Mechanisms of Cancer	ITGB1,HAT1,PRKAR2A,ADCY6,CRK,HIF1A,FZD1,RAC3,PTK2,ADCY9,FOS,CASP6,CDK8,MAP2K2,RHOT1,FGFR4,CAMK2B,CTNND1,PSEN1
p53 Signaling	CASP6,GADD45B,STAG1,FGFR4,ADGRB1,HIF1A,PML,ST13
IGF-1 Signaling	PTK2,FOS,CSNK2A1,MAP2K2,FGFR4,FOXO3,PRKAR2A,SOCS5
Regulation of Actin-based Motility by Rho	ITGB1,MYL9,MPRIP,RHOT1,PFN2,MYLK,RAC3
Male IUGR HFCS Diet versus Chow Diet	
Mitochondrial Function	**GSR,PDHA1,ATP5PF,NDUFB11,NDUFA9,APH1A,MAPK10,COX5A,NDUFA12,UQCR11,ATP5S,BCL2,UQCRB**
Assembly of RNA Polymerase I Complex	**TAF1C,TBP,UBTF**
RAR Activation	PBRM1,RDH10,ADCY6,PDPK1,SMARCD1,SMARCD3,ADH7,IGFBP3,MAPK10,SORBS3,CSNK2B,ADCY10,PML,SMAD1
Protein Ubiquitination Pathway	PSMD9,HSPA6,UBE2V2,FBXW7,PSMD3,DNAJA1,DNAJB14,UBE2D2,PSME1,UBE2B,PSMC6,PSMB2,USP16,USP47,ANAPC5,UBE2E3,UBC
CDK5 Signaling	GNAS,PPP2R3A,PPP2CA,ADCY6,MAPK10,PPP2R2C,MAPK7,ADCY10,GNAL

Supplementary Table 3: Causal Networks

Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target Molecules in Dataset
Female IUGR Chow vs Female CON Chow						
RB1	1.152	transcription regulator	Inhibited	-2.358	3.65E-03	CDC6,CLDN3,COX4I1,EI24,HSBP1,MCM7,MRPL11,MRPL53,MYL6B,NDUFB8
HOXA10		transcription regulator	Activated	2	4.76E-02	APOE,CYBB,HOXA11,KLF10,NDRG2
Male IUGR Chow vs Male CON Chow						
None						
Female CON HFCS Diet versus Chow Diet						
MED13	-1.03	transcription regulator	Inhibited	-2.236	3.35E-09	CD36,CIDEA,CIDEC,FASN,GPD1,PPARG,SCD,THRSP
AHR	1.166	ligand-dependent nuclear receptor	Inhibited	-2.284	2.33E-07	CDKN2C,COL1A1,COL1A2,COL3A1,COL5A1,COL6A3,FABP4,FBLN2,GAS1,GPAM
FBXW7	-1.044	enzyme	Inhibited	-2.216	1.00E-06	CD36,CIDEC,FABP4,GPAM,HSPE1,PPARG
HAND2		transcription regulator	Inhibited	-2.213	6.05E-05	COL1A1,COL1A2,COL3A1,ECM2,FAP
TBX5		transcription regulator	Inhibited	-2.213	8.48E-05	COL1A1,COL1A2,COL3A1,ECM2,FAP
EOMES	1.002	transcription regulator	Inhibited	-2	4.54E-04	ANXA1,COL3A1,COL6A3,PMP22,SOX2
MYOCD	1.032	transcription regulator	Inhibited	-2.213	6.86E-04	COL1A1,COL1A2,COL3A1,ECM2,FAP
GATA4	1.081	transcription regulator	Inhibited	-2.213	2.80E-03	COL1A1,COL1A2,COL3A1,CTHRC1,ECM2,FAP
SPDEF		transcription regulator	Inhibited	-2	3.67E-03	COL1A1,COL5A1,COL6A2,COL6A3

PPARA	-1.069	ligand-dependent nuclear receptor	Activated	2.453	5.43E-09	CD36,CDKN2C,CEACAM1,CIDEA,CIDEC,ELOVL5,FABP4,FABP5,FASN,FGB
IGF2BP1	-1.232	translation regulator	Activated	2.449	1.58E-08	COL1A1,COL1A2,COL5A1,COL6A2,COL6A3,LGALS1
SREBF1	-1.086	transcription regulator	Activated	2.928	1.36E-07	ACLY,ALDOC,CIDEA,FABP5,FASN,GCK,GPAM,NSDHL,PLTP,PMP22
PPARG	2.294	ligand-dependent nuclear receptor	Activated	2.959	2.41E-07	ACLY,AGPAT2,CAV1,CAV2,CD36,CIDEA,CIDEC,COL1A1,COL1A2,FABP4
KLF15	1.118	transcription regulator	Activated	2.355	1.69E-06	CD36,FABP5,FASN,GPAM,PPARG,SCD
SREBF2	-1.001	transcription regulator	Activated	2.599	2.82E-06	ACLY,ALDOC,FABP5,FASN,NSDHL,SCD,THRSP
TP53	1.075	transcription regulator	Activated	2.719	1.46E-05	ACLY,ANXA1,ANXA8/ANXA8L1,CAV1,CAV2,COL1A1,COL1A2,COL3A1,COL6A2,FABP4
NR1I2		ligand-dependent nuclear receptor	Activated	2.104	1.20E-02	CD36,FASN,GSTM5,PPARG,SCD
Female IUGR HFCS Diet versus Chow Diet						
SMARCA4	-1.095	transcription regulator	Activated	2.111	3.54E-02	ARL16,CDK20,CLK1,GPX1,HNMT,HYI,ITGA7,KHDRBS3,MAFF,MT1H
Male CON HFCS Diet versus Chow Diet						
CREB1	1.188	transcription regulator	Activated	2.159	3.45E-04	AVP,CH25H,FOS,GADD45B,INHA,JUNB,MSMO1,PSEN1,PTGS2,RHEB
AR	-1.297	ligand-dependent nuclear receptor	Activated	2.092	7.49E-03	ABCC4,AMD1,CALU,CCDC85B,CCT3,CLDN11,CLSTN1,DHCR7,DSC2,FKBP5
CREM		transcription regulator	Activated	2.207	1.21E-02	CH25H,FOS,GADD45B,INHA,JUNB,MSMO1,SERTAD1,SPTY2D1

SMAD3		transcription regulator	Activated	2.916	1.84E-02	FOS,INHA,ITGB1,JUNB,JUND,mir-21,PTGS2,TBX3,TNC
SRF	1.216	transcription regulator	Activated	2.195	3.12E-02	CAPRIN1,EIF6,FHL2,FOS,ITGB1,JUNB,MYL9,MYLK,PTGS2,TAGLN
Male IUGR HFCS Diet versus Chow Diet						
PARP1	-1.867	enzyme	Inhibited	-2.588	3.09E-02	GBP6,ICAM1,OPRM1,POU2F1,TGFA,TLR9,TNFRSF10B

Supplementary Table 4. Normalized and transformed values of identified metabolites F=female, M=male, CON

Metabolite	**Unique mass**	**RT_dim1(sec)**	**RT_dim2(sec)**	**F1_CON_0**	**F2_CON_0**
Pentanoic acid, trimethylsilyl ester	75	590	1.33	20340	2250
Decane	57	630	1.18	5930	6970
Decanoic acid, trimethylsilyl ester	147	635	1.05	300	380
Benzene, 1,2,3-trimethyl-	105	640	1.99	900	1210
Ethanedioic acid, bis(trimethylsilyl) ester	147	645	1.11	1200	2030
Indane	117	655	2.22	330	440
3-t-Pentylcyclopentanone	69	670	1.25	#N/A	#N/A
2-Hepten-4-one, 6-methyl-	69	680	1.29	#N/A	#N/A
Tridecane	57	685	1.18	750	470
Benzene, 2-ethyl-1,4-dimethyl-/Benzene, 4-ethyl-1,2-dimethyl-	119	700	1.88	1790	2240
2H-Pyran-2-one, tetrahydro-6-methyl-	42	700	4.4	1430	1680
2,4,6,8-Tetramethyl-1-undecene	57	720	1.2	1220	1070
N,N-Dimethyloctylamine/3-Buten-1-amine, N,N-dimethyl-	58	790	1.39	920	1280
Propanoic acid, 2-oxo-3-(trimethylsilyl)-, trimethylsilyl ester	119	795	2.02	#N/A	#N/A
Heptanoic acid, trimethylsilyl ester	75	890	1.49	1220	980
2-Methoxyphenol trimethylsilyl ether	166	970	2.11	1230	1010
Urea, N,N'-bis(trimethylsilyl)-	147	990	1.98	260	460
3-Ethylphenol, trimethylsilyl ether	179	995	1.82	1000	880
Benzeneacetic acid, trimethylsilyl ester	73	1075	2.28	41110	61820
1,2-Benzenediol bis(trimethylsilyl) ether	73	1135	1.64	1640	4010
3-Octenoic acid, trimethylsilyl ester	73	1190	1.61	#N/A	750
4-Methylcatechol, bis(trimethylsilyl) ether	73	1255	1.61	#N/A	#N/A
Benzenepropanoic acid, trimethylsilyl ester	104	1265	2.22	3300	3860
Mercaptoacetic acid, bis(trimethylsilyl)-	73	1330	0.97	#N/A	#N/A

Benzenepropanoic acid, 4-[(trimethylsilyl)oxy]-‡-[[(trimethylsilyl)oxy]imino]-, trimethylsilyl ester	75	1350	1.52	#N/A	#N/A
Benzoic acid, 2-[(trimethylsilyl)oxy]-, trimethylsilyl ester	73	1420	1.91	1700	900
Trimethylsilyl 2,4-dichlorobenzoate	173	1460	2.28	1140	1230
Benzenepropanoic acid, ‡-[(trimethylsilyl)oxy]-, trimethylsilyl ester	73	1530	1.78	1010	430
3-Phenyl-3-trimethylsilyloxypropanoic acid, trimethylsilyl ester	73	1545	1.75	380	710
Benzeneacetic acid, 3-[(trimethylsilyl)oxy]-, trimethylsilyl ester/Benzeneacetic acid, 4-[(trimethylsilyl)oxy]-, trimethylsilyl ester	73	1595	1.94	640	740
3-Phenyl-3-(trimethylsilyloxy)butan-2-one	73	1605	1.84	400	460
Dodecanoic acid, trimethylsilyl ester	75	1620	1.55	280	130
Benzene, 1,2,3,4-tetramethyl-	73	1685	2.18	#N/A	#N/A
1-Pentadecanamine, N,N-dimethyl-	58	1690	1.53	5930	13880
1-Octanamine, N-methyl-N-octyl-	58	1725	1.5	890	1450
n-Tridecanoic acid, trimethylsilyl ester	73	1750	1.54	#N/A	100
Azelaic acid, bis(trimethylsilyl) ester	75	1800	1.72	1110	1710
Glycine, N-benzoyl-, trimethylsilyl ester	105	1815	3.26	2940	4900
Benzenepropanoic acid, 3-methoxy-4[(trimethylsilyl)oxy]-, trimethylsilyl ester	73	1910	2.1	2130	940
n-Pentadecanoic acid, trimethylsilyl ester	75	1945	1.53	140	240
1H-Indole-3-acetic acid, 1-(trimethylsilyl)-, trimethylsilyl ester	202	1975	2.7	30360	36110
Dodecanedioic acid, bis(trimethylsilyl) ester	73	1980	1.61	10	2730
1,11-Undecanedioic acid, di(trimethylsilyl) ester	73	2030	1.72	450	660
1H-Indole-3-propanoic acid, 1-(trimethylsilyl)-, trimethylsilyl ester	73	2115	2.52	400	580
N-Methyl-N-benzyltetradecanamine	91	2155	2.04	190	220

L-Tryptophan, N,1-bis(trimethylsilyl)-, trimethylsilyl ester	73	2235	2.05	#N/A	260
9,12-Octadecadienoic acid (Z,Z)-, trimethylsilyl ester	75	2265	1.77	3360	5130
trans-9-Octadecenoic acid, trimethylsilyl ester	129	2275	1.69	2530	30100
Octadecanoic acid, trimethylsilyl ester	341	2305	1.6	202050	136170
Arachidonic acid, trimethylsilyl ester	75	2415	1.94	#N/A	320
Sebacic acid, bis(trimethylsilyl) ester	73	2495	1.47	2250	2460
Hexanoic acid, trimethylsilyl ester	73	2510	1.47	650	230
Tetracosanoic acid, trimethylsilyl ester	117	2840	1.67	190	210
Cholesterol trimethylsilyl ether	129	3080	2.23	1650	5820

= Control, IUGR = Interuterine Growth Restricted, 0 = Chow Diet, 7 = HFCS diet.

F3_CON_0	F1_IUGR_0	F2_IUGR_0	F3_IUGR_0	M1_CON_0	M2_CON_0	M3_CON_0	M1_IUGR_0	M3_IUGR_0
14080	4700	12900	4710	3190	1740	55450	#N/A	2920
9720	12680	14330	10110	11700	21150	34050	58760	13930
950	1120	#N/A	750	#N/A	1160	1560	#N/A	470
1720	2100	2390	1660	3490	3290	5520	8150	2060
2700	#N/A	5210	#N/A	6820	#N/A	#N/A	9990	4400
640	770	910	620	1170	1210	2070	2710	740
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
530	1520	1800	750	1190	1830	2820	5020	1580
2960	3960	4650	3230	1520	5580	9110	14640	3740
4120	1180	3770	840	7450	1930	770	10980	400
1980	2450	3150	1030	#N/A	#N/A	#N/A	#N/A	#N/A
5730	2740	3130	1640	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
3310	10	1160	1290	#N/A	1230	3260	#N/A	280
610	690	440	1060	#N/A	#N/A	#N/A	#N/A	#N/A
910	270	#N/A	#N/A	3670	#N/A	#N/A	6720	2050
2990	2840	2790	500	1470	#N/A	4480	2610	1930
79030	27840	46200	61650	79340	13050	60420	4870	45250
8470	6820	3790	5330	2480	19070	31360	1560	2410
3080	490	#N/A	730	#N/A	1330	1600	#N/A	1100
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
4070	1730	3760	1690	2340	#N/A	14320	3210	1510
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A

#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
2260	850	1440	760	4670	1250	3920	20370	3740
5700	1440	2360	1390	4020	1950	10600	3620	8120
2500	580	1280	7610	2430	18500	3510	10330	4330
1340	500	830	#N/A	2110	#N/A	1470	2890	2250
1400	#N/A	#N/A	960	2160	1870	3640	2790	2180
500	#N/A	#N/A	290	#N/A	#N/A	#N/A	#N/A	#N/A
830	430	380	420	350	620	2040	#N/A	290
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
21830	21030	10400	10910	4040	17870	#N/A	4350	3900
7440	2890	3120	1940	5150	6430	#N/A	4460	3310
350	260	#N/A	100	#N/A	#N/A	#N/A	#N/A	#N/A
3950	850	1790	1110	1750	910	5110	#N/A	3360
11790	3530	10200	2170	15620	1640	17760	#N/A	32690
2740	740	700	1480	7860	2760	2390	4600	3540
280	270	320	490	#N/A	#N/A	#N/A	#N/A	#N/A
39760	11890	56080	28830	90110	80290	58760	68830	80450
3200	1970	2180	220	5330	#N/A	1120	2180	4320
1050	510	550	510	#N/A	#N/A	#N/A	#N/A	#N/A
1060	650	790	310	780	#N/A	#N/A	#N/A	1110
1320	280	280	180	#N/A	#N/A	#N/A	#N/A	#N/A

510	#N/A	#N/A	280	1000	#N/A	#N/A	1500	900
20620	8100	2370	5500	#N/A	#N/A	#N/A	#N/A	#N/A
12770	42790	5390	5050	7090	22420	#N/A	7090	17090
5100	152790	118920	167840	40780	51910	#N/A	63300	83360
600	780	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
9920	3310	1940	4470	#N/A	#N/A	#N/A	#N/A	#N/A
1240	230	270	440	#N/A	#N/A	#N/A	#N/A	#N/A
230	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
2620	4810	1930	1440	1100	#N/A	#N/A	#N/A	620

F1_CON_7	F2_CON_7	F3_CON_7	F1_IUGR_7	F2_IUGR_7	F3_IUGR_7	M1_CON_7	M2_CON_7	M3_CON_7
34490	4610	12340	5150	51530	6850	#N/A	3700	1690
10430	18050	17210	17720	11050	18310	37830	26510	8570
#N/A	670	850	810	800	750	860	1270	870
1590	2300	2870	2830	2790	2690	5830	4150	2850
2790	6580	10480	4740	6870	3690	90	21020	7250
610	200	1080	960	1140	1040	2150	1590	1080
1760	1110	2590	1170	2540	1240	#N/A	4220	#N/A
#N/A	#N/A	1320	#N/A	#N/A	#N/A	2940	2050	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
2980	1220	4890	4930	1200	4030	10040	7290	1790
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
3010	19140	14560	12340	9430	16820	4130	5210	4440
800	1750	3660	1490	2150	1310	2710	5280	2260
1520	1820	4800	2830	7260	2420	#N/A	3280	2760
920	#N/A	550	#N/A	#N/A	990	#N/A	#N/A	980
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
1870	270	1600	1090	2100	1390	700	1730	1660
124190	8220	50380	84580	33830	52880	32370	20330	62060
5570	14900	17290	12190	4080	23240	1920	8070	2720
#N/A	2460	1310	#N/A	610	610	#N/A	790	11970
#N/A	#N/A	2020	1620	870	1230	#N/A	1040	#N/A
7920	880	5930	2550	5910	2690	3310	1290	1510
#N/A	#N/A	380	#N/A	#N/A	570	410	#N/A	#N/A

#N/A	3540	1660	1370	#N/A	1540	#N/A	#N/A	40
1650	1330	2070	1290	#N/A	1910	4200	2930	5090
740	7280	4190	7770	4440	2010	3270	14930	7950
#N/A	#N/A	660	500	#N/A	890	4740	4060	1770
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	340	930	#N/A	510	670	2750	2350	2200
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
580	930	420	1270	710	1320	1670	840	1350
3530	4610	5800	5650	5210	4980	11920	8350	6060
15380	27570	24490	20410	22620	38450	4760	16390	13610
890	2570	12830	8160	6940	3100	4340	5050	4400
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
630	790	3190	860	670	1450	4260	3950	6560
950	1430	4500	2840	2560	5240	17850	19770	32400
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
33780	33670	15570	22290	18990	18540	163420	106450	92210
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A

#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
14520	#N/A	1780	1550	6320	2000	#N/A	1280	1810
12830	1760	5190	3180	1750	3570	1150	3770	3480
26260	3830	7910	3180	51570	5500	2100	4770	4560
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
930	#N/A	900	#N/A	4120	600	#N/A	800	330
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
7230	710	5590	2840	5020	1500	#N/A	#N/A	4640

M1_IUGR_7	M2_IUGR_7	M3_IUGR_7
2290	60	#N/A
15420	29650	28400
#N/A	740	740
2320	4190	4020
2130	1710	3480
780	1580	1540
3300	#N/A	#N/A
#N/A	#N/A	2020
#N/A	#N/A	#N/A
4020	7750	6670
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
7980	15730	12050
1040	2260	1870
1860	2560	2120
#N/A	1130	#N/A
#N/A	#N/A	#N/A
600	1140	#N/A
20800	11480	16320
4830	15600	4980
1980	1110	910
#N/A	3610	870
#N/A	#N/A	440
470	680	560

#N/A	1300	#N/A
3060	2060	4420
151220	9160	12000
1480	#N/A	3640
#N/A	#N/A	#N/A
1880	970	3270
#N/A	#N/A	#N/A
270	790	400
4800	9110	8560
7090	31410	4860
9130	12690	12380
#N/A	#N/A	#N/A
2680	1710	3880
7130	5230	10870
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
38360	58870	163330
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A

#N/A	#N/A	#N/A
610	970	#N/A
1540	2530	610
1920	4780	830
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
#N/A	#N/A	#N/A
#N/A	820	#N/A

Supplementary Table 5. Identifiers of metabolites including NIST Identifier, common name, HMDB ID, KEGG ID, PubChem ID, Class

NIST Identifier	Common Name	HMDB	KEGG	PubChem	Chemical class	Pathway
Pentanoic acid, trimethylsilyl ester	Valeric acid	HMDB0000892	C00803	7991	Fatty Acid	NA
Decane	Decane	HMDB0031450	NA	15600	Hydrocarbon	NA
Benzene, 1,2,3-trimethyl-	Hemimellitene	HMDB0059901	NA	10686	benzenoid	Degradation of Aromatic Compounds
Ethanedioic acid, bis(trimethylsilyl) ester	oxalic acid	HMDB0002329	C00209	971	carboxylic acid	metabolism of glyocylic acid and ascorbic acid excreted in urine
Indane	Indane	HMDB0059837	NA	10326	benzenoid	Degradation of Aromatic Compounds
3-Ethylphenol, trimethylsilyl ether	3-Ethylphenol	HMDB0059873	C14386	6997	benzenoid	Degradation of Aromatic Compounds
Benzene, 2-ethyl-1,4-dimethyl-	2-ethyl-p-xylene	HMDB0059890 (Predicted)	NA	15653	benzenoid	Degradation of Aromatic Compounds
Heptanoic acid, trimethylsilyl ester	Heptanoic acid	HMDB0000666	C17714	8094	carboxylic acid	NA
Benzeneacetic acid, trimethylsilyl ester	Phenylacetic acid	HMDB00209	C07086	999	carboxylic acid	Phenylalanine metabolism
1,2-Benzenediol bis(trimethylsilyl) ether	pyrocatechol	HMDB00957	C00090	289	benzenoid	Aminobenzoate degradation
Benzoic acid, 2-[(trimethylsilyl)oxy]-, trimethylsilyl ester	salicylic acid	HMDB01895	C00805	338	carboxylic acid	Phenylalanine metabolism
Dodecanoic acid, trimethylsilyl ester	Lauric acid	HMDB00638	C02679	3893	Fatty Acid	fatty acid synthesis
1-Pentadecanamine, N,N-dimethyl-	N,N-dimethyl-1-Pentadecanamine	No result	NA	87232	amine	NA
1-Octanamine, N-methyl-N-octyl-	N-methyl-N-octyl-1-Octanamine	No result	NA	78202	amine	NA

Azelaic acid, bis(trimethylsilyl) ester	nonanedioic acid	HMDB00784	C08261	2266	Fatty Acid	NA
Glycine, N-benzoyl-, trimethylsilyl ester	hippuric acid	HMDB00714	C01586	464	carboxylic acid	Phenylalanine metabolism
1H-Indole-3-acetic acid, 1-(trimethylsilyl)-, trimethylsilyl ester	Indoleacetic acid	HMDB00197	C00954	802	Indoles	tryptophan metabolism
trans-9-Octadecenoic acid, trimethylsilyl ester	Elaidic acid	HMDB0000573	C00712	445639	Fatty acid	Biosynthesis of unsaturated fatty acids
Octadecanoic acid, trimethylsilyl ester	Stearic acid	HMDB00827	C01530	5281	Fatty acid	Biosynthesis of unsaturated fatty acids
N,N-Dimethyloctylamine	N,N-Dimethyloctylamine	No result	NA	16224	amine	NA
Benzenepropanoic acid, trimethylsilyl ester	hydrocinnamic acid	HMDB00764	C05629	107	phenylpropanoids	phenyalanine metablism
Benzeneacetic acid, 3-[(trimethylsilyl)oxy]-, trimethylsilyl ester	3-hydroxyphenylacetic acid	HMDB0000440	C05593	12122	phenol	tyrosine metabolism associated with phenylketonuria
3-Octenoic acid, trimethylsilyl ester	(Z)-3-Octenoic acid	No result	NA	5282716	Fatty Acid	NA
Benzenepropanoic acid, ‡-[(trimethylsilyl)oxy]-, trimethylsilyl ester	Phenyllactic acid	HMDB0000779	C01479	3848	phenylpropanoids	phenyalanine metablism
Cholesterol trimethylsilyl ether	Cholesterol	HMDB0000067	C00187	11025495	sterol	Steroid biosynthesis
N-Methyl-N-benzyltetradecanamine	N-Methyl-N-benzyltetradecanamine	No result	NA	584166	amine	NA
Trimethylsilyl 2,4-dichlorobenzoate	2,4-dichlorobenzoate	No result	NA	5787	benzenoid	Degradation of Aromatic Compounds
Decanoic acid, trimethylsilyl ester	Capric acid	HMDB000511	NA	2669	dicarboxylic acid	normal uninary acid

9,12-Octadecadienoic acid (Z,Z)-, trimethylsilyl ester	Linoleic acid	HMDB00673	C01595	5280450	Fatty Acid	Linoleic acid metabolism/Biosynthesis of unsaturated fatty acids
2-Methoxyphenol trimethylsilyl ether	Catechol mono methyl ester	HMDB01398	C01502	460	benzenoid	Aminobenzoate degradation
Sebacic acid, bis(trimethylsilyl) ester	Decanedioic acid	HMDB00792	C08277	5192	Fatty Acid	NA
Propanoic acid, 2-oxo-3-(trimethylsilyl)-, trimethylsilyl ester	(S)3-hydroxyisobutyric acid (3-HIBA)	HMDB0000023	C06001	440873	hydroxy acid	Valine, leucine and isolucine degradation
Benzene, 1,2,3,4-tetramethyl-	prehnitene	HMDB0059823	NA	10236	benzenoid	Degradation of Aromatic Compounds
Benzenepropanoic acid, 4-[(trimethylsilyl)oxy]-‡-[[(trimethylsilyl)oxy]imino]-, trimethylsilyl ester	4-Hydroxyphenylpyruvic acid (4-HPPA)	HMDB0000707	C01179	979	benzenoid	Phenylalanine, tyrosine and tryptophan biosynthesis/ Ubiquinone and other terpenoid-quinone biosynthesis
3-t-Pentylcyclopentanone	3-t-Pentylcyclopentanone	No result	NA	551379	Ketone	NA
2-Hepten-4-one, 6-methyl-	6-methyl-2-Hepten-4-one	No result	NA	12502788	Ketone	NA
4-Methylcatechol, bis(trimethylsilyl) ether	4-methylcatechol	HMDB0000873	C06730	9958	benzenoid	Benzoate degradation/Degradation of Aromatic Compounds
Mercaptoacetic acid, bis(trimethylsilyl)-	Mercaptoacetic acid	No result	C02086	1133	carboxylic acid	NA
2H-Pyran-2-one, tetrahydro-6-methyl-	delta Hexalactone	HMDB0000453	NA	13204	lactons	NA
Benzenepropanoic acid, 3-methoxy-4[(trimethylsilyl)oxy]-, trimethylsilyl ester	dihydroferulic acid 3-(4-hydroxy-3-methoxyphenyl) propanoic acid	HMDB0062121	NA	14340	phenylpropanoids	NA

1H-Indole-3-propanoic acid, 1-(trimethylsilyl)-, trimethylsilyl ester	Indole-3-propionic acid	HMDB0002302	NA	3744	Indoles	tryptophan metabolism
Tridecane	Tridecane	HMDB0034284	C13834	12388	hydrocarbons	NA
3-Phenyl-3-trimethylsilyloxypropanoic acid, trimethylsilyl ester	3-hydroxy-3-phenylpropanoic acid	HMDB0124925 (predicted)	NA	92959	phenylpropanoids	related to phenyl pyruvic acid metabolism
Urea, N,N'-bis(trimethylsilyl)-	Urea	HMDB00294	C00086	1176	amide	Arginine biosynthesis
3-Phenyl-3-(trimethylsilyloxy)butan-2-one	3-hydroxy-3-phenylbutan-2-one	No result	NA	233220	ketone	NA
L-Tryptophan, N,1-bis(trimethylsilyl)-, trimethylsilyl ester	L-Tryptophan	HMDB00929	C00078	6305	amino acid	tryptophan metabolism
1,11-Undecanedioic acid, di(trimethylsilyl) ester	Undecanedioic acid	HMDB00888	NA	15816	Fatty Acid	NA
Dodecanedioic acid, bis(trimethylsilyl) ester	Dodecanedioic acid	HMDB0000623	C02678	12736	Fatty Acid	NA
n-Pentadecanoic acid, trimethylsilyl ester	Pentadecanoic acid	HMDB0000826	C16537	13849	Fatty acid	NA
Hexanoic acid, trimethylsilyl ester	caproic acid	HMDB0000535	C01585	8892	Fatty Acid	Beta Oxidation of Very Long Chain Fatty Acids
2,4,6,8-Tetramethyl-1-undecene	2,4,6,8-Tetramethyl-1-undecene	No result	NA	536235	Hydrocarbon	NA
n-Tridecanoic acid, trimethylsilyl ester	Tridecanoic acid	HMDB00910	C17076	12530	Fatty Acid	NA
Arachidonic acid, trimethylsilyl ester	Arachidonic acid	HMDB01043	C00219	444899	Fatty Acid	Biosynthesis of unsaturated fatty acids
Tetracosanoic acid, trimethylsilyl ester	lignoceric acid	HMDB0002003	C08320	11197	Fatty Acid	Biosynthesis of unsaturated fatty acids

and Pathway. X = present in all animals, O = not present in all animals.

F CON Chow	F IUGR Chow	M CON Chow	M IUGR Chow	F CON HFCS	F IUGR HFCS	M CON HFCS	M IUGR HFCS
X	X	X	O	X	X	O	O
X	X	X	X	X	X	X	X
X	X	X	X	X	X	X	X
X	O	O	X	X	X	X	X
X	X	X	X	X	X	X	X
X	X	O	X	X	X	X	O
X	X	X	X	X	X	X	X
X	X	X	O	X	X	O	X
X	X	X	X	X	X	X	X
X	X	X	X	X	X	X	X
X	X	X	X	X	O	X	X
X	X	X	O	X	X	X	X
X	X	O	X	X	X	X	X
X	X	O	X	X	X	X	X

X X X O X X X X
X X X O X X X X

X X X X X X X X
X X O X X X X X
X X O X X X X X

X X O O X X X X
X X O X X X X O

X O X X O O X X
O O O O O O O X

X X X X O X O O
X X O O X X O O

X X X X X X O X

X X X X X X X X
O O O O O X X O

X	X		O	O	X	O	O
X	X	O	O	O	O	O	O
X	X			O	O	O	O
				X	X	X	X
				X	X	X	X
				O	O	O	O
				X	X	O	O
				X	O	X	O
				O	X	O	O
				O	X	O	X
X	X	X	X				
X	X	X	X				

X	X	O	O
X	X	X	X
X	O	O	X
X	O	O	X
X	O	O	O
O	O	O	X
X	X	O	O
X	X	O	O
X	X		
X	X		
X	X		
O	O		
O	O		
X			

Supplementary Table 6: HFCS Diet vs Chow Diet Gene

Gene Symbol	Gene Name	Accession No.	CON Chow F Mean	CON HFHS F Mean	p-val CON F HFHS vs. CON F Chow	Ratio CON F HFHS vs. CON F Chow	REFSEQ ID	NEPHRON (MEAN RPKM)	COLLECTING DUCT (MEAN RPKM)
COL6A3	collagen type VI alpha 3 chain(COL6A3)	NM_004369	103.1	136.4	0.00078	1.288			
ACLY	ATP citrate lyase(ACLY)	NM_001096	317	434.6	0.00096	1.374			
		BQ186959	111.6	101.8	0.00115	0.891			
NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	NM_002530	102.8	119.4	0.0013	1.13			
		XM_944079	122.9	159.3	0.00131	1.257			
PPP1CA	protein phosphatase 1 catalytic subunit alpha(PPP1CA)	NM_002708	121.5	107.1	0.00182	0.861			
		AW081577	104.5	123.6	0.00203	1.156			
		XM_944499	109.3	100.2	0.0026	0.897			
C1QTNF6	C1q and tumor necrosis factor related protein 6(C1QTNF6)	NM_031910	106.2	114.9	0.00271	1.136	NM_017193	356.13	8.18
C1QTNF6	C1q and tumor necrosis factor related protein 6(C1QTNF6)	NM_031910	110.3	128.7	0.00271	1.136	NM_017193	356.13	8.18

SMAGP	small cell adhesion glycoprotein(SMAGP)	NM_001033873	190.5	156.5	0.00286	0.813	NM_017193	356.13	8.18
SIDT2	SID1 transmembrane family member 2(SIDT2)	NM_001040455	350	417.7	0.00289	1.205	NM_017193	356.13	8.18
FAP	fibroblast activation protein alpha(FAP)	NM_004460	96.4	127.9	0.0029	1.298			
ISPD	isoprenoid synthase domain containing(ISPD)	NM_001101417	118.8	104	0.00308	0.854			
		XM_941979	99.2	125.3	0.00341	1.217			
ABCA9	ATP binding cassette subfamily A member 9(ABCA9)	NM_080283	115.9	144.3	0.00348	1.218			
CEP63	centrosomal protein 63(CEP63)	NM_025180	139.3	186.9	0.00359	1.326			
SCD	stearoyl-CoA desaturase(SCD)	NM_005063	116.4	281.9	0.00363	2.346			
CD248	CD248 molecule(CD248)	NM_020404	120.3	190.8	0.00367	1.546			
DCUN1D5	defective in cullin neddylation 1 domain containing 5(DCUN1D5)	AK094744	121.4	108.2	0.00378	0.87			
ISM1	isthmin 1(ISM1)	NM_080826	93.4	114	0.00384	1.189			
GORAB	golgin, RAB6 interacting(GORAB)	NM_152281	114.4	130.8	0.00439	1.118			
NUAK1	NUAK family kinase 1(NUAK1)	NM_014840	266.5	438.6	0.00475	1.605			

MRPL34	mitochondrial ribosomal protein L34(MRPL34)	NM_023937	399.5	330.5	0.00481	0.823
		XM_044178	107.6	90.6	0.00495	0.832
POSTN	periostin(POSTN)	NM_006475	91.7	128.2	0.00508	1.367
NFASC	neurofascin(NFASC)	NM_001005387	102.8	118.8	0.0052	1.126
CPXM1	carboxypeptidase X, M14 family member 1(CPXM1)	NM_019609	116.2	154.4	0.00551	1.302
PCSK5	proprotein convertase subtilisin/kexin type 5(PCSK5)	NM_006200	111.9	151.8	0.00588	1.325
CRK	CRK proto-oncogene, adaptor protein(CRK)	NM_016823	150.3	166.2	0.00589	1.287
CRK	CRK proto-oncogene, adaptor protein(CRK)	NM_016823	153.7	144.3	0.00589	1.287
CRK	CRK proto-oncogene, adaptor protein(CRK)	NM_016823	260.4	339.6	0.00589	1.287
COL6A3	collagen type VI alpha 3 chain(COL6A3)	NM_057165	305	592.9	0.00608	1.983
ECM2	extracellular matrix protein 2(ECM2)	NM_001393	105.9	139.8	0.0061	1.292
ECM2	extracellular matrix protein 2(ECM2)	NM_001393	204.9	348.7	0.0061	1.292
NSDHL	NAD(P) dependent steroid dehydrogenase-like(NSDHL)	NM_015922	185.9	232.8	0.00695	1.235

PMEPA1	prostate transmembrane protein, androgen induced 1(PMEPA1)	NM_199169	119.3	126.9	0.0071	1.383
PMEPA1	prostate transmembrane protein, androgen induced 1(PMEPA1)	NM_199169	134	189.8	0.0071	1.383
KCNH2	potassium voltage-gated channel subfamily H member 2(KCNH2)	NM_172056	108.1	127.8	0.00748	1.153
THBS2	thrombospondin 2(THBS2)	NM_003247	143.9	291.4	0.00795	1.976
		XM_001724468	114.1	132.4	0.00859	1.129
OLFML2B	olfactomedin like 2B(OLFML2B)	NM_015441	132.8	169.1	0.00893	1.242
SRPX	sushi repeat containing protein, X-linked(SRPX)	NM_006307	165.6	376.1	0.00915	2.23
YIF1B	Yip1 interacting factor homolog B, membrane trafficking protein(YIF1B)	NM_033557	124	110.9	0.00937	0.876
MPV17L	MPV17 mitochondrial inner membrane protein like(MPV17L)	NM_173803	109.6	95.4	0.00967	0.858
		AA447555	118.4	99.9	0.00973	0.827
XRCC5	X-ray repair cross complementing 5(XRCC5)	NM_021141	161.5	137.8	0.00996	0.845

		XM_927228	109.4	124.3	0.01005	1.111
		DB302602	106.4	130.3	0.0105	1.194
TBC1D8B	TBC1 domain family member 8B(TBC1D8B)	NM_017752	113.6	108.2	0.01075	0.82
TBC1D8B	TBC1 domain family member 8B(TBC1D8B)	NM_017752	176.8	144.8	0.01075	0.82
ZNF467	zinc finger protein 467(ZNF467)	NM_207336	264.2	196.8	0.01105	0.755
COL5A1	collagen type V alpha 1 chain(COL5A1)	NM_000093	107.3	135.9	0.01115	1.241
PLA2G2E	phospholipase A2 group IIE(PLA2G2E)	NM_014589	117.2	107.4	0.01122	0.894
PPM1A	protein phosphatase, Mg2+/Mn2+ dependent 1A(PPM1A)	NM_177952	108.1	128.4	0.01159	1.16
PPM1A	protein phosphatase, Mg2+/Mn2+ dependent 1A(PPM1A)	NM_177952	216	207	0.01159	1.16
		XM_0017199616	115.5	103.7	0.0116	0.875
SSRP1	structure specific recognition protein 1(SSRP1)	NM_003146	101.1	119.6	0.01178	1.148
hspe1	heat shock protein family E (Hsp10) member 1(HSPE1)	NM_002157	203.9	299.6	0.01219	1.495
hspe1	heat shock protein family E (Hsp10) member 1(HSPE1)	NM_002157	1594.2	1583.5	0.01219	1.495

MT2A	metallothionein 2A(MT2A)	NM_005953	1492.9	2670.6	0.01243	1.87
LINC00560	long intergenic non-protein coding RNA 560(LINC00560)	BC043278	99.1	116.9	0.01259	1.142
		XM_928029	152.5	132.6	0.0127	0.861
MS4A3	membrane spanning 4-domains A3(MS4A3)	NM_001031666	103.5	87.4	0.0129	0.824
ADORA1	adenosine A1 receptor(ADORA1)	NM_000674	112.9	113.5	0.0132	1.264
ADORA1	adenosine A1 receptor(ADORA1)	NM_000674	177.8	227.4	0.0132	1.264
		XM_209824	111	125	0.0134	1.097
HNRNPUL2	heterogeneous nuclear ribonucleoprotein U like 2(HNRNPUL2)	NM_001079559	117.9	106.5	0.0135	0.885
		XM_929413	122.6	110.3	0.01383	0.884
PDGFRL	platelet derived growth factor receptor like(PDGFRL)	NM_006207	117.9	143.4	0.01399	1.186
		CN304166	104.5	120.1	0.01405	1.118
CILP	cartilage intermediate layer protein(CILP)	NM_003613	115.1	117.1	0.01464	1.504
CILP	cartilage intermediate layer protein(CILP)	NM_003613	141	218.5	0.01464	1.504

NAA60	N(alpha)-acetyltransferase 60, NatF catalytic subunit(NAA60)	NM_001083601	250.3	198.7	0.01467	0.804			
EIF2S1	eukaryotic translation initiation factor 2 subunit alpha(EIF2S1)	NM_004094	101.6	118.4	0.01484	1.14	NM_053502	4.02	18.01
LARS	leucyl-tRNA synthetase(LARS)	NM_020117	112.4	100.7	0.01492	0.884	NM_053502	4.02	18.01
TSHR	thyroid stimulating hormone receptor(TSHR)	NM_000369	109.8	139.1	0.01514	1.235	NM_053502	4.02	18.01
TSHR	thyroid stimulating hormone receptor(TSHR)	NM_000369	118.7	145.8	0.01514	1.235	NM_053502	4.02	18.01
KCNJ14	potassium voltage-gated channel subfamily J member 14(KCNJ14)	NM_013348	123.1	112.7	0.01535	0.899			
COL3A1	collagen type III alpha 1 chain(COL3A1)	NM_000090	114	165.3	0.01547	1.425			
TRIM51EP	tripartite motif-containing 51E, pseudogene(TRIM51EP)	NM_001136118	133.3	153.7	0.0157	1.125			
PMP22	peripheral myelin protein 22(PMP22)	NM_153321	140.7	211.1	0.01582	1.461			
PMP22	peripheral myelin protein 22(PMP22)	NM_153321	304.6	629.2	0.01582	1.461			

SRRM2	serine/arginine repetitive matrix 2(SRRM2)	NM_016333	2133.6	2612	0.01594	1.25			
hamp	hepcidin antimicrobial peptide(HAMP)	NM_021175	136.1	114.2	0.01607	0.82	NM_001009670	33.30	2.04
TBC1D7	TBC1 domain family member 7(TBC1D7)	NM_016495	188.3	231.6	0.01623	1.212			
EFNA3	ephrin A3(EFNA3)	NM_004952	153.1	134.1	0.01654	0.859			
NRDC	nardilysin convertase(NRDC)	NM_002525	473.1	377.4	0.01664	0.808			
CAPN6	calpain 6(CAPN6)	NM_014289	100.2	117.3	0.01678	1.141			
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial(GPAM)	NM_020918	95.4	123.8	0.0168	3.075			
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial(GPAM)	NM_020918	195.7	626.4	0.0168	3.075			
ABCA8	ATP binding cassette subfamily A member 8(ABCA8)	NM_007168	202.1	315.8	0.01685	1.509			
HAVCR1P1	hepatitis A virus cellular receptor 1 pseudogene 1(HAVCR1P1)	NR_003603	107.9	181.6	0.01745	1.577			
HAVCR1P1	hepatitis A virus cellular receptor 1 pseudogene 1(HAVCR1P1)	NR_003603	115.5	149.5	0.01745	1.577			
		XM_927208	140.8	125.7	0.01803	0.877			

Hpvc1	human papillomavirus (type 18) E5 central sequence-like 1(HPVC1)	NR_004422	111.2	103.6	0.01808	0.915
HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1(HACE1)	NM_020771	127.4	113.4	0.01813	0.878
		XM_939334	138	123.1	0.01831	0.878
ECM2	extracellular matrix protein 2(ECM2)	NM_001393	105.9	139.8	0.01923	1.67
COL6A5	collagen type VI alpha 5 chain(COL6A5)	NM_153264	104.1	123.1	0.01926	1.149
COL6A5	collagen type VI alpha 5 chain(COL6A5)	NM_153264	109.8	111.8	0.01926	1.149
SKP2	S-phase kinase associated protein 2(SKP2)	NM_032637	103.7	126.8	0.01927	1.193
TOB1	transducer of ERBB2, 1(TOB1)	NM_005749	1031.1	568.8	0.01938	0.556
ASB8	ankyrin repeat and SOCS box containing 8(ASB8)	NM_024095	118.5	110.9	0.02023	0.913
ASB8	ankyrin repeat and SOCS box containing 8(ASB8)	NM_024095	121.6	105.5	0.02023	0.913

AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2(AGPAT2)	NM_006412	116	160.4	0.02024	1.347
FASTK	Fas activated serine/threonine kinase(FASTK)	NM_033015	120.1	113.9	0.02038	0.86
FASTK	Fas activated serine/threonine kinase(FASTK)	NM_033015	212.1	183	0.02038	0.86
ASAH1	N-acylsphingosine amidohydrolase 1(ASAH1)	NM_177924	122.3	113.9	0.02039	0.912
GPD1	glycerol-3-phosphate dehydrogenase 1(GPD1)	NM_005276	101.2	125	0.02046	1.207
MFAP5	microfibrillar associated protein 5(MFAP5)	NM_003480	172.5	294.7	0.02054	1.67
C1orf87	chromosome 1 open reading frame 87(C1orf87)	NM_152377	101.7	98.6	0.02062	0.893
C1orf87	chromosome 1 open reading frame 87(C1orf87)	NM_152377	115.4	105.5	0.02062	0.893
		XM_944183	114.3	126.6	0.02101	1.083
TRIM45	tripartite motif containing 45(TRIM45)	NM_025188	161	145.9	0.02102	0.894
COL1A1	collagen type I alpha 1 chain(COL1A1)	NM_000088	225.5	1069.5	0.02116	4.674

		AW135045	148.4	136.1	0.02128	0.902
PXK	PX domain containing serine/threonine kinase like(PXK)	NM_017771	190.4	157.8	0.02146	0.831
		XM_938510	106.5	126	0.0215	1.151
		XM_925919	112	101.5	0.02158	0.883
		XM_941821	117.9	129.5	0.02159	1.074
MCMDC2	minichromosome maintenance domain containing 2(MCMDC2)	NM_173518	113.7	115.6	0.02195	1.363
MCMDC2	minichromosome maintenance domain containing 2(MCMDC2)	NM_173518	3072.3	4141	0.02195	1.363
MMADHC	methylmalonic aciduria and homocystinuria, cblD type(MMADHC)	NM_015702	232.8	223.2	0.02229	0.753
MMADHC	methylmalonic aciduria and homocystinuria, cblD type(MMADHC)	NM_015702	637.9	568.3	0.02229	0.753
MMADHC	methylmalonic aciduria and homocystinuria, cblD type(MMADHC)	NM_015702	659.1	482.7	0.02229	0.753
COL1A2	collagen type I alpha 2 chain(COL1A2)	NM_000089	184.3	825.5	0.02232	3.163
COL1A2	collagen type I alpha 2 chain(COL1A2)	NM_000089	499.5	1554.2	0.02232	3.163

		XM_001726262	98.8	114.1	0.02255	1.12
TUBA3FP	tubulin alpha 3f pseudogene(TUBA3FP)	NR_003608	120.7	112.3	0.02259	0.91
FBLN2	fibulin 2(FBLN2)	NM_001998	115.3	182.4	0.02275	2.255
FBLN2	fibulin 2(FBLN2)	NM_001998	181	416.8	0.02275	2.255
		XM_001134012	208.6	459.5	0.02279	2.21
FBLN2	fibulin 2(FBLN2)	NM_001998	115.3	182.4	0.02301	1.546
PI15	peptidase inhibitor 15(PI15)	NM_015886	113.6	109.2	0.02312	1.222
PI15	peptidase inhibitor 15(PI15)	NM_015886	121	151	0.02312	1.222
		XM_927196	98.2	112.7	0.0234	1.124
MIR591	microRNA 591(MIR591)	NR_030322	144.2	126	0.02363	0.861
COG4	component of oligomeric golgi complex 4(COG4)	NM_015386	103.1	121.6	0.02364	1.15
		AK129542	131.2	120.2	0.02374	0.902
GSTM5	glutathione S-transferase mu 5(GSTM5)	NM_000851	179.1	262.6	0.02394	1.442
CCDC78	coiled-coil domain containing 78(CCDC78)	NM_173476	141.9	122.2	0.02415	0.843

ELOVL5	ELOVL fatty acid elongase 5(ELOVL5)	NM_021814	103.7	133.2	0.02431	1.256
PPTC7	PTC7 protein phosphatase homolog(PPTC7)	NM_139283	282	207.2	0.0247	0.726
SLC29A1	solute carrier family 29 member 1 (Augustine blood group)(SLC29A1)	NM_001078174	122.3	137.1	0.02484	1.314
SLC29A1	solute carrier family 29 member 1 (Augustine blood group)(SLC29A1)	NM_001078174	162.9	217.2	0.02484	1.314
CTHRC1	collagen triple helix repeat containing 1(CTHRC1)	NM_138455	104.2	140.4	0.02514	1.375
CTHRC1	collagen triple helix repeat containing 1(CTHRC1)	NM_138455	119	165.9	0.02514	1.375
UBC	ubiquitin C(UBC)	NM_021009	10602.5	9083.6	0.02538	0.818
UBC	ubiquitin C(UBC)	NM_021009	12020.7	12013.2	0.02538	0.818
		XM_001718145	121.7	109.3	0.0256	0.88
SOX2	SRY-box 2(SOX2)	NM_003106	91.1	108	0.02573	1.154
DACH1	dachshund family transcription factor 1(DACH1)	NM_080759	138.1	170.6	0.02581	1.195

YBEY	ybeY metallopeptidase (putative)(YBEY)	NM_058181	104.5	105.4	0.02612	0.81			
YBEY	ybeY metallopeptidase (putative)(YBEY)	NM_058181	297.8	252.3	0.02612	0.81			
YBEY	ybeY metallopeptidase (putative)(YBEY)	NM_058181	301	246	0.02612	0.81			
RNASE3	ribonuclease A family member 3(RNASE3)	NM_002935	84.8	183.7	0.0262	2.088			
		XM_001126483	127.7	115.4	0.02629	0.886			
ANXA1	annexin A1(ANXA1)	NM_000700	270.9	944.9	0.02645	3.411			
THRSP	thyroid hormone responsive(THRSP)	NM_003251	110.3	389	0.02685	3.374	NM_001107943	0.63	112.77
EP400NL	EP400 N-terminal like(EP400NL)	NM_182613	96.8	110.7	0.02693	1.118			
		XM_001726438	141.4	158.5	0.02724	1.097			
POLR2J3	RNA polymerase II subunit J3(POLR2J3)	NM_001097615	525.7	409.8	0.02754	0.774			
HPX	hemopexin(HPX)	NM_000613	145.1	109.6	0.0279	0.737			
TOPBP1	topoisomerase (DNA) II binding protein 1(TOPBP1)	NM_007027	110.4	133.2	0.02799	1.18			
FASN	fatty acid synthase(FASN)	NM_004104	337	1891.8	0.02802	5.576			
COL1A2	collagen type I alpha 2 chain(COL1A2)	NM_000089	184.3	825.5	0.02838	4.39			

PGLYRP2	peptidoglycan recognition protein 2(PGLYRP2)	NM_052890	121.6	106.1	0.02847	0.852			
RERE	arginine-glutamic acid dipeptide repeats(RERE)	NM_012102	320.9	368.4	0.02849	1.153			
TRIM10	tripartite motif containing 10(TRIM10)	NM_006778	123.6	115.6	0.02856	0.917			
TVP23B	trans-golgi network vesicle protein 23 homolog B(TVP23B)	NM_016078	108.5	95.1	0.02884	0.862			
TVP23B	trans-golgi network vesicle protein 23 homolog B(TVP23B)	NM_016078	139.9	133.8	0.02884	0.862			
		XM_933591	118.5	104.7	0.0289	0.867			
		XR_019367	144.5	121.6	0.02909	0.831	NM_134372	22.51	0.03
DDX19B	DEAD-box helicase 19B(DDX19B)	NM_001014451	97.9	112.5	0.02916	1.12			
DDX19B	DEAD-box helicase 19B(DDX19B)	NM_001014451	184.1	187.7	0.02916	1.12			
PPARG	peroxisome proliferator activated receptor gamma(PPARG)	NM_015869	90.1	115.6	0.02917	1.247			
PPARG	peroxisome proliferator activated receptor gamma(PPARG)	NM_015869	225.9	651.8	0.02917	1.247			
CCKAR	cholecystokinin A receptor(CCKAR)	NM_000730	109.5	125.2	0.0293	1.116			

FABP5	fatty acid binding protein 5(FABP5)	NM_001444	95	136.3	0.0293	1.398
FABP5	fatty acid binding protein 5(FABP5)	NM_001444	240.5	510.9	0.0293	1.398
SPRY1	sprouty RTK signaling antagonist 1(SPRY1)	NM_199327	500.4	756.6	0.02948	1.547
		XM_001722644	116.6	104.8	0.02949	0.88
NDUFB11	NADH:ubiquinone oxidoreductase subunit B11(NDUFB11)	NM_019056	1498.6	1252.4	0.02956	0.842
		XM_943964	119.2	107.1	0.02975	0.879
		XM_294093	105	120.4	0.02978	1.117
KLF10	Kruppel like factor 10(KLF10)	NM_005655	154.5	141.3	0.02987	0.832
KLF10	Kruppel like factor 10(KLF10)	NM_005655	192.8	157.9	0.02987	0.832
LGALS1	galectin 1(LGALS1)	NM_002305	681.2	1942.4	0.0299	2.938
CAV2	caveolin 2(CAV2)	NM_001233	203.8	356.4	0.02991	1.732
CAV2	caveolin 2(CAV2)	NM_001233	258	425.7	0.02991	1.732
FABP4	fatty acid binding protein 4(FABP4)	NM_001442	282.6	6897.1	0.03005	24.735
DYNAP	dynactin associated protein(DYNAP)	NM_173629	116	106.5	0.03015	0.899

ATP5G2	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C2 (subunit 9)(ATP5G2)	NM_005176	224.2	182.4	0.03039	0.787			
ATP5G2	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C2 (subunit 9)(ATP5G2)	NM_005176	2815.4	2479.8	0.03039	0.787			
		DB337880	102.2	119.2	0.03082	1.138			
PON3	paraoxonase 3(PON3)	NM_000940	111.4	97.8	0.03097	0.857	NM_001031645	1.93	10.04
CTHRC1	collagen triple helix repeat containing 1(CTHRC1)	NM_138455	104.2	140.4	0.03101	1.317			
AMBN	ameloblastin(AMBN)	NM_016519	108.1	99.6	0.03109	0.902			
		AI446524	98.8	116.4	0.03117	1.144			
		XM_932043	118.7	104.5	0.03119	0.865			
VN1R5	vomeronasal 1 receptor 5 (gene/pseudogene)(VN1R5)	NM_173858	139.3	123.6	0.03126	0.871			
FBXL8	F-box and leucine rich repeat protein 8(FBXL8)	NM_018378	128.1	152.9	0.0314	1.162			
		AI698256	112.9	135.6	0.03157	1.174			

OPN1SW	opsin 1 (cone pigments), short-wave-sensitive(OPN1SW)	NM_001708	99.1	119.9	0.03174	1.179			
		XR_037520	117.1	132.8	0.03186	1.107			
THYN1	thymocyte nuclear protein 1(THYN1)	NM_199297	140.8	176.6	0.03214	1.23			
CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1(CEACAM1)	NM_001712	120	105	0.03226	0.858			
CPXM2	carboxypeptidase X, M14 family member 2(CPXM2)	NM_198148	172.8	232.9	0.03227	1.31			
DSG2	desmoglein 2(DSG2)	NM_001943	121.4	110.8	0.03236	0.891			
GID4	GID complex subunit 4 homolog(GID4)	NM_024052	99.4	115	0.03247	1.122			
GID4	GID complex subunit 4 homolog(GID4)	NM_024052	131.9	129.3	0.03247	1.122	NM_144748	66.99	0.14
		XM_933382	133.4	113.7	0.03258	0.834			
HEYL	hes related family bHLH transcription factor with YRPW motif-like(HEYL)	NM_014571	168.8	269.8	0.03269	1.587			
GSN	gelsolin(GSN)	NM_198252	209.4	641.6	0.03271	2.981			
SFRP5	secreted frizzled related protein 5(SFRP5)	NM_003015	115.7	135.1	0.03275	1.137			

TIPARP	TCDD inducible poly(ADP-ribose) polymerase(TIPARP)	NM_015508	396.4	317	0.03275	0.827			
MT1IP	metallothionein 1I, pseudogene(MT1IP)	NM_175621	1211.2	2412.2	0.03281	2.159			
NBPF11	neuroblastoma breakpoint family member 11(NBPF11)	NM_183372	110	121.4	0.03288	1.078			
		XM_940358	99.1	113.2	0.03291	1.106			
MID1IP1	MID1 interacting protein 1(MID1IP1)	NM_021242	116	116.2	0.03294	0.815	NM_001107793	77.29	6.85
MID1IP1	MID1 interacting protein 1(MID1IP1)	NM_021242	199.5	159.5	0.03294	0.815	NM_001107793	77.29	6.85
		XM_931329	118.7	106.5	0.03309	0.879	NM_001107793	77.29	6.85
prdm9	PR/SET domain 9(PRDM9)	NM_020227	114	126.6	0.03339	1.088	NM_001107793	77.29	6.85
CALR	calreticulin(CALR)	NM_004343	203.4	172.4	0.03356	0.848			
HSPB2	heat shock protein family B (small) member 2(HSPB2)	NM_001541	116.3	101.6	0.03388	0.858			
FABP5	fatty acid binding protein 5(FABP5)	NM_001444	95	136.3	0.03391	2.085			
GAS1	growth arrest specific 1(GAS1)	NM_002048	271	394.7	0.034	1.42			

TDGP1	thymine-DNA glycosylase pseudogene 1(TDGP1)	NR_024382	100.4	115.6	0.03429	1.123
IKZF2	IKAROS family zinc finger 2(IKZF2)	NM_016260	114.7	131.1	0.03431	1.12
KCNJ4	potassium voltage-gated channel subfamily J member 4(KCNJ4)	NM_152868	102.1	120.4	0.0344	1.139
KCNJ4	potassium voltage-gated channel subfamily J member 4(KCNJ4)	NM_152868	108.7	117.6	0.0344	1.139
GCK	glucokinase(GCK)	NM_033508	86.1	106.6	0.03459	1.21
CIDEC	cell death inducing DFFA like effector c(CIDEC)	NM_022094	104.1	301.9	0.03469	2.79
CIDEC	cell death inducing DFFA like effector c(CIDEC)	NM_022094	105	119.1	0.03469	2.79
GSTA1	glutathione S-transferase alpha 1(GSTA1)	NM_145740	107.6	99.2	0.03469	0.683
GSTA1	glutathione S-transferase alpha 1(GSTA1)	NM_145740	148.6	104.7	0.03469	0.683
LOC101927635	uncharacterized LOC101927635(LOC101927635)	BG119374	122.9	109.5	0.03525	0.87

mrap	melanocortin 2 receptor accessory protein(MRAP)	NM_178817	114.3	198.3	0.03526	1.676
RNASE2	ribonuclease A family member 2(RNASE2)	NM_002934	92.9	130.1	0.03553	1.361
		XM_940764	98.8	117.4	0.03563	1.164
fgl1	fibrinogen like 1(FGL1)	NM_201553	167.9	116	0.03579	0.671
COL6A2	collagen type VI alpha 2 chain(COL6A2)	NM_001849	167.7	217	0.03627	1.269
COL6A2	collagen type VI alpha 2 chain(COL6A2)	NM_001849	189.9	306.3	0.03627	1.269
CACNG2	calcium voltage-gated channel auxiliary subunit gamma 2(CACNG2)	NM_006078	102.5	91.8	0.03629	0.879
NCALD	neurocalcin delta(NCALD)	NM_032041	304.1	452	0.03661	1.512
		XR_038776	132.3	116.8	0.03678	0.866
RNF146	ring finger protein 146(RNF146)	NM_030963	117.2	104.1	0.0368	0.867
RNF146	ring finger protein 146(RNF146)	NM_030963	152.3	145.6	0.0368	0.867
COL6A2	collagen type VI alpha 2 chain(COL6A2)	NM_001849	167.7	217	0.03704	1.571
		XM_001716052	117.9	108.2	0.03716	0.902

c12orf4	chromosome 12 open reading frame 4(C12orf4)	NM_020374	140.5	125.3	0.03717	0.872			
MT1P3	metallothionein 1 pseudogene 3(MT1P3)	NM_080757	1313.1	2470.2	0.03767	1.995			
NDUFA10	NADH:ubiquinone oxidoreductase subunit A10(NDUFA10)	NM_004544	103.7	111.8	0.03787	1.25			
NDUFA10	NADH:ubiquinone oxidoreductase subunit A10(NDUFA10)	NM_004544	105.1	133.8	0.03787	1.25			
GAGE4	G antigen 4(GAGE4)	NM_001474	103	124.1	0.03808	1.171			
MIR1185-1	microRNA 1185-1(MIR1185-1)	NR_031575	138.9	155.8	0.03814	1.092			
NUGGC	nuclear GTPase, germinal center associated(NUGGC)	NM_001010906	117.8	104.9	0.03852	0.872			
ZNF585A	zinc finger protein 585A(ZNF585A)	NM_199126	137.4	117.7	0.0386	0.834			
BPY2B	basic charge, Y-linked, 2B(BPY2B)	NM_001002760	111.9	101.8	0.03865	0.89	NM_001009603	28.32	0.90
GMFB	glia maturation factor beta(GMFB)	NM_004124	114.4	134.3	0.03872	1.145			
igsf11	immunoglobulin superfamily member 11(IGSF11)	NM_152538	121.3	145.2	0.03895	1.171			
		XM_938166	161.6	291.2	0.03911	1.759			

NLRP1	NLR family pyrin domain containing 1(NLRP1)	NM_033007	113	105.6	0.03931	0.916
		XM_0011130020	130.6	118.2	0.0394	0.898
PHF10	PHD finger protein 10(PHF10)	NM_133325	120.3	140.2	0.03946	1.133
CD36	CD36 molecule(CD36)	NM_000072	183.5	1068.4	0.03979	5.653
WWOX	WW domain containing oxidoreductase(WWOX)	NM_130791	123.6	141.3	0.03993	1.113
ALB	albumin(ALB)	NM_000477	1072.9	336.1	0.03999	0.286
ALB	albumin(ALB)	NM_000477	1474.5	661.3	0.03999	0.286
FGF18	fibroblast growth factor 18(FGF18)	NM_003862	119.7	111.1	0.04018	0.911
TRAF4	TNF receptor associated factor 4(TRAF4)	NM_004295	117.9	106.1	0.04081	0.879
TNN	tenascin N(TNN)	NM_022093	113.7	137.7	0.04092	1.184
CDKN2C	cyclin dependent kinase inhibitor 2C(CDKN2C)	NM_078626	151.8	336.4	0.04102	2.146
		XM_0017211172	177.4	313.4	0.04104	1.74
PODN	podocan(PODN)	NM_153703	104.5	134.7	0.04122	1.26

FAM19A4	family with sequence similarity 19 member A4, C-C motif chemokine like(FAM19A4)	NM_001005527	103.4	115.9	0.04132	1.097
FAM19A4	family with sequence similarity 19 member A4, C-C motif chemokine like(FAM19A4)	NM_001005527	106.9	121.3	0.04132	1.097
		XM_290985	103.8	126.5	0.04149	1.18
GLRB	glycine receptor beta(GLRB)	NM_000824	146.3	255.4	0.04167	1.678
TRPV4	transient receptor potential cation channel subfamily V member 4(TRPV4)	NM_021625	132.3	110.5	0.04167	0.823
		XM_001726471	109.8	137.9	0.04173	1.23
ORM1	orosomucoid 1(ORM1)	NM_000607	141.1	97.6	0.04187	0.671
TAB3	TGF-beta activated kinase 1/MAP3K7 binding protein 3(TAB3)	NM_152787	99.3	113.8	0.04197	1.117
		XR_017659	96.9	113.8	0.042	1.133
SLC1A2	solute carrier family 1 member 2(SLC1A2)	NM_004171	118.3	106.1	0.04214	0.883
PCBP2	poly(rC) binding protein 2(PCBP2)	NM_001128913	115.9	101.3	0.04224	0.853

ZIC4	Zic family member 4(ZIC4)	NM_032153	122.2	112.7	0.04233	0.905
		AW044615	109.8	100.2	0.04238	0.893
TIGD6	tigger transposable element derived 6(TIGD6)	NM_030953	121.5	114.4	0.04251	0.921
LY9	lymphocyte antigen 9(LY9)	NM_001033667	84.8	125.1	0.04273	1.441
GC	GC, vitamin D binding protein(GC)	NM_000583	172	110	0.04291	0.619
abl1	ABL proto-oncogene 1, non-receptor tyrosine kinase(ABL1)	NM_005157	591.2	660.4	0.043	1.125
PCYOX1	prenylcysteine oxidase 1(PCYOX1)	NM_016297	132.5	160.6	0.04301	1.181
PCYOX1	prenylcysteine oxidase 1(PCYOX1)	NM_016297	505.8	655.5	0.04301	1.181
CRCP	CGRP receptor component(CRCP)	NM_014478	116.7	110.1	0.04322	1.398
CRCP	CGRP receptor component(CRCP)	NM_014478	2497.8	3480.4	0.04322	1.398
FAM124A	family with sequence similarity 124 member A(FAM124A)	NM_145019	111.8	103.6	0.04331	0.906
FGB	fibrinogen beta chain(FGB)	NM_005141	113.2	95.6	0.04334	0.827
PTAR1	protein prenyltransferase alpha subunit repeat containing 1(PTAR1)	NM_001099666	203.8	240	0.04337	1.149

FAM196A	family with sequence similarity 196 member A(FAM196A)	NM_001039762	85.1	111.8	0.04343	1.271
FGG	fibrinogen gamma chain(FGG)	NM_000509	188.8	94.8	0.04344	0.479
		XM_944654	107.9	120.1	0.04361	1.086
FAM3D	family with sequence similarity 3 member D(FAM3D)	NM_138805	135.4	120.8	0.04408	0.881
GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1(GBGT1)	NM_021996	102.9	119.4	0.04427	1.135
CADM3	cell adhesion molecule 3(CADM3)	NM_021189	102.8	120.9	0.04434	1.143
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2(AGPAT2)	NM_001012727	138.4	213.5	0.04444	1.507
		NM_198289	121.8	596.8	0.0445	4.655
		AA906391	145.2	172.4	0.04457	1.17
TGM5	transglutaminase 5(TGM5)	NM_201631	104.3	116.6	0.04462	1.094
CASKIN2	CASK interacting protein 2(CASKIN2)	NM_020753	116.9	108	0.04484	0.905
		AK002088	91.1	105.7	0.045	1.129
		XM_001725227	115	135.7	0.04521	1.147

PNPLA2	patatin like phospholipase domain containing 2(PNPLA2)	NM_020376	282.3	634.6	0.04534	2.133
NACA	nascent polypeptide-associated complex alpha subunit(NACA)	NM_005594	4000.5	3255.1	0.04555	0.822
NACA	nascent polypeptide-associated complex alpha subunit(NACA)	NM_005594	5969.1	5262.2	0.04555	0.822
METRN	meteorin, glial cell differentiation regulator(METRN)	NM_024042	129.9	108	0.04557	0.821
JADE1	jade family PHD finger 1(JADE1)	NM_024900	215	183.4	0.04598	0.844
CIDEA	cell death-inducing DFFA-like effector a(CIDEA)	NM_001279	101.9	1110.9	0.04601	10.315
ADGRB1	adhesion G protein-coupled receptor B1(ADGRB1)	NM_001702	123.6	111.7	0.04606	0.883
PLCL1	phospholipase C like 1(PLCL1)	NM_006226	116.7	104.4	0.04609	0.884
C14orf180	chromosome 14 open reading frame 180(C14orf180)	NM_001008404	93.9	124.9	0.04611	1.3
CAV1	caveolin 1(CAV1)	NM_001753	157.8	503.2	0.04625	3.01
CAV1	caveolin 1(CAV1)	NM_001753	159	206.6	0.04625	3.01

ALDOC	aldolase, fructose-bisphosphate C(ALDOC)	NM_005165	342	1042.5	0.04629	2.928
TDRD1	tudor domain containing 1(TDRD1)	NM_198795	194.2	244.2	0.04638	1.388
TDRD1	tudor domain containing 1(TDRD1)	NM_198795	247.7	334.6	0.04638	1.388
YTHDF2	YTH N6-methyladenosine RNA binding protein 2(YTHDF2)	NM_016258	288.1	238.7	0.04649	0.845
PSMD8	proteasome 26S subunit, non-ATPase 8(PSMD8)	NM_002812	333.6	278.8	0.0467	0.828
UBN2	ubinuclein 2(UBN2)	NM_173569	161.5	187.1	0.04678	1.142
UBN2	ubinuclein 2(UBN2)	NM_173569	234.7	243	0.04678	1.142
ADIRF	adipogenesis regulatory factor(ADIRF)	NM_006829	2009.5	3414.7	0.0469	1.753
c2orf42	chromosome 2 open reading frame 42(C2orf42)	NM_017880	125.3	110	0.04719	0.861
MAR2	membrane associated ring-CH-type finger 2(MARCH2)	NM_001005416	114.7	132	0.04764	1.121
MAR2	membrane associated ring-CH-type finger 2(MARCH2)	NM_001005416	154	163.8	0.04764	1.121

NPSR1-AS1	NPSR1 antisense RNA 1(NPSR1-AS1)	NM_207285	136.8	127.8	0.04773	0.915
		XM_001130790	132.7	630.3	0.04805	4.52
ZNF652	zinc finger protein 652(ZNF652)	NM_014897	4290.7	5557.2	0.04818	1.309
KCNV2	potassium voltage-gated channel modifier subfamily V member 2(KCNV2)	NM_133497	102.7	117.1	0.04832	1.107
		XR_015597	94.3	112.9	0.04842	1.166
HECTD2	HECT domain E3 ubiquitin protein ligase 2(HECTD2)	NM_182765	137.6	138	0.04849	0.862
HECTD2	HECT domain E3 ubiquitin protein ligase 2(HECTD2)	NM_182765	143.7	126.4	0.04849	0.862
TAF6	TATA-box binding protein associated factor 6(TAF6)	NM_005641	113.1	126.7	0.04867	1.089
		XM_001131201	110.9	126.7	0.04884	1.106
c1orf216	chromosome 1 open reading frame 216(C1orf216)	NM_152374	123.1	139.7	0.04918	1.104
		XM_001732853	113.6	104.2	0.04945	0.896
		CK299443	155.9	140.5	0.04954	0.888

PPARG	peroxisome proliferator activated receptor gamma(PPARG)	NM_138712	116.5	275.5	0.04973	2.294
PLTP	phospholipid transfer protein(PLTP)	NM_182676	205.3	322.8	0.04998	1.567
APOPT1	apoptogenic 1, mitochondrial(APOPT1)	NM_032374	1407.8	1812.9	0.05	1.328

Gene Symbol	**Gene Name**	**Accession No.**	**IUGR Chow F Mean**	**IUGR HFHS F Mean**	**p-val IUGR F HFHS vs. IUGR F Chow**	**Ratio IUGR F HFHS vs. IUGR F Chow**	**REFSEQ ID**	**NEPHRON (MEAN RPKM)**	**COLLECTING DUCT (MEAN RPKM)**
		XR_038951	520.6	329.4	0.00017	0.656			
FNTB	farnesyltransferase, CAAX box, beta(FNTB)	NM_002028	399.5	281.9	0.00023	0.724			
CCT7	chaperonin containing TCP1 subunit 7(CCT7)	NM_006429	644.7	445.7	0.00104	0.745			
ODC1	ornithine decarboxylase 1(ODC1)	NM_002539	725.5	484.4	0.0011	0.726			
		XM_001719540	150.1	130.9	0.00111	0.859			
ACTR5	ARP5 actin-related protein 5 homolog(ACTR5)	NM_024855	134	122.4	0.00143	0.885			
EIF3M	eukaryotic translation initiation factor 3 subunit M(EIF3M)	NM_006360	464.5	327.5	0.00153	0.655			

EIF4A1	eukaryotic translation initiation factor 4A1(EIF4A1)	NM_001416	586.5	372.4	0.00153	0.655			
		XM_934376	149.6	133.4	0.00194	0.875	NM_017193	356.13	8.18
FLJ41170	uncharacterized LOC440200(FLJ41170)	NM_001004332	183.1	236.5	0.00197	1.391	NM_017193	356.13	8.18
		XM_001713654	9306.3	6648.7	0.00201	0.835	NM_017193	356.13	8.18
RPS26P11	ribosomal protein S26 pseudogene 11(RPS26P11)	NR_002309	9176.8	5893.9	0.00255	0.745	NM_017193	356.13	8.18
SMAGP	small cell adhesion glycoprotein(SMAGP)	NM_001033873	235.3	188.5	0.00284	0.826			
JAM2	junctional adhesion molecule 2(JAM2)	NM_021219	130	158	0.003	1.202			
RPS3A	ribosomal protein S3A(RPS3A)	NM_001006	8852.1	6542.5	0.00312	0.75			
RPS3A	ribosomal protein S3A(RPS3A)	NM_001006	9567.1	7835.2	0.00312	0.75			
RPS3A	ribosomal protein S3A(RPS3A)	NM_001006	9708	6189.4	0.00312	0.75			
IFT52	intraflagellar transport 52(IFT52)	NM_016004	203.8	268.1	0.00337	1.368			
		BU928253	128.8	153.7	0.00349	1.144			
POMP	proteasome maturation protein(POMP)	NM_015932	536.2	386.2	0.00355	0.746			
MSLNL	mesothelin-like(MSLNL)	NM_001025190	114.5	148.6	0.00364	1.22			

MSLNL	mesothelin-like(MSLNL)	NM_001025190	123.2	139.9	0.00364	1.22
		AA759151	111	135.2	0.00375	1.166
		XM_927511	128.4	119.5	0.00389	0.899
PDPK1	3-phosphoinositide dependent protein kinase 1(PDPK1)	NM_031268	139.4	122.7	0.00392	0.869
PDPK1	3-phosphoinositide dependent protein kinase 1(PDPK1)	NM_031268	574	543.4	0.00392	0.869
		CA433902	187.2	222.9	0.00423	1.229
PPP1CC	protein phosphatase 1 catalytic subunit gamma(PPP1CC)	NM_002710	2359.4	1509.3	0.00427	0.709
		XM_943956	110.5	132.6	0.00429	1.135
TRIM36	tripartite motif containing 36(TRIM36)	NM_001017397	133	157	0.00445	1.145
CLUL1	clusterin like 1(CLUL1)	NM_014410	325.6	432.9	0.0045	1.482
NETO1	neuropilin and tolloid like 1(NETO1)	AK123319	136.2	119.8	0.00453	0.846
SNORA1	small nucleolar RNA, H/ACA box 1(SNORA1)	NR_003026	128.2	113.9	0.00483	0.853
		XM_941785	106.4	126.8	0.00491	1.122
NGEF	neuronal guanine nucleotide exchange factor(NGEF)	NM_019850	164.2	201.6	0.00498	1.231

MT1H	metallothionein 1H(MT1H)	NM_005951	97.7	143.8	0.00502	1.354
MT1H	metallothionein 1H(MT1H)	NM_005951	1671.5	4509.3	0.00502	1.354
		XR_018412	132.9	120.8	0.00508	0.874
MAIP1	matrix AAA peptidase interacting protein 1(MAIP1)	NM_024520	232.1	168.4	0.00533	0.726
CREB1	cAMP responsive element binding protein 1(CREB1)	NM_004379	119.2	126.4	0.00542	1.623
CREB1	cAMP responsive element binding protein 1(CREB1)	NM_004379	1238.6	1821.8	0.00542	1.623
CREB1	cAMP responsive element binding protein 1(CREB1)	NM_004379	11307.8	13499	0.00542	1.623
		XM_938755	2625.7	1447	0.00543	0.639
neurl4	neuralized E3 ubiquitin protein ligase 4(NEURL4)	NM_032442	261	323.4	0.00549	1.313
FAAP20	Fanconi anemia core complex associated protein 20(FAAP20)	NM_182533	118.1	149.6	0.00564	1.211
FAAP24	Fanconi anemia core complex associated protein 24(FAAP24)	NM_152266	169.3	171.7	0.00564	1.211
IARS	isoleucyl-tRNA synthetase(IARS)	NM_002161	2887.6	3967.8	0.00567	1.516

ZNF584	zinc finger protein 584(ZNF584)	NM_173548	132.1	160.3	0.00573	1.165
		XM_001720172	722	461.2	0.00594	0.674
USP21	ubiquitin specific peptidase 21(USP21)	NM_012475	142.8	137.2	0.00597	0.822
USP21	ubiquitin specific peptidase 21(USP21)	NM_012475	217.3	175.3	0.00597	0.822
BCL2	BCL2, apoptosis regulator(BCL2)	NM_000633	138.4	127.4	0.00605	0.641
BCL2L1	BCL2 like 1(BCL2L1)	NM_138578	424	265.5	0.00605	0.641
RFX5	regulatory factor X5(RFX5)	NM_001025603	141.5	114.3	0.00609	0.79
		XR_037398	261	192.5	0.00621	0.731
		XR_037508	200.3	165.4	0.00641	0.84
PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1(PITPNC1)	NM_181671	201.7	153.3	0.00649	0.773
POLE3	DNA polymerase epsilon 3, accessory subunit(POLE3)	NM_017443	402.9	289.5	0.00651	0.744
rbm12	RNA binding motif protein 12(RBM12)	NM_006047	163.5	137.4	0.00683	0.832
rbm12	RNA binding motif protein 12(RBM12)	NM_006047	216.6	170.7	0.00683	0.832
TMEM50B	transmembrane protein 50B(TMEM50B)	NM_006134	177.2	216.2	0.00683	1.283

TMEM50B	transmembrane protein 50B(TMEM50B)	NM_006134	568	512.4	0.00683	1.283
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	108.6	129.1	0.00689	1.131
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	230.5	219.5	0.00689	1.131
		XM_937648	134.9	162.9	0.0071	1.181
SLC35A2	solute carrier family 35 member A2(SLC35A2)	NM_001032289	139.6	129.3	0.00729	0.906
SLC35A2	solute carrier family 35 member A2(SLC35A2)	NM_001032289	409.1	388.8	0.00729	0.906
cyb5r3	cytochrome b5 reductase 3(CYB5R3)	NM_000398	170.6	150.8	0.00731	0.877
		XM_0011288786	505.2	1486.6	0.00756	3.49
MIR1253	microRNA 1253(MIR1253)	NR_031654	191.4	221.4	0.00782	1.2
VAV3	vav guanine nucleotide exchange factor 3(VAV3)	NM_006113	163.6	141.1	0.00788	0.854
VAV3	vav guanine nucleotide exchange factor 3(VAV3)	NM_006113	282.9	264.9	0.00788	0.854
VAV3	vav guanine nucleotide exchange factor 3(VAV3)	NM_006113	495.5	559.3	0.00788	0.854

OR2G2	olfactory receptor family 2 subfamily G member 2(OR2G2)	NM_001001915	167.2	202.2	0.00793	1.277			
RPL10A	ribosomal protein L10a(RPL10A)	NM_007104	1974.5	1104.7	0.00797	0.627	NM_053502	4.02	18.01
RPL10A	ribosomal protein L10a(RPL10A)	NM_007104	6681.9	5179.3	0.00797	0.627	NM_053502	4.02	18.01
		XR_015351	119.9	140.9	0.00801	1.154	NM_053502	4.02	18.01
DHX40	DEAH-box helicase 40(DHX40)	NM_024612	172.7	146.6	0.00811	0.847	NM_053502	4.02	18.01
DHX40	DEAH-box helicase 40(DHX40)	NM_024612	182.5	176.2	0.00811	0.847			
DHX40	DEAH-box helicase 40(DHX40)	NM_024612	196.8	215.6	0.00811	0.847			
MIR1185-1	microRNA 1185-1(MIR1185-1)	NR_031575	141.9	164.5	0.00818	1.135			
		XM_926231	244.2	159.5	0.00818	0.666			
SMOC1	SPARC related modular calcium binding 1(SMOC1)	NM_001034852	122.7	148.9	0.00865	1.179			
SMOC1	SPARC related modular calcium binding 1(SMOC1)	NM_001034852	132.9	136.2	0.00865	1.179			
ANKRD10	ankyrin repeat domain 10(ANKRD10)	NM_017664	229.6	204.5	0.00871	0.87	NM_001009670	33.30	2.04
ANKRA2	ankyrin repeat family A member 2(ANKRA2)	NM_023039	150	135.5	0.00871	0.87			

		XR_018394	1706	752.9	0.00882	0.475
prorsd1p	prolyl-tRNA synthetase associated domain containing 1, pseudogene(PRORSD1P)	NM_001080459	157.9	134.1	0.00901	0.828
TAOK2	TAO kinase 2(TAOK2)	NM_016151	214.1	253.9	0.00906	1.273
		XR_038898	250	168.4	0.00906	0.659
MCMDC2	minichromosome maintenance domain containing 2(MCMDC2)	NM_173518	119.4	134.8	0.00946	1.382
MCMDC2	minichromosome maintenance domain containing 2(MCMDC2)	NM_173518	4139.8	4970.2	0.00946	1.382
SLC35B2	solute carrier family 35 member B2(SLC35B2)	NM_178148	147.6	173.3	0.00948	1.163
GLE1	GLE1, RNA export mediator(GLE1)	NM_001003722	300.9	399.2	0.00968	1.483
PTPA	protein phosphatase 2 phosphatase activator(PTPA)	NM_178003	121.1	148.7	0.00975	1.167
RHBDL2	rhomboid like 2(RHBDL2)	NM_017821	146.7	182.8	0.00976	1.263
RHBDL2	rhomboid like 2(RHBDL2)	NM_017821	518.6	594.4	0.00976	1.263
SEH1L	SEH1 like nucleoporin(SEH1L)	NM_001013437	209.3	160.1	0.00976	0.76

SEH1L	SEH1 like nucleoporin(SEH1L)	NM_001013437	273.8	261.4	0.00976	0.76
		XR_017380	139.3	114.5	0.00979	0.812
EEF1B2	eukaryotic translation elongation factor 1 beta 2(EEF1B2)	NM_001037663	7295.5	5026	0.0098	0.797
		XR_038867	179.9	142.7	0.00981	0.799
		XM_944646	156.4	177.6	0.01007	1.163
		XM_001132307	112.5	139.4	0.01019	1.177
MUC4	mucin 4, cell surface associated(MUC4)	NM_018406	115	137.6	0.01036	1.137
DDX19B	DEAD-box helicase 19B(DDX19B)	NM_001014451	165	133.6	0.01038	0.799
SP3	Sp3 transcription factor(SP3)	NM_003111	131.7	118.4	0.01047	0.87
		XR_039278	2439.5	1596.3	0.01057	0.724
FUT6	fucosyltransferase 6(FUT6)	NM_000150	114	131.2	0.01061	1.686
FUT7	fucosyltransferase 7(FUT7)	NM_004479	291	423.6	0.01061	1.686
		XM_929340	173.3	128.3	0.01073	0.722
		XM_929340	4436.9	3161.7	0.01073	0.722
		AW183894	1115.9	1640.1	0.01111	1.644

KCNC1	potassium voltage-gated channel subfamily C member 1(KCNC1)	AK125480	137.2	170.3	0.01117	1.223
SPCS2	signal peptidase complex subunit 2(SPCS2)	NM_014752	1017.4	606.7	0.01129	0.642
		AI539492	211.5	290.5	0.01131	1.474
		XM_933970	507.4	329.2	0.01136	0.674
NDUFAF7	NADH:ubiquinone oxidoreductase complex assembly factor 7(NDUFAF7)	NM_144736	142.2	129.7	0.01143	1.471
NDUFAF7	NADH:ubiquinone oxidoreductase complex assembly factor 7(NDUFAF7)	NM_144736	314.6	418.4	0.01143	1.471
RIPK4	receptor interacting serine/threonine kinase 4(RIPK4)	NM_020639	128.8	154.9	0.01146	1.162
MAPK7	mitogen-activated protein kinase 7(MAPK7)	NM_139032	130.6	134.8	0.01154	0.854
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1(MAPK8IP1)	NM_005456	177	151.9	0.01154	0.854
MRPL3	mitochondrial ribosomal protein L3(MRPL3)	NM_007208	124.7	148.7	0.01165	1.137

EIF4E2	eukaryotic translation initiation factor 4E family member 2(EIF4E2)	NM_004846	1861.8	1286.1	0.01191	0.771
		XM_001715717	160.7	131.4	0.01204	0.809
		XM_001715717	415.3	342.5	0.01204	0.809
BBS1	Bardet-Biedl syndrome 1(BBS1)	NM_024649	179.1	201.5	0.01237	1.141
		CR605357	133	158.6	0.01242	1.17
CYP4A11	cytochrome P450 family 4 subfamily A member 11(CYP4A11)	NM_000778	146.1	134.9	0.01252	0.905
LOC105378397	uncharacterized LOC105378397(LOC105378397)	BX092644	178.7	230.7	0.01256	1.343
CCNK	cyclin K(CCNK)	NM_003858	122.3	109.6	0.01258	0.865
TMEM106C	transmembrane protein 106C(TMEM106C)	NM_024056	527.8	681.4	0.01262	1.508
cenpv	centromere protein V(CENPV)	NM_181716	208.1	258.5	0.01267	1.313
CENPX	centromere protein X(CENPX)	NM_144998	416.2	502.5	0.01267	1.313
TMEM267	transmembrane protein 267(TMEM267)	NM_022483	2771.5	4189.6	0.01278	1.703
RPL7A	ribosomal protein L7a(RPL7A)	NM_000972	320.5	241.5	0.01279	0.759

		XR_036919	4757.2	2981.9	0.01296	0.746
EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1(EEPD1)	NM_030636	295.4	224.9	0.01307	0.778
MAR5	membrane associated ring-CH-type finger 5(MARCH5)	NM_017824	101.3	113.9	0.01308	1.137
MAR6	membrane associated ring-CH-type finger 6(MARCH6)	NM_005885	103.4	125.5	0.01308	1.137
		XR_039439	155.4	129.1	0.0132	0.495
		XR_039439	1435	675.3	0.0132	0.495
		XR_016832	224.8	168.2	0.01326	0.752
		XR_038101	843.9	504.2	0.01336	0.628
EPB41L5	erythrocyte membrane protein band 4.1 like 5(EPB41L5)	NM_020909	1038.6	725.5	0.01341	0.752
		XR_038433	297.4	177.6	0.01345	0.569
		XR_038433	2121.1	1243.5	0.01345	0.569
MPZL1	myelin protein zero like 1(MPZL1)	NM_024569	121.6	102	0.01348	0.812
		XM_001131877	117.6	139.7	0.0135	1.136

RUSC1	RUN and SH3 domain containing 1(RUSC1)	NM_014328	662.7	832.5	0.01363	1.51			
THBS3	thrombospondin 3(THBS3)	NM_007112	300.1	347.7	0.01364	1.277			
		NM_001039755	5325.7	6709	0.0137	1.431			
HBP1	HMG-box transcription factor 1(HBP1)	NM_012257	180.7	166.6	0.01374	0.744			
HBQ1	hemoglobin subunit theta 1(HBQ1)	NM_005331	337	242.9	0.01374	0.744			
RPL19P9	ribosomal protein L19 pseudogene 9(RPL19P9)	NM_001080544	660.6	436.1	0.01375	0.724			
RPL19P9	ribosomal protein L19 pseudogene 9(RPL19P9)	NM_001080544	6597.3	4381.6	0.01375	0.724			
		XR_038693	1302	690.7	0.01381	0.563			
		XR_038693	1767.9	1231.7	0.01381	0.563			
		XM_001723164	151.5	167.3	0.01411	1.098			
		XR_037282	263.9	176.4	0.01417	0.673	NM_001107943	0.63	112.77
MAFF	MAF bZIP transcription factor F(MAFF)	NM_012323	146.7	136.4	0.01423	1.957			
MAFG	MAF bZIP transcription factor G(MAFG)	NM_002359	487.8	800.6	0.01423	1.957			
		XM_001133677	106.4	116.7	0.01429	0.882			

		XM_001133677	138.9	123.4	0.01429	0.882			
MAP2K7	mitogen-activated protein kinase kinase 7(MAP2K7)	NM_145185	127.2	113.2	0.0143	0.864			
PIPSL	PIP5K1A and PSMD4-like, pseudogene(PIPSL)	NR_002319	223.4	172.6	0.01452	0.774			
ARL17B	ADP ribosylation factor like GTPase 17B(ARL17B)	NM_001039083	4156	5459.5	0.01458	1.473			
		XM_937758	805.8	480	0.01463	0.638			
c21orf59	chromosome 21 open reading frame 59(C21orf59)	NM_021254	1267.9	1675.6	0.01472	1.473			
PI4KA	phosphatidylinositol 4-kinase alpha(PI4KA)	NM_002650	252.8	190.5	0.01475	0.761			
ZNF280D	zinc finger protein 280D(ZNF280D)	NM_001002844	113.1	106.4	0.0148	0.885			
		XM_929608	100	124.1	0.01487	1.172			
GPRC5A	G protein-coupled receptor class C group 5 member A(GPRC5A)	NM_003979	118.4	137.2	0.01491	1.115			
		XR_017653	2142.3	1463.8	0.01502	0.77	NM_134372	22.51	0.03
		XM_927468	125.8	115.6	0.01503	0.884			
TRNT1	tRNA nucleotidyl transferase 1(TRNT1)	NM_182916	117.5	105.4	0.01514	0.851			

TRNT1	tRNA nucleotidyl transferase 1(TRNT1)	NM_182916	126.2	120.2	0.01514	0.851
		XM_001719035	522.4	338.7	0.01515	0.674
ZDHHC24	zinc finger DHHC-type containing 24(ZDHHC24)	NM_207340	262.6	290.4	0.01519	1.181
EWSR1	EWS RNA binding protein 1(EWSR1)	NM_005243	222.5	298.9	0.01527	1.489
MROH7	maestro heat like repeat family member 7(MROH7)	NM_001039464	215.5	355.7	0.01531	1.862
PLCD4	phospholipase C delta 4(PLCD4)	NM_032726	179.8	254.8	0.01535	1.534
FAM63A	family with sequence similarity 63 member A(FAM63A)	NM_018379	124.1	148.6	0.01536	1.429
FAM63B	family with sequence similarity 63 member B(FAM63B)	NM_001040450	626.5	784.2	0.01536	1.429
		XR_016872	308.9	200.2	0.01544	0.646
SLC35E1	solute carrier family 35 member E1(SLC35E1)	NM_024881	121.9	121.4	0.01558	1.543
SLC35E1	solute carrier family 35 member E1(SLC35E1)	NM_024881	1336.2	1830.8	0.01558	1.543
		XM_927693	142	164.3	0.01559	1.148
		XM_001721625	2052.7	2763.4	0.0156	1.474

C1orf229	chromosome 1 open reading frame 229(C1orf229)	NM_207401	162	144.4	0.01563	0.886			
ZNF394	zinc finger protein 394(ZNF394)	NM_032164	1925.2	2622.5	0.01565	1.525			
		AW450365	123.5	150.2	0.01567	1.174			
		AA503583	153	130	0.01584	0.811			
ACTB	actin beta(ACTB)	NM_001101	2599.1	1663.7	0.01594	0.593			
ACTB	actin beta(ACTB)	NM_001101	7876.7	3772.5	0.01594	0.593			
ACTB	actin beta(ACTB)	NM_001101	13400.8	8681.3	0.01594	0.593			
RAMP2	receptor activity modifying protein 2(RAMP2)	NM_005854	144.1	167.6	0.01602	1.146	NM_001031645	1.93	10.04
RAMP2	receptor activity modifying protein 2(RAMP2)	NM_005854	159.1	173.6	0.01602	1.146			
		XM_945223	123.9	144.5	0.01603	1.124			
		XM_934920	250.7	170.2	0.01607	0.703			
ZBTB41	zinc finger and BTB domain containing 41(ZBTB41)	NM_194314	132.7	112.5	0.0162	0.831			
		XR_037881	117.9	122.3	0.01671	0.605			
		XR_037881	1416.1	810.5	0.01671	0.605			

		XM_943174	115.6	147.2	0.01677	1.249			
SLC26A10	solute carrier family 26 member 10(SLC26A10)	NM_133489	99.9	105.7	0.01684	0.882			
SLC26A10	solute carrier family 26 member 10(SLC26A10)	NM_133489	144.5	130.6	0.01684	0.882			
POTEKP	POTE ankyrin domain family member K, pseudogene(POTEKP)	NM_001017421	5570.2	2215.8	0.01696	0.53			
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1(ENTPD1)	NM_001098175	276.2	200.2	0.01706	0.738			
		XM_944499	117.6	112.3	0.01711	0.92			
PIGL	phosphatidylinositol glycan anchor biosynthesis class L(PIGL)	NM_004278	128.1	120.8	0.01714	0.905			
		XM_0011129013	153.4	158.6	0.01715	1.741			
		XM_0011129013	355.1	527.1	0.01715	1.741	NM_144748	66.99	0.14
CDK2AP2	cyclin dependent kinase 2 associated protein 2(CDK2AP2)	NM_005851	166.6	209.5	0.01716	1.28			
		XR_015295	5069.4	3031.1	0.01726	0.674			
STK11	serine/threonine kinase 11(STK11)	NM_000455	176.8	145.8	0.0173	0.824			

EID2B	EP300 interacting inhibitor of differentiation 2B(EID2B)	NM_152361	122.4	120.3	0.01733	1.477			
EIF1	eukaryotic translation initiation factor 1(EIF1)	NM_005801	4551.9	6130	0.01733	1.477			
		XM_001720210	238	184.3	0.01735	0.765			
MUC6	mucin 6, oligomeric mucus/gel-forming(MUC6)	NM_005961	129.1	126.6	0.01737	1.502			
MUC6	mucin 6, oligomeric mucus/gel-forming(MUC6)	NM_005961	223.8	209.8	0.01737	1.502			
MUC6	mucin 6, oligomeric mucus/gel-forming(MUC6)	NM_005961	307.2	393.2	0.01737	1.502	NM_001107793	77.29	6.85
ARF1	ADP ribosylation factor 1(ARF1)	NM_001024228	433.4	313.9	0.01755	0.758	NM_001107793	77.29	6.85
		XR_016027	194.3	150.1	0.01759	0.784	NM_001107793	77.29	6.85
ARSB	arylsulfatase B(ARSB)	NM_000046	149.2	133.2	0.01764	0.874	NM_001107793	77.29	6.85
KANK4	KN motif and ankyrin repeat domains 4(KANK4)	NM_181712	105.4	142.7	0.01773	1.263			
KANSL1	KAT8 regulatory NSL complex subunit 1(KANSL1)	NM_015443	133.3	160.8	0.01773	1.263			

		XM_001719452	120.8	136.8	0.01779	1.097
STXBP2	syntaxin binding protein 2(STXBP2)	NM_006949	294.2	347.2	0.01821	1.293
		XR_018937	392.6	238.8	0.01828	0.616
		XR_018937	4367.6	3029.7	0.01828	0.616
TRIM13	tripartite motif containing 13(TRIM13)	NM_001007278	126.8	127	0.01839	1.482
TRIM13	tripartite motif containing 13(TRIM13)	NM_001007278	875.2	1150.2	0.01839	1.482
GNG8	G protein subunit gamma 8(GNG8)	NM_033258	211.1	169.3	0.01839	0.797
CTDSPL2	CTD small phosphatase like 2(CTDSPL2)	NM_016396	1542.2	1003.5	0.01871	0.705
CNGA1	cyclic nucleotide gated channel alpha 1(CNGA1)	NM_000087	147.8	133.6	0.0188	0.869
		XM_001714161	171.2	192	0.01885	1.165
C4BPA	complement component 4 binding protein alpha(C4BPA)	NM_000715	168.7	148.8	0.01889	0.876
		XR_019429	241.6	156.9	0.01905	0.638
LGALS7B	galectin 7B(LGALS7B)	NM_001042507	369	836.2	0.01938	2.701
LGALS8	galectin 8(LGALS8)	NM_201545	983	2633.4	0.01944	2.899

LGALS7B	galectin 7B(LGALS7B)	NM_001042507	628	1540.9	0.01944	2.899
MEX3C	mex-3 RNA binding family member C(MEX3C)	NM_016626	285.5	194.9	0.01952	0.694
		XM_0011255808	172.8	141.4	0.01957	0.808
lgals9	galectin 9(LGALS9)	NM_009587	983	2633.4	0.0196	3.156
PSMA3	proteasome subunit alpha 3(PSMA3)	NM_152132	701.3	478.1	0.0198	0.733
		XR_039108	184.3	148.2	0.01993	0.793
PTGES3	prostaglandin E synthase 3(PTGES3)	NM_006601	302.1	211.8	0.01998	0.711
		XR_018710	109.6	127.1	0.02019	1.107
brms1	breast cancer metastasis suppressor 1(BRMS1)	NM_001024958	543.3	399.1	0.02022	0.855
HSP90AA1	heat shock protein 90 alpha family class A member 1(HSP90AA1)	NM_001017963	150.3	136.6	0.02028	0.889
HSP90AA1	heat shock protein 90 alpha family class A member 1(HSP90AA1)	NM_005348	170	159.3	0.02028	0.889
LOC606724	coronin 1A pseudogene(LOC606724)	NR_002454	3790	5486.9	0.02035	1.588

FAM98B	family with sequence similarity 98 member B(FAM98B)	NM_001042429	361.1	418.5	0.02036	1.25			
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta(YWHAH)	NM_003405	3061.8	1821.7	0.02037	0.668			
GPSM2	G-protein signaling modulator 2(GPSM2)	NM_013296	117	134	0.02039	1.106			
MIR1247	microRNA 1247(MIR1247)	NR_031649	125.6	119.4	0.02039	0.905			
SET	SET nuclear proto-oncogene(SET)	NM_003011	358.1	275.1	0.02042	0.764			
DDX54	DEAD-box helicase 54(DDX54)	NM_024072	4076.4	5394.3	0.02043	1.487			
		BX098521	151.7	199.5	0.02044	1.297			
		XR_001416	248	338.7	0.02063	1.621	NM_001009603	28.32	0.90
		XR_018705	230.8	157.9	0.02067	0.677			
CCDC22	coiled-coil domain containing 22(CCDC22)	NM_014008	155.8	194.2	0.02068	1.29			
DCUN1D1	defective in cullin neddylation 1 domain containing 1(DCUN1D1)	NM_020640	264.6	193.2	0.02078	0.784			

DCTPP1	dCTP pyrophosphatase 1(DCTPP1)	NM_024096	226.5	177.5	0.02078	0.784
RBBP5	RB binding protein 5, histone lysine methyltransferase complex subunit(RBBP5)	NM_005057	134.7	127.2	0.02091	0.916
YY1	YY1 transcription factor(YY1)	NM_003403	457.6	317.6	0.02093	0.721
YY1	YY1 transcription factor(YY1)	NM_003403	994.4	742.5	0.02093	0.721
DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic(DPM1)	NM_003859	233.9	190.1	0.02098	0.825
DPM2	dolichyl-phosphate mannosyltransferase subunit 2, regulatory(DPM2)	NM_003863	509.3	490	0.02098	0.825
LOC101930164	uncharacterized LOC101930164(LOC101930164)	AK026751	177.1	211.8	0.02102	1.241
MYO3A	myosin IIIA(MYO3A)	NM_017433	133.9	124.2	0.02103	0.897
PRRG4	proline rich and Gla domain 4(PRRG4)	NM_024081	188.1	246.5	0.02121	1.372
		XR_018261	1141.9	606.6	0.02123	0.603
NSA2	NSA2, ribosome biogenesis homolog(NSA2)	NM_014886	1514.3	1136.2	0.02126	0.779

NSA2	NSA2, ribosome biogenesis homolog(NSA2)	NM_014886	2216.3	1551.3	0.02126	0.779
ZC3H3	zinc finger CCCH-type containing 3(ZC3H3)	NM_015117	242.7	194.5	0.02133	0.819
		XM_0017211430	3671.5	5101.1	0.02148	1.503
ACVR1	activin A receptor type 1(ACVR1)	NM_001105	220.5	273.4	0.02162	1.345
APH1A	aph-1 homolog A, gamma-secretase subunit(APH1A)	NM_001077628	841.1	566.5	0.02167	0.724
		XR_019029	175.5	155.1	0.02168	0.88
ACTB	actin beta(ACTB)	NM_001101	2599.1	1663.7	0.0217	0.69
ACTB	actin beta(ACTB)	NM_001101	7876.7	3772.5	0.0217	0.69
ACTG1	actin gamma 1(ACTG1)	NM_001614	13400.8	8681.3	0.0217	0.69
		XR_040489	125.3	143.6	0.02172	1.111
ZNF468	zinc finger protein 468(ZNF468)	NM_199132	134.6	147.4	0.02187	1.195
ZNF468	zinc finger protein 468(ZNF468)	NM_199132	143	171.6	0.02187	1.195
BNIP3L	BCL2 interacting protein 3 like(BNIP3L)	NM_004331	106.5	128.3	0.02193	1.146
BNIPL	BCL2 interacting protein like(BNIPL)	NM_138278	136	155.3	0.02193	1.146

FLYWCH1	FLYWCH-type zinc finger 1(FLYWCH1)	NM_020912	146.8	133.3	0.02202	0.884
		XM_938988	1597.3	550.1	0.02221	0.409
POLRMT	RNA polymerase mitochondrial(POLRMT)	NM_005035	252.8	290.7	0.02229	1.226
ETS1	ETS proto-oncogene 1, transcription factor(ETS1)	NM_005238	211	290.5	0.02231	1.423
FASTK	Fas activated serine/threonine kinase(FASTK)	NM_006712	116.3	97	0.02255	0.796
KLF10	Kruppel like factor 10(KLF10)	NM_005655	104.3	127.1	0.02262	1.16
		XM_944246	587.6	345	0.0227	0.62
CEP192	centrosomal protein 192(CEP192)	NM_032142	2713.1	3587.6	0.02299	1.456
ART4	ADP-ribosyltransferase 4 (Dombrock blood group)(ART4)	NM_021071	106.9	131.7	0.02317	1.146
DYNC1LI2	dynein cytoplasmic 1 light intermediate chain 2(DYNC1LI2)	NM_006141	132.2	123.3	0.02332	0.897
		XR_019565	2110.2	1326.2	0.02336	0.704
		XR_019565	3209.1	2022.7	0.02336	0.704
DIXDC1	DIX domain containing 1(DIXDC1)	NM_001037954	135.7	150	0.02338	1.077

		CD237661	289.1	400.2	0.02363	1.601
RPS27A	ribosomal protein S27a(RPS27A)	NM_002954	3219	2388.2	0.02372	0.809
RPS27A	ribosomal protein S27a(RPS27A)	NM_002954	17436.1	14379.2	0.02372	0.809
		BF054947	125.4	141.5	0.02391	1.09
		XR_016385	386.7	274.5	0.02404	0.74
		XM_372319	138.5	160.9	0.02422	1.165
		XR_042295	210.8	303.1	0.02437	1.58
RPL6	ribosomal protein L6(RPL6)	NM_001024662	165.1	148.9	0.0244	0.726
RPL6	ribosomal protein L6(RPL6)	NM_001024662	2434.3	1880.7	0.0244	0.726
RPL6	ribosomal protein L6(RPL6)	NM_001024662	5324.9	3122.2	0.0244	0.726
TBRG4	transforming growth factor beta regulator 4(TBRG4)	NM_004749	159.3	143.5	0.02451	0.886
		XR_039678	173.8	147.4	0.02457	0.85
ZRANB1	zinc finger RANBP2-type containing 1(ZRANB1)	NM_017580	154.2	175.2	0.02463	1.153
ABHD17B	abhydrolase domain containing 17B(ABHD17B)	NM_016014	114.5	126.7	0.02471	0.817

ABHD17C	abhydrolase domain containing 17C(ABHD17C)	NM_021214	154.7	129.6	0.02471	0.817
		XM_001723141	1229.6	827.3	0.02472	0.736
CCT8L1P	chaperonin containing TCP1 subunit 8 like 1, pseudogene(CCT8L1P)	NM_001029866	447.8	297.4	0.0249	0.668
		XR_038984	981.9	612.8	0.02492	0.669
BTG2	BTG anti-proliferation factor 2(BTG2)	NM_006763	282.1	226.1	0.02504	0.813
HNMT	histamine N-methyltransferase(HNMT)	NM_006895	108.5	130.5	0.02506	1.127
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1(HNRNPA1)	NM_031157	113.3	119.9	0.02506	1.127
		AW276479	1131.4	1642	0.02509	1.62
GSKIP	GSK3B interacting protein(GSKIP)	NM_016472	98.9	124.5	0.02511	1.164
PXMP4	peroxisomal membrane protein 4(PXMP4)	NM_183397	150.9	177.8	0.02518	1.171
SHROOM4	shroom family member 4(SHROOM4)	NM_020717	135.1	165.1	0.0252	1.633
SHROOM4	shroom family member 4(SHROOM4)	NM_020717	729	1031.1	0.0252	1.633
ENO1	enolase 1(ENO1)	NM_001428	159.2	193.5	0.02526	1.233

SEC22C	SEC22 homolog C, vesicle trafficking protein(SEC22C)	NM_032970	124.4	114.1	0.02528	0.884
SEC22C	SEC22 homolog C, vesicle trafficking protein(SEC22C)	NM_032970	130.9	135.7	0.02528	0.884
EFCAB5	EF-hand calcium binding domain 5(EFCAB5)	NM_001033562	335.3	263	0.02532	0.811
EIF4E3	eukaryotic translation initiation factor 4E family member 3(EIF4E3)	NM_173359	207.5	174.1	0.02538	1.41
EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2(EIF4EBP2)	NM_004096	232.9	286.3	0.02538	1.41
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	NM_001895	190.8	163.3	0.02543	0.856
		XR_017565	605.1	385.7	0.02553	0.652
		XR_038851	505.1	672.8	0.02554	1.552
TDRD1	tudor domain containing 1(TDRD1)	NM_198795	273.5	350.9	0.02562	1.341
TDRD1	tudor domain containing 1(TDRD1)	NM_198795	346	425.7	0.02562	1.341
		XR_039146	344.3	230.4	0.02562	0.673
		XM_292085	1828.7	890.3	0.02569	0.531

SSPO	SCO-spondin(SSPO)	NM_198455	119.1	153.3	0.02596	1.222			
ATP6V0E1	ATPase H+ transporting V0 subunit e1(ATP6V0E1)	NM_003945	338.6	416.2	0.02619	1.308			
		W91949	129.6	107.7	0.02624	0.791			
GDPD3	glycerophosphodiester phosphodiesterase domain containing 3(GDPD3)	NM_024307	340.3	412.8	0.02631	1.35			
CCT3	chaperonin containing TCP1 subunit 3(CCT3)	NM_005998	466.1	354	0.02635	0.793			
c1orf116	chromosome 1 open reading frame 116(C1orf116)	NM_023938	171.1	202.7	0.02646	1.27			
C1orf122	chromosome 1 open reading frame 122(C1orf122)	NM_198446	232.5	297	0.02646	1.27			
INO80	INO80 complex subunit(INO80)	NM_017553	7156.1	8841.3	0.02655	1.366			
		XM_371314	128.5	149	0.02668	1.129			
GPR37	G protein-coupled receptor 37(GPR37)	NM_005302	167.1	146.3	0.02682	0.87			
TRMO	tRNA methyltransferase O(TRMO)	NM_016481	296	226.6	0.0269	0.775			
		XM_940103	171.6	196.9	0.02703	1.197	NM_144744	0.11	40.01
AKIRIN1	akirin 1(AKIRIN1)	NM_024595	167.7	209.2	0.02705	1.291			

RPS10	ribosomal protein S10(RPS10)	NM_001014	10480.3	6847.8	0.02706	0.756
CLPB	ClpB homolog, mitochondrial AAA ATPase chaperonin(CLPB)	NM_030813	251.7	318.1	0.02707	1.394
RPL36	ribosomal protein L36(RPL36)	NM_033643	1757.7	1029	0.0272	0.689
		XR_037945	139.2	117.9	0.02725	0.833
CDCA8	cell division cycle associated 8(CDCA8)	NM_018101	214.8	163.5	0.02732	0.769
		XM_928122	224.9	260.5	0.02733	1.261
RPL7P9	ribosomal protein L7 pseudogene 9(RPL7P9)	NM_001093763	330.3	242.5	0.02744	0.739
		XM_497182	114.3	104.9	0.02747	0.866
COPS4	COP9 signalosome subunit 4(COPS4)	NM_016129	184.8	147.3	0.02761	0.781
magoh	mago homolog, exon junction complex core component(MAGOH)	NM_002370	158.5	197.2	0.0278	1.242
DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic(DPM1)	NM_003859	135.3	118.4	0.0278	0.854
		XM_938599	827.3	479.3	0.02787	0.628

		XR_038738	359.9	244.6	0.02806	0.701
BRK1	BRICK1, SCAR/WAVE actin nucleating complex subunit(BRK1)	NM_018462	543.3	399.1	0.02812	0.779
		XM_001126896	137.5	127.4	0.02812	0.9
BRIX1	BRX1, biogenesis of ribosomes(BRIX1)	NM_018321	163.7	139.9	0.02812	0.779
		DB337588	119.6	138.6	0.02814	1.116
HS3ST3A1	heparan sulfate-glucosamine 3-sulfotransferase 3A1(HS3ST3A1)	NM_006042	139.9	126.6	0.0282	0.88
		XM_932143	246.4	292.3	0.02853	1.259
C14orf132	chromosome 14 open reading frame 132(C14orf132)	NM_020215	189.3	156.8	0.02853	0.827
		XM_938903	197.6	153.7	0.02877	0.772
ZNF652	zinc finger protein 652(ZNF652)	NM_014897	6050.7	7159.2	0.02886	1.292
MED20	mediator complex subunit 20(MED20)	NM_004275	542.5	381.9	0.02887	0.75
Tceal7	transcription elongation factor A like 7(TCEAL7)	NM_152278	136.7	118.4	0.02892	0.841
ARMC8	armadillo repeat containing 8(ARMC8)	NM_015396	296.8	352.5	0.02894	1.304

MSLN	mesothelin(MSLN)	NM_013404	120.5	139.3	0.02896	1.115
LRRFIP2	LRR binding FLII interacting protein 2(LRRFIP2)	NM_017724	1687.3	2879.9	0.02898	1.937
SHISA4	shisa family member 4(SHISA4)	NM_198149	103.6	122.5	0.02903	1.112
		XR_016670	139.4	125.4	0.02906	0.87
SIL1	SIL1 nucleotide exchange factor(SIL1)	NM_001037633	167.1	180.6	0.02911	1.372
SIL1	SIL1 nucleotide exchange factor(SIL1)	NM_001037633	332.5	405.8	0.02911	1.372
COLGALT1	collagen beta(1-O)galactosyltransferase 1(COLGALT1)	NM_024656	211.1	272.1	0.02925	1.385
PLCD1	phospholipase C delta 1(PLCD1)	NM_006225	212.9	264.2	0.02952	1.277
FCER1G	Fc fragment of IgE receptor Ig(FCER1G)	NM_004106	1717.1	2748.9	0.02961	1.797
		XM_376420	10758.5	7086	0.02965	0.747
ZNF548	zinc finger protein 548(ZNF548)	NM_152909	174.9	153.3	0.02966	0.875
TNPO1	transportin 1(TNPO1)	NM_153188	139.4	132.5	0.02976	0.751
TNPO1	transportin 1(TNPO1)	NM_153188	266.6	235.8	0.02976	0.751
TNPO1	transportin 1(TNPO1)	NM_153188	463.8	330.8	0.02976	0.751
		BX111413	115.3	141.8	0.02997	1.191

CRCP	CGRP receptor component(CRCP)	NM_014478	125.3	131.5	0.03	1.344
CRCT1	cysteine rich C-terminal 1(CRCT1)	NM_019060	3804.2	4477.9	0.03	1.344
TRIM45	tripartite motif containing 45(TRIM45)	NM_025188	179.4	192.9	0.03024	1.101
NEK11	NIMA related kinase 11(NEK11)	NM_145910	118.5	140.4	0.03027	1.14
PSMG1	proteasome assembly chaperone 1(PSMG1)	NM_203433	595	441.6	0.03029	0.784
		BX091766	141.2	160.9	0.03045	1.14
		AK095707	178.6	224.2	0.03046	1.343
BTF3L4	basic transcription factor 3 like 4(BTF3L4)	NM_152265	224.9	184.8	0.03066	0.811
BTG1	BTG anti-proliferation factor 1(BTG1)	NM_001731	282.1	226.1	0.03066	0.811
		XM_937382	120.7	138.1	0.03067	1.094
BICC1	BicC family RNA binding protein 1(BICC1)	NM_001080512	105.2	134.3	0.03069	1.203
		XM_941107	125.4	146	0.03087	1.131
		XM_926370	171.7	134.2	0.03095	0.778
NOXA1	NADPH oxidase activator 1(NOXA1)	NM_006647	269.4	350.3	0.031	1.421
RBM34	RNA binding motif protein 34(RBM34)	NM_015014	123	110.9	0.03116	0.863
ZNF80	zinc finger protein 80(ZNF80)	NM_007136	120.4	140.4	0.0312	1.121

BAIAP2	BAI1 associated protein 2(BAIAP2)	NM_006340	130.3	152.2	0.0313	1.127
BAIAP2	BAI1 associated protein 2(BAIAP2)	NM_017450	195.3	221.3	0.0313	1.127
		CF552427	186.5	227.4	0.03139	1.315
NFYA	nuclear transcription factor Y subunit alpha(NFYA)	NM_002505	138.8	126	0.03151	0.895
CACYBP	calcyclin binding protein(CACYBP)	NM_014412	151.6	140.4	0.03156	0.915
		XR_039373	261.1	185.7	0.03168	0.712
		XM_001720622	150.1	130.2	0.03172	0.851
ZNF2	zinc finger protein 2(ZNF2)	NM_021088	117.1	138.6	0.03172	1.125
OSBPL2	oxysterol binding protein like 2(OSBPL2)	NM_001001691	146.9	170.7	0.03173	1.143
PLAC8L1	PLAC8 like 1(PLAC8L1)	NM_001029869	127.1	117.6	0.03174	0.882
AGXT	alanine-glyoxylate aminotransferase(AGXT)	NM_000030	117.7	140.3	0.03175	1.134
ALAD	aminolevulinate dehydratase(ALAD)	NM_001003945	125.9	139.5	0.03182	1.559
		XM_929418	140.6	130.1	0.03182	0.901
ALAS1	5'-aminolevulinate synthase 1(ALAS1)	NM_000688	282.5	411	0.03182	1.559
CGN	cingulin(CGN)	NM_020770	217.7	177.4	0.03185	0.812

SAE1	SUMO1 activating enzyme subunit 1(SAE1)	NM_005500	793.7	462.1	0.03205	0.628
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	NM_003622	120.6	140.5	0.0321	0.827
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	NM_003622	128.3	110.6	0.0321	0.827
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	NM_003622	183	171.5	0.0321	0.827
ACTR3B	ARP3 actin related protein 3 homolog B(ACTR3B)	NM_020445	310.8	169.9	0.0321	0.555
AKT3	AKT serine/threonine kinase 3(AKT3)	NM_005465	642.2	479.4	0.03212	0.795
		XR_037673	2180.1	1427.4	0.03212	0.712
		XM_941064	124.6	143.6	0.03213	1.104
MOS	v-mos Moloney murine sarcoma viral oncogene homolog(MOS)	NM_005372	116.5	111.6	0.03233	0.909
KIAA0513	KIAA0513(KIAA0513)	NM_014732	389.9	525.8	0.03238	1.61
SLK	STE20 like kinase(SLK)	NM_014720	153.9	138.2	0.03257	0.872
		XM_0017166468	127.3	151	0.03262	1.168

SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1 like(SPECC1L)	NM_015330	130.9	118.1	0.03266	0.855
SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1 like(SPECC1L)	NM_015330	736	609.6	0.03266	0.855
KLHL28	kelch like family member 28(KLHL28)	NM_017658	224.6	210.3	0.03268	1.416
KLHL3	kelch like family member 3(KLHL3)	NM_017415	291.1	369.6	0.03268	1.416
		XM_001717865	124.3	138.6	0.03272	1.082
HINFP	histone H4 transcription factor(HINFP)	NM_015517	276.6	207.7	0.03275	0.756
HIKESHI	Hikeshi, heat shock protein nuclear import factor(HIKESHI)	NM_016401	136.8	132.8	0.03275	0.756
NUMA1	nuclear mitotic apparatus protein 1(NUMA1)	NM_006185	158	149.5	0.03284	0.849
NUMA1	nuclear mitotic apparatus protein 1(NUMA1)	NM_006185	368.7	296	0.03284	0.849
CNIH2	cornichon family AMPA receptor auxiliary protein 2(CNIH2)	NM_182553	396.4	282.3	0.03292	0.736
CNIH1	cornichon family AMPA receptor auxiliary protein 1(CNIH1)	NM_005776	290.2	227.5	0.03292	0.736

		XM_376787	323.8	214.6	0.03295	0.663
GNB3	G protein subunit beta 3(GNB3)	NM_002075	150.3	133.3	0.03302	0.871
		XM_0017222111	1860.4	2514.9	0.03305	1.48
ZKSCAN8	zinc finger with KRAB and SCAN domains 8(ZKSCAN8)	NM_006298	119.2	108.3	0.03323	0.861
		CV318379	146.9	159.7	0.03346	1.073
		XM_938181	11401.5	8116	0.03346	0.793
RPS4X	ribosomal protein S4, X-linked(RPS4X)	NM_001007	4554.2	2742.6	0.03348	0.735
RPS4X	ribosomal protein S4, X-linked(RPS4X)	NM_001007	4921	3536.8	0.03348	0.735
FBXW5	F-box and WD repeat domain containing 5(FBXW5)	NM_018998	173.6	137.2	0.03351	0.794
		XM_927451	138.7	146.7	0.03351	0.68
		XM_927451	727.6	471.4	0.03351	0.68
IL9	interleukin 9(IL9)	NM_000590	291.5	203.4	0.03356	0.735
PAXIP1	PAX interacting protein 1(PAXIP1)	NM_007349	237.5	195.8	0.03361	0.832
AMY1B	amylase, alpha 1B (salivary)(AMY1B)	NM_001008218	127.8	133.2	0.03373	0.655

AMY1C	amylase, alpha 1C (salivary)(AMY1C)	NM_001008219	2362.1	1459.6	0.03373	0.655
SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1(SMARCD1)	NM_003076	315.6	249.2	0.03397	0.811
AFTPH	aftiphilin(AFTPH)	NM_017657	131.3	118.2	0.03407	0.866
IL19	interleukin 19(IL19)	NM_013371	11297.9	13722.9	0.03409	1.276
CEP104	centrosomal protein 104(CEP104)	NM_014704	176.3	167.3	0.03415	1.172
CEP112	centrosomal protein 112(CEP112)	NM_145036	204.2	229.3	0.03415	1.172
RPL36AL	ribosomal protein L36a like(RPL36AL)	NM_001001	273.2	205.1	0.03418	0.761
RPL36AL	ribosomal protein L36a like(RPL36AL)	NM_001001	2736.2	2005.2	0.03418	0.761
GPX3	glutathione peroxidase 3(GPX3)	NM_002084	3152.3	6021.5	0.03421	2.02
		XR_017249	146.2	125.6	0.03424	0.832
EIF4G2	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)	NM_001418	557.7	376.5	0.03426	0.71
EIF4G2	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)	NM_001418	2383.3	1905.2	0.03426	0.71

EIF4G2	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)	NM_001418	4924.9	3901.3	0.03426	0.71			
CGB5	chorionic gonadotropin beta subunit 5(CGB5)	NM_033043	118.3	138.9	0.03426	1.129	NM_017196	14.73	0.69
		AI198908	128.7	116.2	0.03434	0.874	NM_017196	14.73	0.69
TUBA1A	tubulin alpha 1a(TUBA1A)	NM_006009	777.6	439.7	0.03443	0.595			
TUBA1A	tubulin alpha 1a(TUBA1A)	NM_006009	6647.5	4557.3	0.03443	0.595	NM_017196	14.73	0.69
ARHGAP12	Rho GTPase activating protein 12(ARHGAP12)	NM_018287	907.2	943	0.03445	1.153			
		XM_933679	125.4	155.5	0.03449	0.777			
		XM_933679	198	156.2	0.03449	0.777			
SDR42E1	short chain dehydrogenase/reductase family 42E, member 1(SDR42E1)	NM_145168	119.1	135.3	0.03451	1.091	NM_031356	5.43	24.53
		XM_001128866	1655.9	2265.5	0.03495	1.475	NM_031356	5.43	24.53
		XR_017029	113.3	134.8	0.0351	1.142			
HYLS1	HYLS1, centriolar and ciliogenesis associated(HYLS1)	NM_145014	269.1	318.3	0.0351	1.266			
		BF996074	1010.1	1588.9	0.03514	1.785			
		XM_944513	116.1	140.1	0.0352	1.144			

		XR_037873	1822.1	1195.7	0.03524	0.738			
KIF16B	kinesin family member 16B(KIF16B)	NM_024704	649.9	787.4	0.03528	1.355			
PPHLN1	periphilin 1(PPHLN1)	NM_201440	269.4	184.8	0.03533	0.684			
FBXO38	F-box protein 38(FBXO38)	NM_030793	405.8	287	0.03534	0.724			
		XM_001723702	241.1	177.9	0.0354	0.717			
ZNF564	zinc finger protein 564(ZNF564)	NM_144976	288.5	214.5	0.0354	0.771			
ZNF256	zinc finger protein 256(ZNF256)	NM_005773	190.1	141.7	0.03546	0.74			
		BX093647	124.4	136	0.03547	1.056			
CDK6	cyclin dependent kinase 6(CDK6)	NM_001259	711.9	927.2	0.03549	1.454			
RAD9A	RAD9 checkpoint clamp component A(RAD9A)	NM_004584	206.7	259.8	0.03566	1.297			
NECTIN4	nectin cell adhesion molecule 4(NECTIN4)	NM_030916	107.5	131.7	0.03586	1.154	NM_017135	41.45	2.88
CSN1S1	casein alpha s1(CSN1S1)	NM_001890	114.5	135.7	0.0359	1.118	NM_017135	41.45	2.88
		XM_942516	128.7	120.3	0.03591	0.91	NM_017135	41.45	2.88
plekhb2	pleckstrin homology domain containing B2(PLEKHB2)	NM_017958	124.6	126.5	0.0361	1.306	NM_017135	41.45	2.88

plekhb2	pleckstrin homology domain containing B2(PLEKHB2)	NM_017958	161.6	209.6	0.0361	1.306	NM_017135	41.45	2.88
APP	amyloid beta precursor protein(APP)	NM_201414	1835.9	2194.8	0.03616	1.293			
TBC1D25	TBC1 domain family member 25(TBC1D25)	NM_002536	130	130.3	0.03624	0.913			
TBC1D25	TBC1 domain family member 25(TBC1D25)	NM_002536	161.6	147.7	0.03624	0.913			
PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase type 2 beta(PIP4K2B)	NM_138687	2108.7	2678.9	0.03626	1.448			
DLD	dihydrolipoamide dehydrogenase(DLD)	NM_000108	121.3	141.5	0.03626	1.112			
RHAG	Rh-associated glycoprotein(RHAG)	NM_000324	123.4	145.3	0.03629	1.157			
SCRT1	scratch family transcriptional repressor 1(SCRT1)	NM_031309	183.5	164.7	0.0363	0.891			
TXNDC5	thioredoxin domain containing 5(TXNDC5)	NM_022085	203.3	147	0.03632	0.729	NM_001033653	43.46	1.56
ITPKB	inositol-trisphosphate 3-kinase B(ITPKB)	NM_002221	4382.8	5647.3	0.03635	1.399			
ITGA9	integrin subunit alpha 9(ITGA9)	NM_002207	178.2	204.6	0.0364	1.182			
NISCH	nischarin(NISCH)	NM_007184	389.5	455.4	0.03644	1.274			
		XR_019588	9256.9	6133.3	0.03644	0.779			

DAZL	deleted in azoospermia like(DAZL)	NM_001351	185.8	217.9	0.03654	1.23
		XM_937091	142.2	162.4	0.03662	1.134
		XR_041286	1954	1155.3	0.03669	0.707
		XR_041286	5828	3336.9	0.03669	0.707
CCDC103	coiled-coil domain containing 103(CCDC103)	NM_213607	3129.2	3781.1	0.03679	1.348
KHK	ketohexokinase(KHK)	NM_000221	300	214.6	0.03679	0.795
KHDRBS3	KH RNA binding domain containing, signal transduction associated 3(KHDRBS3)	NM_006558	153.4	125.1	0.03679	0.795
HSCB	HscB mitochondrial iron-sulfur cluster cochaperone(HSCB)	NM_172002	213.9	244.4	0.03683	1.189
HSD11B1	hydroxysteroid 11-beta dehydrogenase 1(HSD11B1)	NM_181755	411.9	490.6	0.03683	1.189
CMTM6	CKLF like MARVEL transmembrane domain containing 6(CMTM6)	NM_017801	209.9	235.3	0.03685	1.184
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B(EPB41L4B)	NM_019114	1100.7	755.6	0.03692	0.736

		XR_015954	195.4	151.5	0.03709	0.781			
		XR_038568	1456.6	749.2	0.0371	0.592			
		XR_038568	2160.6	1272.1	0.0371	0.592			
CNOT7	CCR4-NOT transcription complex subunit 7(CNOT7)	NM_013354	300.1	245.7	0.03711	0.835			
CNOT8	CCR4-NOT transcription complex subunit 8(CNOT8)	NM_004779	472.5	373.6	0.03711	0.835			
REXO2	RNA exonuclease 2(REXO2)	NM_015523	1022.6	690.5	0.03718	0.758			
CSTF2	cleavage stimulation factor subunit 2(CSTF2)	NM_001325	163.5	147	0.03721	0.889			
LYPLA1	lysophospholipase I(LYPLA1)	NM_006330	121.9	115.9	0.03728	0.898			
ATP9A	ATPase phospholipid transporting 9A (putative)(ATP9A)	NM_006045	275.1	167.7	0.03729	0.599	NM_134407	50.47	11.16
MRPS18A	mitochondrial ribosomal protein S18A(MRPS18A)	NM_018135	324.5	352.4	0.03732	1.217			
SAMD9	sterile alpha motif domain containing 9(SAMD9)	NM_017654	120.6	141.6	0.03741	1.146			
CEPT1	choline/ethanolamine phosphotransferase 1(CEPT1)	NM_006090	154.2	174.9	0.03741	1.121			

PCDHGB2	protocadherin gamma subfamily B, 2(PCDHGB2)	NM_032096	143.8	130.5	0.03748	0.894
CREB1	cAMP responsive element binding protein 1(CREB1)	NM_004379	128.9	222.5	0.03756	1.945
UBXN6	UBX domain protein 6(UBXN6)	NM_025241	534	616.5	0.03757	1.293
SNAP23	synaptosome associated protein 23(SNAP23)	NM_003825	130.1	127.7	0.03759	0.848
SNAP23	synaptosome associated protein 23(SNAP23)	NM_003825	188	159.5	0.03759	0.848
CCZ1	CCZ1 homolog, vacuolar protein trafficking and biogenesis associated(CCZ1)	NM_015622	1404.8	1039.2	0.03761	0.811
		XR_037525	501.1	353.6	0.03764	0.722
		XR_017589	227.2	170.5	0.03766	0.738
		XM_928982	96.2	117.8	0.03772	1.145
DYRK1B	dual specificity tyrosine phosphorylation regulated kinase 1B(DYRK1B)	NM_006484	145	132.5	0.03774	0.886
		BU078529	120.8	137.8	0.03804	1.097

DSP	desmoplakin(DSP)	NM_001008844	185.5	209.3	0.03811	1.906			
DST	dystonin(DST)	NM_001723	195.6	312.7	0.03811	1.906			
MAX	MYC associated factor X(MAX)	NM_002382	150.3	127.4	0.03814	0.839			
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	210.8	197.6	0.03838	0.84			
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	264.4	221.2	0.03838	0.84			
MRPL47	mitochondrial ribosomal protein L47(MRPL47)	NM_020409	181.6	147.8	0.03839	0.802	NM_001033706	2.42	10.86
		XR_017481	146.9	129.8	0.03843	0.876			
		XR_015611	213.1	161.5	0.03843	0.754			
C1R	complement C1r(C1R)	NM_001733	127.4	103.8	0.03859	0.791			
		XM_934846	144.2	174.7	0.03862	1.208			
		XM_001720379	792.6	491.2	0.03869	0.63			
COMMD6	COMM domain containing 6(COMMD6)	NM_203497	700.5	520	0.03893	0.795	NM_153300	0.14	61.17
		XM_001130742	575	671.1	0.0391	1.465			

		XM_001130742	1793.8	2373.7	0.0391	1.465	NM_032416	108.51	1.87
		XR_038930	7887.1	5231.1	0.03915	0.796			
ACTR8	ARP8 actin-related protein 8 homolog(ACTR8)	NM_022899	169.9	145.6	0.0392	0.855			
EIF2B5	eukaryotic translation initiation factor 2B subunit epsilon(EIF2B5)	NM_003907	450.7	360	0.03923	0.843			
		XR_017804	3711.5	2721.1	0.03927	0.745			
		XR_017804	6448.1	3895.8	0.03927	0.745			
		XM_001724539	729.2	435.7	0.03931	0.651			
		XR_038097	359.1	231.6	0.03941	0.672			
KRT2	keratin 2(KRT2)	NM_000423	280.2	409.7	0.03945	1.712			
EIF2B4	eukaryotic translation initiation factor 2B subunit delta(EIF2B4)	NM_172195	450.7	360	0.03947	0.842			
EIF2B4	eukaryotic translation initiation factor 2B subunit delta(EIF2B4)	NM_015636	398.2	321.2	0.03947	0.842			
h2afy	H2A histone family member Y(H2AFY)	NM_138609	203.6	176	0.03952	0.79			
H2AFY2	H2A histone family member Y2(H2AFY2)	NM_018649	317.1	244.3	0.03952	0.79			

		XM_001715145	4374.5	5415.3	0.03959	1.418			
CUTA	cutA divalent cation tolerance homolog(CUTA)	NM_001014840	172.7	223.9	0.03966	1.433			
NCCRP1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)(NCCRP1)	NM_001001414	110.2	132.7	0.03967	1.163	NM_001191088	10.07	0.03
NCCRP1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)(NCCRP1)	NM_001001414	150.6	162.5	0.03967	1.163	NM_001191088	10.07	0.03
		XM_943583	177.1	199.1	0.03969	1.141	NM_001191088	10.07	0.03
NIP7	NIP7, nucleolar pre-rRNA processing protein(NIP7)	NM_016101	238	183.9	0.03981	0.791			
IMPACT	impact RWD domain protein(IMPACT)	NM_018439	191.3	163.5	0.03986	0.853			
		XM_001725448	162.6	147.2	0.03987	0.884			
		XM_932890	350.2	472.2	0.0399	1.572	NM_012496	1095.39	8.76
SPAG9	sperm associated antigen 9(SPAG9)	NM_003971	134.7	123.2	0.04018	0.887			
SPAG9	sperm associated antigen 9(SPAG9)	NM_003971	152.5	146.2	0.04018	0.887			
RPL7	ribosomal protein L7(RPL7)	NM_000971	456.2	334.9	0.04021	0.774			

TAGAP	T-cell activation RhoGTPase activating protein(TAGAP)	NM_054114	137.6	116.2	0.04031	0.825
SIVA1	SIVA1 apoptosis inducing factor(SIVA1)	NM_006427	265.6	244	0.04034	0.765
SIVA1	SIVA1 apoptosis inducing factor(SIVA1)	NM_006427	303.4	228.5	0.04034	0.765
WAPL	WAPL cohesin release factor(WAPL)	NM_015045	274.2	229.6	0.04046	0.86
IFRD2	interferon related developmental regulator 2(IFRD2)	NM_006764	105.8	128	0.04062	1.151
SPCS2P4	signal peptidase complex subunit 2 homolog (S. cerevisiae) pseudogene 4(SPCS2P4)	NM_001080536	268.6	202	0.04067	0.741
		XM_001715568	146.4	164.2	0.04069	1.108
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3(SRGAP3)	NM_001033117	124.3	157.2	0.04079	1.232
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3(SRGAP3)	NM_001033117	195.8	246.7	0.04079	1.232
MT1B	metallothionein 1B(MT1B)	NM_005947	1509.5	5464.9	0.04085	3.475
ZNF583	zinc finger protein 583(ZNF583)	NM_152478	136.1	121.5	0.04086	0.881
NOP14	NOP14 nucleolar protein(NOP14)	NM_003703	121.1	144.3	0.04086	1.152

FBXO30	F-box protein 30(FBXO30)	NM_032145	136	116.2	0.04094	0.842
FBXO32	F-box protein 32(FBXO32)	NM_058229	154.8	154.4	0.04094	0.842
OGFOD1	2-oxoglutarate and iron dependent oxygenase domain containing 1(OGFOD1)	NM_018233	128.5	113.4	0.04099	0.851
OGFOD1	2-oxoglutarate and iron dependent oxygenase domain containing 1(OGFOD1)	NM_018233	132.2	128.5	0.04099	0.851
DYRK1A	dual specificity tyrosine phosphorylation regulated kinase 1A(DYRK1A)	NM_130438	274.5	200.8	0.04102	0.716
DYRK1A	dual specificity tyrosine phosphorylation regulated kinase 1A(DYRK1A)	NM_130437	135.2	138.6	0.04102	0.716
RPL17P39	ribosomal protein L17 pseudogene 39(RPL17P39)	NM_001093733	880.1	593.3	0.04125	0.735
MCHR2	melanin concentrating hormone receptor 2(MCHR2)	NM_032503	132.4	161.4	0.04131	1.191
		XM_0017188864	238.7	158.9	0.04134	0.653
		XM_936640	120	137.9	0.0414	1.103

KLK10	kallikrein related peptidase 10(KLK10)	NM_002776	576.6	407.6	0.04141	0.747
FAM131B	family with sequence similarity 131 member B(FAM131B)	NM_014690	141.3	130	0.04142	0.894
ZNF100	zinc finger protein 100(ZNF100)	NM_173531	127.9	147.3	0.04142	1.119
MANBAL	mannosidase beta like(MANBAL)	NM_001003897	250	286.6	0.04144	1.226
BTBD6	BTB domain containing 6(BTBD6)	NM_033271	187.2	158	0.04147	0.851
NOSTRIN	nitric oxide synthase trafficking(NOSTRIN)	NM_052946	223.1	288.6	0.04147	1.434
BTBD3	BTB domain containing 3(BTBD3)	NM_014962	121.8	122.7	0.04147	0.851
HAX1	HCLS1 associated protein X-1(HAX1)	NM_006118	119.9	137.9	0.04151	1.107
		XM_001132706	123	113.9	0.04153	0.888
TOPORS	TOP1 binding arginine/serine rich protein(TOPORS)	NM_005802	136.1	120.4	0.04162	0.858
		AI215519	149.9	167.1	0.04181	1.127
		BG058337	238	287.3	0.04181	1.391
PAQR9	progestin and adipoQ receptor family member 9(PAQR9)	NM_198504	128.3	264.7	0.04194	2.447
ZFX	zinc finger protein, X-linked(ZFX)	NM_003410	127.2	115.6	0.04196	0.877

ZSCAN2	zinc finger and SCAN domain containing 2(ZSCAN2)	NM_017894	124.8	140.2	0.04197	1.084			
		XM_944905	142.5	159.9	0.0421	1.098			
KRTAP4-7	keratin associated protein 4-7(KRTAP4-7)	NM_033061	170.2	199.7	0.04217	1.181			
NRG3	neuregulin 3(NRG3)	NM_001010848	199.5	227.4	0.04225	1.213	NM_013059	21.02	0.11
		XR_041205	1685.5	963.5	0.04225	0.66			
ADAMTSL4	ADAMTS like 4(ADAMTSL4)	NM_025008	172.3	150.6	0.04228	0.865			
		XM_001717156	5234.3	3571.6	0.04231	0.82			
CDYL2	chromodomain Y-like 2(CDYL2)	AK023660	96.8	149.2	0.04232	1.591			
MED1	mediator complex subunit 1(MED1)	NM_004774	204.6	169.2	0.04239	0.827			
MED1	mediator complex subunit 1(MED1)	NM_004774	307.3	332	0.04239	0.827			
RTN4IP1	reticulon 4 interacting protein 1(RTN4IP1)	NM_032730	190.4	217.2	0.04241	1.158			
FNBP1L	formin binding protein 1 like(FNBP1L)	NM_001024948	122.4	146.7	0.04244	1.138			
		XR_037721	388.4	306.5	0.04263	0.837			
LY86	lymphocyte antigen 86(LY86)	NM_004271	110	145.1	0.04263	1.304			
KIAA0319L	KIAA0319 like(KIAA0319L)	NM_024874	329	264.8	0.04271	0.82			

		XM_001133527	123.9	127.7	0.04274	1.157			
		XM_001133527	142.3	165.4	0.04274	1.157			
		XM_001726456	155	139.4	0.04277	0.889	NM_012816	19.78	2.28
ZNF283	zinc finger protein 283(ZNF283)	NM_181845	114.2	106.6	0.0428	0.878	NM_012816	19.78	2.28
HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1(HERPUD1)	NM_001010990	278.9	211.9	0.04286	0.775			
AATK	apoptosis associated tyrosine kinase(AATK)	NM_001080395	323.6	368.1	0.0429	1.24			
		XM_944968	107.3	125.4	0.04293	1.095			
QRFPR	pyroglutamylated RFamide peptide receptor(QRFPR)	NM_198179	1460.7	1944.9	0.04295	1.456			
LRRC3DN	LRRC3 downstream neighbor (non-protein coding)(LRRC3DN)	AL117578	125.1	118.2	0.04296	0.902			
MEIG1	meiosis/spermiogenesis associated 1(MEIG1)	NM_001080836	129.8	146.9	0.04297	1.102			
MOCS1	molybdenum cofactor synthesis 1(MOCS1)	NM_005943	234.1	268.7	0.04301	1.237			
CLK1	CDC like kinase 1(CLK1)	NM_004071	219.6	172.9	0.04302	0.787			
SNRPD2	small nuclear ribonucleoprotein D2 polypeptide(SNRPD2)	NM_004597	221.5	182.7	0.04304	0.818			

SNORA18	small nucleolar RNA, H/ACA box 18(SNORA18)	NR_002959	172	154.4	0.04316	0.892			
IL17RE	interleukin 17 receptor E(IL17RE)	NM_153483	120.4	137.7	0.04321	1.093			
MYO3B	myosin IIIB(MYO3B)	NM_138995	696.5	949	0.04324	1.567			
		XM_001721589	739.6	475.3	0.04328	0.679			
SRSF1	serine and arginine rich splicing factor 1(SRSF1)	NM_001078166	1563.3	1172.5	0.0433	0.803			
		XM_933437	161.6	189.5	0.0433	1.176			
		XR_018316	715.5	385.9	0.0434	0.559			
		XM_001732883	123.4	112.3	0.04342	0.878			
HDLBP	high density lipoprotein binding protein(HDLBP)	NM_203346	312.5	375	0.04353	1.404			
HDLBP	high density lipoprotein binding protein(HDLBP)	NM_005336	111.9	118.4	0.04353	1.404			
		XM_936822	199.4	156.9	0.04358	0.781			
		XR_015495	137.6	122.6	0.04358	0.87	NM_031544	4.79	38.59
SERPINB7	serpin family B member 7(SERPINB7)	NM_003784	123.3	145.1	0.04377	1.234	NM_031544	4.79	38.59

SERPINB7	serpin family B member 7(SERPINB7)	NM_003784	171.6	205.1	0.04377	1.234
FKBP14	FK506 binding protein 14(FKBP14)	NM_017946	142.6	156	0.04379	1.371
FKBP1A	FK506 binding protein 1A(FKBP1A)	NM_000801	2187.3	2702.4	0.04379	1.371
PPA2	pyrophosphatase (inorganic) 2(PPA2)	NM_006903	4900.5	5967	0.04389	1.367
RPL21P16	ribosomal protein L21 pseudogene 16(RPL21P16)	NM_001139505	117	104.5	0.04391	0.864
		XR_037860	625.2	358.5	0.04396	0.608
CDCA4	cell division cycle associated 4(CDCA4)	NM_145701	134.6	101.2	0.04402	0.741
		XR_038543	5646.2	3974	0.04404	0.775
RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1(RAP1GDS1)	NM_021159	215.8	175.3	0.04412	0.831
TRAPPC2	trafficking protein particle complex 2(TRAPPC2)	NM_001011658	140.7	131.4	0.04412	0.918
		XR_039407	620.8	465	0.04422	0.801
NANS	N-acetylneuraminate synthase(NANS)	NM_018946	223.9	169	0.04426	0.748
SEC23A	Sec23 homolog A, coat complex II component(SEC23A)	NM_006364	115.2	133.6	0.04427	1.109

SEC23A	Sec23 homolog A, coat complex II component(SEC23A)	NM_006364	132.4	130.5	0.04427	1.109
ADAMDEC1	ADAM like decysin 1(ADAMDEC1)	NM_014479	121.7	106.7	0.04427	0.86
RHEB	Ras homolog enriched in brain(RHEB)	NM_005614	376	314.4	0.0443	0.861
RNA5S9	RNA, 5S ribosomal 9(RNA5S9)	NR_023371	186.3	225.7	0.0443	1.246
RAX2	retina and anterior neural fold homeobox 2(RAX2)	NM_032753	174.1	214.2	0.0444	1.273
RAX2	retina and anterior neural fold homeobox 2(RAX2)	NM_032753	1050.1	1081.8	0.0444	1.273
XRCC2	X-ray repair cross complementing 2(XRCC2)	NM_005431	118.1	123.6	0.04448	1.462
XRCC2	X-ray repair cross complementing 2(XRCC2)	NM_005431	1119.2	1461.7	0.04448	1.462
		XR_015615	212.3	247.8	0.04478	1.255
		XR_038081	104.2	124.1	0.04482	1.134
LNPEP	leucyl and cystinyl aminopeptidase(LNPEP)	NM_005575	1079.3	1296.6	0.04486	1.342
BNIP1	BCL2 interacting protein 1(BNIP1)	NM_013980	2942.2	4061.6	0.04487	1.536

		NM_001080831	206.3	168	0.0449	0.82
AKTIP	AKT interacting protein(AKTIP)	NM_001012398	117.9	111.6	0.04493	0.881
SUGP1	SURP and G-patch domain containing 1(SUGP1)	NM_182812	189.5	213.6	0.04506	1.172
		XR_037117	201.4	150.5	0.0452	0.664
		XR_037117	1539.6	919.6	0.0452	0.664
		XM_937469	111.1	133.5	0.04522	1.142
		XM_001725687	1333	862.6	0.04531	0.72
		BM977869	133.1	121.8	0.04538	0.89
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	99.8	106.1	0.04544	0.876
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	116.2	112.9	0.04544	0.876
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	120.1	110.9	0.04544	0.876
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	130.5	119.2	0.04544	0.876
		XM_045290	611.7	424.1	0.04551	0.745
ZDHHC1	zinc finger DHHC-type containing 1(ZDHHC1)	NM_013304	240.9	295.7	0.04553	1.287
DMC1	DNA meiotic recombinase 1(DMC1)	NM_007068	321.1	355.3	0.04558	1.21

RPS21	ribosomal protein S21(RPS21)	NM_001024	165.5	149.7	0.04564	0.898
		XM_0017199081	312.4	211.5	0.04572	0.682
		XM_935907	658.5	437.2	0.04581	0.702
SLC10A7	solute carrier family 10 member 7(SLC10A7)	NM_001029998	132.8	127.5	0.04595	0.932
SLC10A7	solute carrier family 10 member 7(SLC10A7)	NM_001029998	150.1	141.2	0.04595	0.932
		BU622756	122.4	141.6	0.04598	1.108
SNHG8	small nucleolar RNA host gene 8(SNHG8)	NR_003584	607.7	410.6	0.046	0.724
ZKSCAN3	zinc finger with KRAB and SCAN domains 3(ZKSCAN3)	NM_024493	132.8	124.1	0.04603	0.896
NECAB2	N-terminal EF-hand calcium binding protein 2(NECAB2)	NM_019065	166.7	183.6	0.04606	1.104
KYAT1	kynurenine aminotransferase 1(KYAT1)	NM_004059	155.2	136.1	0.04607	0.857
MFSD14C	major facilitator superfamily domain containing 14C(MFSD14C)	NR_002894	3646.4	4446.2	0.04622	1.378
GLE1	GLE1, RNA export mediator(GLE1)	NM_001003722	468.2	977	0.04625	2.408
		XM_929297	131.5	147.9	0.04627	1.092

CBX5	chromobox 5(CBX5)	NM_012117	173.6	145.5	0.04627	0.821
TPM1	tropomyosin 1 (alpha)(TPM1)	NM_001018008	130.7	155.5	0.04645	1.158
TPM1	tropomyosin 1 (alpha)(TPM1)	NM_001018008	141.1	143.1	0.04645	1.158
GRK3	G protein-coupled receptor kinase 3(GRK3)	NM_005160	1794	2516.4	0.04659	1.552
RANBP1	RAN binding protein 1(RANBP1)	NM_002882	344.3	225	0.04659	0.677
RANBP1	RAN binding protein 1(RANBP1)	NM_002882	879.4	649.2	0.04659	0.677
ANXA1	annexin A1(ANXA1)	NM_000700	277.1	186	0.04679	0.663
		XR_040497	152.9	188.2	0.04695	1.212
		XM_939730	126.9	148.6	0.04695	1.123
ZNF549	zinc finger protein 549(ZNF549)	NM_153263	178.3	196.9	0.04698	1.137
ZNF549	zinc finger protein 549(ZNF549)	NM_153263	6038.9	7142.4	0.04698	1.137
		XM_927228	137.4	131.4	0.04711	0.927
		BI827719	117.1	135.8	0.04713	1.102
GUSB	glucuronidase beta(GUSB)	NM_000181	454.5	489.2	0.04715	1.158
HMGN3	high mobility group nucleosomal binding domain 3(HMGN3)	NM_004242	1643.4	877.1	0.04716	0.603

HMGN2	high mobility group nucleosomal binding domain 2(HMGN2)	NM_005517	177.1	154.4	0.04716	0.603
AMACR	alpha-methylacyl-CoA racemase(AMACR)	NM_203382	168.3	125.4	0.04725	0.726
SPOPL	speckle type BTB/POZ protein like(SPOPL)	NM_001001664	148.1	127.6	0.04729	0.849
		XM_001719439	302.5	194.1	0.04737	0.638
		XR_039723	346	218.3	0.04738	0.652
CDC123	cell division cycle 123(CDC123)	NM_006023	126.8	148.1	0.04739	1.139
ZNF600	zinc finger protein 600(ZNF600)	NM_198457	243.7	303.9	0.04742	1.353
PIGO	phosphatidylinositol glycan anchor biosynthesis class O(PIGO)	NM_152850	207.2	251.3	0.04745	1.247
WBP11	WW domain binding protein 11(WBP11)	NM_016312	436.2	358.1	0.04749	0.867
PDCD7	programmed cell death 7(PDCD7)	NM_005707	333.5	266.3	0.04761	0.828
PDCD7	programmed cell death 7(PDCD7)	NM_005707	24825.1	30661.9	0.04761	0.828
TRPV5	transient receptor potential cation channel subfamily V member 5(TRPV5)	NM_019841	189.7	224.8	0.04764	1.241
tfcp2	transcription factor CP2(TFCP2)	NM_005653	206.7	170.4	0.0477	0.837

		XM_944813	121.3	138.3	0.04772	1.084
		XM_943208	145.5	159.1	0.04772	1.081
SH2D1A	SH2 domain containing 1A(SH2D1A)	NM_002351	120.3	114.5	0.04772	0.895
YPEL2	yippee like 2(YPEL2)	NM_001005404	160	141.3	0.04795	0.867
GET4	golgi to ER traffic protein 4(GET4)	NM_015949	102.4	126.3	0.04797	1.171
RPS7	ribosomal protein S7(RPS7)	NM_001011	145.4	127.6	0.04804	0.852
RPS7	ribosomal protein S7(RPS7)	NM_001011	194.3	202.8	0.04804	0.852
		XM_001722060	1000.1	1216.9	0.04813	1.363
CCNG2	cyclin G2(CCNG2)	NM_004354	125	116.1	0.04814	0.678
CCNH	cyclin H(CCNH)	NM_001239	226.2	154.9	0.04814	0.678
RPS8	ribosomal protein S8(RPS8)	NM_001012	1470.6	725	0.04814	0.592
		XM_001715097	129.9	149.6	0.04821	1.136
HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B(HNRNPAB)	NM_004499	146.7	132	0.04826	0.877
SNRPF	small nuclear ribonucleoprotein polypeptide F(SNRPF)	NM_003095	641.8	423.4	0.04829	0.681

SNRPF	small nuclear ribonucleoprotein polypeptide F(SNRPF)	NM_003095	1328.4	906.8	0.04829	0.681			
DSC3	desmocollin 3(DSC3)	NM_024423	111.2	182.1	0.04845	1.811			
TMEM54	transmembrane protein 54(TMEM54)	NM_033504	145.8	179.7	0.04849	1.251			
CDK7	cyclin dependent kinase 7(CDK7)	NM_001799	719.1	859.7	0.04854	1.352			
SGSM2	small G protein signaling modulator 2(SGSM2)	NM_014853	912.5	950.8	0.04855	1.16			
		XM_939709	186	214.1	0.04856	1.229			
ERAP2	endoplasmic reticulum aminopeptidase 2(ERAP2)	NM_022350	206.1	179.1	0.0487	1.453			
ERBB2	erb-b2 receptor tyrosine kinase 2(ERBB2)	NM_004448	5897.6	7862.8	0.0487	1.453			
		DB336496	165.9	196.3	0.04875	1.22			
NOC4L	nucleolar complex associated 4 homolog(NOC4L)	NM_024078	117.2	136.9	0.04876	1.124			
NOC4L	nucleolar complex associated 4 homolog(NOC4L)	NM_024078	177.9	206.1	0.04876	1.124	NM_031012	19.39	0.85
		XR_039555	179.2	126.1	0.04876	0.683			
RPL23	ribosomal protein L23(RPL23)	NM_000978	5124.5	3196.8	0.04884	0.747			

ACTL6A	actin like 6A(ACTL6A)	NM_004301	1214.3	784.4	0.04888	0.684			
OSTC	oligosaccharyltransferase complex non-catalytic subunit(OSTC)	NM_021227	199.2	178.3	0.04891	0.751	NM_012904	10.16	55.22
OSTC	oligosaccharyltransferase complex non-catalytic subunit(OSTC)	NM_021227	757.8	544.9	0.04891	0.751			
BAIAP2	BAI1 associated protein 2(BAIAP2)	NM_006340	127.9	121.8	0.04894	0.918			
CRHR1	corticotropin releasing hormone receptor 1(CRHR1)	NM_004382	99.8	151.5	0.04895	1.552			
		AI738931	137.8	172.3	0.04898	1.258			
MBLAC2	metallo-beta-lactamase domain containing 2(MBLAC2)	NM_203406	127.6	120.1	0.04907	0.915			
LSM5	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated(LSM5)	NM_012322	177.6	142.4	0.04934	0.796			
LSM7	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated(LSM7)	NM_016199	566.5	466.3	0.04934	0.796			
rps15a	ribosomal protein S15a(RPS15A)	NM_001019	182.9	136.5	0.04938	0.741			
rps15a	ribosomal protein S15a(RPS15A)	NM_001019	1616	913.9	0.04938	0.741			
RPS14	ribosomal protein S14(RPS14)	NM_001025070	8805.8	5307.3	0.04948	0.725			

		XM_001724343	839.5	430.9	0.04948	0.571			
		XM_928464	435.7	340.4	0.0495	0.831	NM_012823	17.52	0.04
		XR_038937	954.2	614.2	0.04961	0.694			
DRD3	dopamine receptor D3(DRD3)	NM_000796	113.3	125.7	0.04964	0.895			
DRG1	developmentally regulated GTP binding protein 1(DRG1)	NM_004147	146.9	133.5	0.04964	0.895			
		XR_038410	135.6	120.5	0.04965	0.866			
CCDC53	coiled-coil domain containing 53(CCDC53)	NM_016053	365.4	244.6	0.04973	0.687			
TBCE	tubulin folding cofactor E(TBCE)	NM_001079515	415.5	461.1	0.04975	1.225			
		XR_017366	139	124.6	0.04983	0.886			
		XM_930344	500.6	383.9	0.04997	0.799			
RHBDD3	rhomboid domain containing 3(RHBDD3)	NM_012265	207.7	257.5	0.05	1.319			

Gene Symbol	**Gene Name**	**Accession No.**	**CON Chow M Mean**	**CON HFHS M Mean**	**p-val CON M HFHS vs. CON M Chow**	**Ratio CON M HFHS vs. CON M Chow**	**REFSEQ ID**	**NEPHRON (MEAN RPKM)**	**COLLECTING DUCT (MEAN RPKM)**
		XM_927511	115.2	97.2	0.00001	0.813			

ADCK2	aarF domain containing kinase 2(ADCK2)	NM_052853	107.3	133.3	0.00016	1.171			
RPS26	ribosomal protein S26(RPS26)	NM_001029	89.2	109.3	0.00018	1.183			
RPS26	ribosomal protein S26(RPS26)	NM_001029	1360.8	1666	0.00018	1.183			
C3	complement C3(C3)	NM_000064	116.5	99.5	0.00024	0.805			
SLC38A3	solute carrier family 38 member 3(SLC38A3)	NM_006841	210.4	129.1	0.00044	0.564			
		XM_372319	144.1	116.9	0.00046	0.762			
KLF9	Kruppel like factor 9(KLF9)	NM_001206	332.5	774.2	0.00046	1.981			
MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like(MTHFD2L)	NM_001004346	95.7	122.6	0.00063	1.219	NM_017193	356.13	8.18
TSPAN1	tetraspanin 1(TSPAN1)	NM_005727	96	132.6	0.00076	1.291	NM_017193	356.13	8.18
		XM_001715244	115.4	105.2	0.00082	0.864	NM_017193	356.13	8.18
SNRPC	small nuclear ribonucleoprotein polypeptide C(SNRPC)	NM_003093	237.3	363.8	0.00102	1.336	NM_017193	356.13	8.18
SNRPC	small nuclear ribonucleoprotein polypeptide C(SNRPC)	NM_003093	355.1	429.4	0.00102	1.336			
PHF14	PHD finger protein 14(PHF14)	NM_014660	120.2	109.4	0.00107	0.883			

		XM_001723369	125.5	110.8	0.00135	0.85
ATP6V0E2	ATPase H+ transporting V0 subunit e2(ATP6V0E2)	NM_145230	1451.1	1696	0.00139	1.281
ATP6V0E1	ATPase H+ transporting V0 subunit e1(ATP6V0E1)	NM_003945	625.7	926.7	0.00139	1.281
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2(UGGT2)	NM_020121	135.8	193.7	0.00139	1.276
EFNB2	ephrin B2(EFNB2)	NM_004093	99.5	121	0.00143	1.17
IRF2BP2	interferon regulatory factor 2 binding protein 2(IRF2BP2)	NM_182972	165.2	239.2	0.00163	1.302
IRF2BPL	interferon regulatory factor 2 binding protein like(IRF2BPL)	NM_024496	218.4	267.1	0.00163	1.302
KCNH4	potassium voltage-gated channel subfamily H member 4(KCNH4)	NM_012285	108.7	135	0.002	1.181
BZW1	basic leucine zipper and W2 domains 1(BZW1)	NM_014670	124.8	114.3	0.00206	0.878
MYLK	myosin light chain kinase(MYLK)	NM_053026	142.6	204	0.00209	1.297
		XM_929153	99.5	131.8	0.00212	1.246

ADPRHL2	ADP-ribosylhydrolase like 2(ADPRHL2)	NM_017825	145.2	133.9	0.00222	0.856
SHARPIN	SHANK associated RH domain interactor(SHARPIN)	NM_030974	114.9	152.9	0.00224	1.261
		XM_933942	144.2	131.5	0.00226	0.86
CDAN1	codanin 1(CDAN1)	NM_138477	200.4	163.3	0.00254	0.732
POTEE	POTE ankyrin domain family member E(POTEE)	NM_001083538	102.3	133.2	0.00259	1.239
C8orf59	chromosome 8 open reading frame 59(C8orf59)	NM_001099672	268.8	691.5	0.00279	2.227
PHF7	PHD finger protein 7(PHF7)	NM_016483	116.6	108.1	0.00286	0.891
ARSB	arylsulfatase B(ARSB)	NM_000046	124.2	109.9	0.00294	0.848
ARSD	arylsulfatase D(ARSD)	NM_001669	149.8	144.3	0.00294	0.848
NEDD8	neural precursor cell expressed, developmentally down-regulated 8(NEDD8)	NM_006156	265.5	457.3	0.00295	1.49
NEDD8	neural precursor cell expressed, developmentally down-regulated 8(NEDD8)	NM_006156	2116.6	2390.9	0.00295	1.49
Amy1a	amylase, alpha 1A (salivary)(AMY1A)	NM_001008221	94	117	0.00296	1.191

KALRN	kalirin, RhoGEF kinase(KALRN)	NM_003947	3577.2	5517.9	0.00297	1.382
LRBA	LPS responsive beige-like anchor protein(LRBA)	NM_006726	104.3	129.4	0.00298	1.196
		XM_938867	98.8	117.9	0.003	1.168
LYPD6B	LY6/PLAUR domain containing 6B(LYPD6B)	NM_177964	135.8	123	0.00306	0.861
CES5A	carboxylesterase 5A(CES5A)	NM_145024	120.8	105	0.00307	0.818
		XM_945223	118	104.2	0.00314	0.851
CPNE1	copine 1(CPNE1)	NM_152931	96.3	119.8	0.00315	1.186
		AI082160	151	131.1	0.00332	0.818
CASP6	caspase 6(CASP6)	NM_001226	94.5	118	0.00333	1.193
CASP6	caspase 6(CASP6)	NM_032992	108.7	115.2	0.00333	1.193
RSRC2	arginine and serine rich coiled-coil 2(RSRC2)	NM_023012	127.2	139.8	0.00359	1.329
RSRC2	arginine and serine rich coiled-coil 2(RSRC2)	NM_023012	585.6	906.9	0.00359	1.329
TIGD1	tigger transposable element derived 1(TIGD1)	NM_145702	107.1	98.1	0.0036	0.865
SLCO3A1	solute carrier organic anion transporter family member 3A1(SLCO3A1)	NM_013272	98.3	138.1	0.00374	1.349

SLCO3A1	solute carrier organic anion transporter family member 3A1(SLCO3A1)	NM_013272	130.5	204.6	0.00374	1.349
		XM_001717918	126.8	112.3	0.00389	0.848
bag4	BCL2 associated athanogene 4(BAG4)	NM_004874	120.2	107	0.00402	0.852
ARMCX6	armadillo repeat containing, X-linked 6(ARMCX6)	NM_019007	99	114.4	0.00404	1.292
ARMT1	acidic residue methyltransferase 1(ARMT1)	NM_024573	115.1	160.1	0.00404	1.292
		XM_927848	123	149.3	0.00405	1.158
CNRIP1	cannabinoid receptor interacting protein 1(CNRIP1)	NM_015463	96.3	119.1	0.00412	1.194
SCARNA12	small Cajal body-specific RNA 12(SCARNA12)	NR_003010	128	164	0.00432	1.201
		XM_933083	143.5	127.5	0.00439	0.848
BPHL	biphenyl hydrolase like(BPHL)	NM_004332	106.6	95.8	0.00458	0.852
MIR21	microRNA 21(MIR21)	NR_029493	104	177.3	0.00469	1.562

NPIPB15	nuclear pore complex interacting protein family member B15(NPIPB15)	NM_001018059	118.4	107.9	0.00493	0.86
RTBDN	retbindin(RTBDN)	NM_001080997	130.6	122.6	0.00515	0.897
KHDRBS3	KH RNA binding domain containing, signal transduction associated 3(KHDRBS3)	NM_006558	558.2	965.9	0.00558	1.485
ODF3L2	outer dense fiber of sperm tails 3 like 2(ODF3L2)	NM_182577	137.8	124	0.00563	0.854
MS4A6A	membrane spanning 4-domains A6A(MS4A6A)	NM_022349	98.3	118.2	0.00567	1.16
VRK3	vaccinia related kinase 3(VRK3)	NM_001025778	106.9	104.7	0.00571	0.867
VRK3	vaccinia related kinase 3(VRK3)	NM_001025778	167.3	155.2	0.00571	0.867
NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147133	121.5	116.9	0.00592	0.866
NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147133	181.8	169	0.00592	0.866
		AV649055	126.1	113.6	0.00593	0.854
SON	SON DNA binding protein(SON)	NM_138927	119.6	153.9	0.00594	1.189
SON	SON DNA binding protein(SON)	NM_138927	171.9	234	0.00594	1.189

SON	SON DNA binding protein(SON)	NM_138927	1267.9	1431.2	0.00594	1.189	NM_053502	4.02	18.01
CLDN14	claudin 14(CLDN14)	NM_012130	124.8	393.1	0.00605	2.736	NM_053502	4.02	18.01
CHRNA6	cholinergic receptor nicotinic alpha 6 subunit(CHRNA6)	NM_004198	116.5	103.1	0.00626	0.82	NM_053502	4.02	18.01
BCLAF1	BCL2 associated transcription factor 1(BCLAF1)	NM_001077440	107.8	128.6	0.00629	1.504	NM_053502	4.02	18.01
BCO1	beta-carotene oxygenase 1(BCO1)	NM_017429	556.2	960.4	0.00629	1.504			
dnase2	deoxyribonuclease 2, lysosomal(DNASE2)	NM_001375	107.8	132.5	0.00635	1.163			
ZFP36L1	ZFP36 ring finger protein like 1(ZFP36L1)	NM_004926	802.6	1633.2	0.00639	1.854			
		XM_931775	134.4	125.6	0.00661	0.887			
TICAM1	toll like receptor adaptor molecule 1(TICAM1)	NM_182919	94.4	122.5	0.00681	1.255			
TICAM1	toll like receptor adaptor molecule 1(TICAM1)	NM_182919	114.1	118.3	0.00681	1.255			
		AW274669	124.3	110.5	0.00689	0.861	NM_001009670	33.30	2.04
RUNDC1	RUN domain containing 1(RUNDC1)	NM_173079	97.3	127.8	0.00692	1.262			
MLPH	melanophilin(MLPH)	NM_001042467	128.6	115.1	0.00698	0.861			

		XR_001434	123.5	114.5	0.00698	0.88
LOC100190986	uncharacterized LOC100190986(LOC100190986)	NR_024456	123.5	109	0.00701	0.852
BRIX1	BRX1, biogenesis of ribosomes(BRIX1)	NM_018321	121.9	109.5	0.00741	0.871
ALG13	ALG13, UDP-N-acetylglucosaminyltransferase subunit(ALG13)	NM_018466	131	121.9	0.00742	0.874
KLF7	Kruppel like factor 7(KLF7)	NM_003709	159.5	275.6	0.00745	1.504
ankrd40	ankyrin repeat domain 40(ANKRD40)	NM_052855	114.4	199.7	0.00753	1.599
OGFOD1	2-oxoglutarate and iron dependent oxygenase domain containing 1(OGFOD1)	NM_018233	99.3	130	0.00761	1.228
OGFOD1	2-oxoglutarate and iron dependent oxygenase domain containing 1(OGFOD1)	NM_018233	108.8	120.6	0.00761	1.228
ACYP1	acylphosphatase 1(ACYP1)	NM_001107	147.2	120.3	0.00766	0.776
		XM_001723164	130.4	153.2	0.00769	1.108
ATCAY	ATCAY, caytaxin(ATCAY)	NM_033064	110.4	135.2	0.00773	1.172
WDFY3	WD repeat and FYVE domain containing 3(WDFY3)	NM_178583	113.6	103.2	0.00775	0.856

		XR_038195	115.5	105.7	0.00799	0.883
DNMT3L	DNA methyltransferase 3 like(DNMT3L)	NM_013369	135.1	124.2	0.00805	0.868
DNMT3B	DNA methyltransferase 3 beta(DNMT3B)	NM_006892	100.9	100.9	0.00805	0.868
OPRM1	opioid receptor mu 1(OPRM1)	NM_001008505	109	127.7	0.00808	1.105
OPRM1	opioid receptor mu 1(OPRM1)	NM_001008505	178.1	175	0.00808	1.105
ADIPOQ	adiponectin, C1Q and collagen domain containing(ADIPOQ)	NM_004797	91.8	113.8	0.00808	1.184
CACNB1	calcium voltage-gated channel auxiliary subunit beta 1(CACNB1)	NM_199247	123	112.6	0.00821	0.888
ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)(ENTPD6)	NM_001247	86.8	106.3	0.00831	1.194
ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7(ENTPD7)	NM_020354	101.7	105.3	0.00831	1.194
rab41	RAB41, member RAS oncogene family(RAB41)	NM_001032726	159.4	138.4	0.00832	0.823
FAM83F	family with sequence similarity 83 member F(FAM83F)	NM_138435	124.2	103.8	0.00838	0.795

PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	90.1	96.1	0.00851	0.845
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	113.2	103.8	0.00851	0.845
PGA3	pepsinogen 3, group I (pepsinogen A)(PGA3)	NM_001079807	130.2	116.3	0.00851	0.845
SNX13	sorting nexin 13(SNX13)	NM_015132	124	166.1	0.00852	1.259
TDGP1	thymine-DNA glycosylase pseudogene 1(TDGP1)	NR_024382	94.7	117.4	0.00859	1.164
CCT5	chaperonin containing TCP1 subunit 5(CCT5)	NM_012073	453.4	761.3	0.00873	1.48
PRAM1	PML-RARA regulated adaptor molecule 1(PRAM1)	NM_032152	117.5	111	0.00876	0.897
SDIM1	stress responsive DNAJB4 interacting membrane protein 1(SDIM1)	AK129633	111.7	100.4	0.00883	0.846
RHBDL1	rhomboid like 1(RHBDL1)	NM_003961	125.4	110.9	0.00884	0.858
RBM48	RNA binding motif protein 48(RBM48)	NM_032120	111.5	147.3	0.00888	1.228
RBM48	RNA binding motif protein 48(RBM48)	NM_032120	113.2	123.3	0.00888	1.228
PBXIP1	PBX homeobox interacting protein 1(PBXIP1)	NM_020524	161.6	143.6	0.00892	0.842
		NM_001004302	103.3	131.4	0.00904	1.218

		XM_001126650	93.7	111.4	0.00908	1.155
LMBRD1	LMBR1 domain containing 1(LMBRD1)	NM_018368	147.4	118.6	0.00911	0.755
		XR_019076	93.7	108.9	0.0092	1.124
		AI351498	120.3	109.6	0.00935	0.879
TRIM3	tripartite motif containing 3(TRIM3)	NM_006458	150.2	141.6	0.0094	0.809
TRIM3	tripartite motif containing 3(TRIM3)	NM_006458	207.4	183.2	0.0094	0.809
		XM_001131286	127.8	120.4	0.00948	0.887
		BG951912	120.2	108.2	0.0095	0.873
ALX3	ALX homeobox 3(ALX3)	NM_006492	116.8	226.2	0.00957	1.705
ALX1	ALX homeobox 1(ALX1)	NM_006982	91.2	242.9	0.00957	1.705
TUBA3FP	tubulin alpha 3f pseudogene(TUBA3FP)	NR_003608	118.3	110.9	0.00964	0.896
TSNAX	translin associated factor X(TSNAX)	NM_005999	167.6	278.8	0.00969	1.43
		XM_941665	377.1	707.9	0.00979	1.679
TAGLN	transgelin(TAGLN)	NM_001001522	126.5	115	0.00986	0.86
FAM193A	family with sequence similarity 193 member A(FAM193A)	NM_003704	246	398.6	0.00989	1.403

RNF146	ring finger protein 146(RNF146)	NM_030963	99.4	102.1	0.00991	1.355
RNF146	ring finger protein 146(RNF146)	NM_030963	122.5	189.7	0.00991	1.355
		BX105500	111.7	98.4	0.00991	0.852
PCYOX1L	prenylcysteine oxidase 1 like(PCYOX1L)	NM_024028	100.8	119.2	0.00991	1.136
SQLE	squalene epoxidase(SQLE)	NM_003129	103	141.6	0.00998	1.296
SQLE	squalene epoxidase(SQLE)	NM_003129	105	115.6	0.00998	1.296
		CR593338	122.9	114.7	0.00999	0.873
KDM4B	lysine demethylase 4B(KDM4B)	NM_015015	333.1	517.7	0.01009	1.343
UBE2DNL	ubiquitin conjugating enzyme E2 D N-terminal like (pseudogene)(UBE2DNL)	NR_024062	105.1	95.2	0.01014	0.861
C11orf58	chromosome 11 open reading frame 58(C11orf58)	NM_001142705	191.7	170.1	0.01023	0.818
PRKAR2A	protein kinase cAMP-dependent type II regulatory subunit alpha(PRKAR2A)	NM_004157	98.8	121.2	0.01026	1.171
DNAJC10	DnaJ heat shock protein family (Hsp40) member C10(DNAJC10)	NM_018981	102.7	114.7	0.01029	1.362

DNAJC11	DnaJ heat shock protein family (Hsp40) member C11(DNAJC11)	NM_018198	514.6	812.9	0.01029	1.362			
DNAH6	dynein axonemal heavy chain 6(DNAH6)	AB051484	149.9	117.8	0.01039	0.756			
RHEB	Ras homolog enriched in brain(RHEB)	NM_005614	256	358.2	0.01042	1.225			
DHX15	DEAH-box helicase 15(DHX15)	NM_001358	230	328	0.01045	1.632			
DHX16	DEAH-box helicase 16(DHX16)	NM_003587	752.7	1388.1	0.01045	1.632			
		XM_001126824	150.6	135.5	0.01048	0.85			
		XM_001716052	110.8	100.1	0.01052	0.87			
AMY1B	amylase, alpha 1B (salivary)(AMY1B)	NM_001008218	112.2	120.4	0.01056	1.624			
AMY1C	amylase, alpha 1C (salivary)(AMY1C)	NM_001008219	1317.4	2434.2	0.01056	1.624			
TMEM123	transmembrane protein 123(TMEM123)	NM_052932	418.7	722.5	0.01061	1.498	NM_001107943	0.63	112.77
LEO1	LEO1 homolog, Paf1/RNA polymerase II complex component(LEO1)	NM_138792	107.1	125	0.01068	1.12			
QKI	QKI, KH domain containing RNA binding(QKI)	NM_006775	96.4	119.5	0.01078	1.165			

QKI	QKI, KH domain containing RNA binding(QKI)	NM_006775	105.3	119.9	0.01078	1.165
		XM_937684	132.4	125.1	0.01083	0.894
MIR33B	microRNA 33b(MIR33B)	NR_030361	88.7	105.8	0.01083	1.168
HNRNPK	heterogeneous nuclear ribonucleoprotein K(HNRNPK)	NM_031263	184.4	274.4	0.01088	1.348
HNRNPK	heterogeneous nuclear ribonucleoprotein K(HNRNPK)	NM_031263	825.9	1283.7	0.01088	1.348
HNRNPK	heterogeneous nuclear ribonucleoprotein K(HNRNPK)	NM_031263	988.8	1505.9	0.01088	1.348
		XM_001716310	107	100.3	0.01118	0.89
		XM_936314	127.8	114.9	0.01119	0.86
FBXW5	F-box and WD repeat domain containing 5(FBXW5)	NM_178226	251.7	240.3	0.01125	0.839
		XM_496269	99.6	121.5	0.01127	1.159
GSTM1	glutathione S-transferase mu 1(GSTM1)	NM_000561	98.9	115.8	0.01133	1.126

ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif 6(ADAMTS6)	NM_197941	170.6	291.4	0.01137	1.484	NM_134372	22.51	0.03
FHOD1	formin homology 2 domain containing 1(FHOD1)	NM_013241	296.4	997	0.01144	2.926			
		XM_001715275	115	106.1	0.01146	0.877			
		XM_934672	106.9	102.5	0.01155	0.918			
CYP39A1	cytochrome P450 family 39 subfamily A member 1(CYP39A1)	NM_016593	134.6	121	0.01157	0.858			
HSD17B4	hydroxysteroid 17-beta dehydrogenase 4(HSD17B4)	NM_000414	97.4	225.8	0.01161	2.07			
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	104.2	119.7	0.01162	1.113			
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	204.8	217.2	0.01162	1.113			
RBPMS	RNA binding protein with multiple splicing(RBPMS)	NM_001008710	109.3	149.7	0.01162	1.274			
PHLDA1	pleckstrin homology like domain family A member 1(PHLDA1)	NM_007350	110.5	108.7	0.01165	1.361			
PHLDA1	pleckstrin homology like domain family A member 1(PHLDA1)	NM_007350	186.5	293	0.01165	1.361			

ZFHX4	zinc finger homeobox 4(ZFHX4)	NM_024721	80.5	98.4	0.01169	1.213
rbm12	RNA binding motif protein 12(RBM12)	NM_006047	121.2	152.4	0.0118	1.177
rbm12	RNA binding motif protein 12(RBM12)	NM_006047	138.8	179.8	0.0118	1.177
		DB336481	136.1	128.4	0.0118	0.882
HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2(HSD3B2)	NM_000198	98.5	113.7	0.01189	1.111
CCDC87	coiled-coil domain containing 87(CCDC87)	NM_018219	116.5	102.2	0.01196	0.848
SLC35A2	solute carrier family 35 member A2(SLC35A2)	NM_001032289	109.9	126.1	0.01206	1.094
SLC35A2	solute carrier family 35 member A2(SLC35A2)	NM_001032289	345.8	386	0.01206	1.094
		AW044615	120.4	110.6	0.01257	0.877
		XM_001720423	149.9	130	0.01262	0.833
Snora41	small nucleolar RNA, H/ACA box 41(SNORA41)	NR_002590	109.5	143.7	0.01267	1.264
RBFOX2	RNA binding protein, fox-1 homolog 2(RBFOX2)	NM_001082576	234.9	422.2	0.0128	1.554

HTR3A	5-hydroxytryptamine receptor 3A(HTR3A)	NM_000869	106.4	96.9	0.01282	0.871	NM_001031645	1.93	10.04
HTR3A	5-hydroxytryptamine receptor 3A(HTR3A)	NM_213621	147.9	157.9	0.01282	0.871			
MATR3	matrin 3(MATR3)	NM_199189	97.7	103.8	0.01297	1.418			
MATR3	matrin 3(MATR3)	NM_199189	100.8	111	0.01297	1.418			
MATR3	matrin 3(MATR3)	NM_199189	1659.9	2694.5	0.01297	1.418			
MTX1	metaxin 1(MTX1)	NM_198883	171.5	158.1	0.01297	0.84			
MOXD1	monooxygenase DBH like 1(MOXD1)	NM_015529	102.9	168.3	0.01312	1.524			
TMEM136	transmembrane protein 136(TMEM136)	NM_174926	86.9	106.7	0.01314	1.197			
AHCTF1	AT-hook containing transcription factor 1(AHCTF1)	NM_015446	1763.1	731.7	0.01316	0.351			
AP4E1	adaptor related protein complex 4 epsilon 1 subunit(AP4E1)	NM_007347	168.8	150.5	0.01317	0.84			
MAPKBP1	mitogen-activated protein kinase binding protein 1(MAPKBP1)	NM_014994	125.3	135	0.01326	1.139			
MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5(MAPKAPK5)	NM_139078	91.6	107.7	0.01326	1.139			

SF3A3	splicing factor 3a subunit 3(SF3A3)	NM_006802	817.1	1234.5	0.01327	1.327			
IFT172	intraflagellar transport 172(IFT172)	NM_015662	164.7	216.9	0.01331	1.2			
B3GAT1	beta-1,3-glucuronyltransferase 1(B3GAT1)	NM_054025	102.7	124.5	0.01357	1.164			
RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)(RAC3)	NM_005052	238.8	189.4	0.01379	0.732	NM_144748	66.99	0.14
		XM_371878	94.4	114.5	0.01381	1.173			
MSANTD4	Myb/SANT DNA binding domain containing 4 with coiled-coils(MSANTD4)	NM_032424	171.2	239.6	0.01392	1.249			
SEBOX	SEBOX homeobox(SEBOX)	NM_001080837	114.6	106.1	0.01403	0.876			
NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D(NAPEPLD)	NM_198990	117.5	121.5	0.01417	1.212			
NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D(NAPEPLD)	NM_198990	151.5	203.1	0.01417	1.212			
CHAD	chondroadherin(CHAD)	NM_001267	100	122.7	0.01418	1.187			

PPIE	peptidylprolyl isomerase E(PPIE)	NM_006112	124.6	165.2	0.01427	1.224			
		XR_037672	112.5	135.6	0.01433	1.148			
HAUS2	HAUS augmin like complex subunit 2(HAUS2)	NM_018097	172.6	247	0.01436	1.288	NM_001107793	77.29	6.85
HAT1	histone acetyltransferase 1(HAT1)	NM_003642	134.1	151	0.01436	1.288	NM_001107793	77.29	6.85
		XM_931506	106.7	125.6	0.01442	1.128	NM_001107793	77.29	6.85
HOXD3	homeobox D3(HOXD3)	NM_006898	201.9	444.6	0.0146	1.94	NM_001107793	77.29	6.85
BTLA	B and T lymphocyte associated(BTLA)	NM_181780	105	97.1	0.01464	0.878			
FAM26D	family with sequence similarity 26 member D(FAM26D)	NM_153036	106.6	112.5	0.01474	0.902			
FAM26F	family with sequence similarity 26 member F(FAM26F)	NM_001010919	121.7	114.9	0.01474	0.902			
PI15	peptidase inhibitor 15(PI15)	NM_015886	95.2	113.2	0.01484	1.136			
PI15	peptidase inhibitor 15(PI15)	NM_015886	136.8	127.6	0.01484	1.136			

ELP2	elongator acetyltransferase complex subunit 2(ELP2)	NM_018255	133.4	268.5	0.01485	1.733
ELOVL6	ELOVL fatty acid elongase 6(ELOVL6)	NM_024090	113.7	173.4	0.01485	1.733
FNDC4	fibronectin type III domain containing 4(FNDC4)	NM_022823	338.7	599.5	0.01487	1.536
CAPRIN2	caprin family member 2(CAPRIN2)	NM_023925	160.4	234.6	0.01487	1.311
MPHOSPH6	M-phase phosphoprotein 6(MPHOSPH6)	NM_005792	127.5	164.8	0.01492	1.202
CPSF4	cleavage and polyadenylation specific factor 4(CPSF4)	NM_001081559	152.5	191.1	0.01498	1.18
CPSF3L	cleavage and polyadenylation specific factor 3-like(CPSF3L)	NM_017871	97.9	122.7	0.01498	1.18
		XM_001132711	142.6	127.2	0.01513	0.848
CCDC124	coiled-coil domain containing 124(CCDC124)	NM_138442	91.1	110.5	0.0153	1.189
RARB	retinoic acid receptor beta(RARB)	NM_000965	122.7	195.1	0.01545	1.398
RARB	retinoic acid receptor beta(RARB)	NM_000965	126.3	251.4	0.01545	1.398

MSLNL	mesothelin-like(MSLNL)	NM_001025190	108.4	101	0.01554	0.856
MSLNL	mesothelin-like(MSLNL)	NM_001025190	113.5	102	0.01554	0.856
rtf1	RTF1 homolog, Paf1/RNA polymerase II complex component(RTF1)	NM_015138	152.7	142.8	0.01576	0.873
FZD1	frizzled class receptor 1(FZD1)	NM_003505	117.6	110.1	0.01589	0.88
FZD2	frizzled class receptor 2(FZD2)	NM_001466	251.1	258.2	0.01589	0.88
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	NM_001895	125.5	163.4	0.01591	1.199
SYTL2	synaptotagmin like 2(SYTL2)	NM_032943	90.5	116.1	0.01595	1.231
tmem132a	transmembrane protein 132A(TMEM132A)	NM_178031	98.8	130.8	0.01611	1.252
MORF4L2	mortality factor 4 like 2(MORF4L2)	NM_012286	583.1	916.9	0.01613	1.377
		NM_001004349	124.5	112.3	0.01613	0.847
GDI1	GDP dissociation inhibitor 1(GDI1)	NM_001493	141.8	130.3	0.01614	0.876
CDHR5	cadherin related family member 5(CDHR5)	NM_021924	140.3	129.6	0.01617	0.872
ZCCHC8	zinc finger CCHC-type containing 8(ZCCHC8)	NM_017612	150	193.1	0.01618	1.171
NOXO1	NADPH oxidase organizer 1(NOXO1)	NM_172167	142.3	115.5	0.01621	0.757

ORAI3	ORAI calcium release-activated calcium modulator 3(ORAI3)	NM_152288	180.3	165.3	0.01627	0.85			
mgarp	mitochondria localized glutamic acid rich protein(MGARP)	NM_032623	87.5	107.8	0.01629	1.203			
mgarp	mitochondria localized glutamic acid rich protein(MGARP)	NM_032623	97.1	148.2	0.01629	1.203			
MT1X	metallothionein 1X(MT1X)	NM_005952	6772.5	2593.9	0.01632	0.32			
ZNF174	zinc finger protein 174(ZNF174)	NM_001032292	108.9	108.1	0.01637	1.156			
ZNF174	zinc finger protein 174(ZNF174)	NM_001032292	110.7	135.4	0.01637	1.156	NM_001009603	28.32	0.90
H2AFJ	H2A histone family member J(H2AFJ)	NM_018267	111.7	104.7	0.01649	0.888			
DCAF4L1	DDB1 and CUL4 associated factor 4 like 1(DCAF4L1)	NM_001029955	99.8	117.6	0.01649	1.121			
FLYWCH1	FLYWCH-type zinc finger 1(FLYWCH1)	NM_020912	124.4	112.4	0.01661	0.874			
LRRC46	leucine rich repeat containing 46(LRRC46)	NM_033413	113.2	103.7	0.01672	0.856			
LRRC45	leucine rich repeat containing 45(LRRC45)	NM_144999	110.5	99.2	0.01672	0.856			
NME3	NME/NM23 nucleoside diphosphate kinase 3(NME3)	NM_002513	1065.4	800.5	0.01674	0.659			

LIPT1	lipoyltransferase 1(LIPT1)	NM_015929	101.6	127.9	0.01677	1.198
LITAF	lipopolysaccharide induced TNF factor(LITAF)	NM_004862	109	116.6	0.01677	1.198
HM13	histocompatibility minor 13(HM13)	NM_178580	132.4	145.5	0.01679	1.248
HM13	histocompatibility minor 13(HM13)	NM_178582	175	246.4	0.01679	1.248
CCZ1	CCZ1 homolog, vacuolar protein trafficking and biogenesis associated(CCZ1)	NM_015622	868.3	1276	0.01691	1.288
		XM_943482	115.3	107.2	0.01716	0.878
ITPA	inosine triphosphatase(ITPA)	NM_033453	1119.3	1967.5	0.01725	1.573
ITM2C	integral membrane protein 2C(ITM2C)	NM_001012516	735.9	1104.2	0.01725	1.573
LOC105378397	uncharacterized LOC105378397(LOC105378397)	BX092644	201.8	162.1	0.01735	0.754
CSNK1G1	casein kinase 1 gamma 1(CSNK1G1)	NM_022048	142.1	200.6	0.01737	1.399
csnk1e	casein kinase 1 epsilon(CSNK1E)	NM_152221	127.6	197.4	0.01737	1.399
TSACC	TSSK6 activating cochaperone(TSACC)	NM_144627	106.5	133.2	0.01756	1.213
ZNF77	zinc finger protein 77(ZNF77)	NM_021217	108.6	137.3	0.0176	1.194

TMEM237	transmembrane protein 237(TMEM237)	NM_001044385	145.7	225.7	0.01761	1.367
PCM1	pericentriolar material 1(PCM1)	NM_006197	268.7	361.1	0.01767	1.172
PCM1	pericentriolar material 1(PCM1)	NM_006197	382.6	494	0.01767	1.172
GSTO1	glutathione S-transferase omega 1(GSTO1)	NM_004832	122.2	115.2	0.0177	0.905
		XM_001714310	111.4	105.1	0.01797	0.9
PPIL2	peptidylprolyl isomerase like 2(PPIL2)	NM_014337	132.2	117.2	0.01812	0.844
PPIL2	peptidylprolyl isomerase like 2(PPIL2)	NM_014337	182.9	188.4	0.01812	0.844
PHF12	PHD finger protein 12(PHF12)	NM_020889	114	135.7	0.01823	1.14
TTC19	tetratricopeptide repeat domain 19(TTC19)	NM_017775	97.6	113.4	0.01824	1.114
CAMK1D	calcium/calmodulin dependent protein kinase ID(CAMK1D)	AK097377	263.2	521.1	0.01826	1.717
DUSP10	dual specificity phosphatase 10(DUSP10)	NM_007207	103.7	94.9	0.01855	0.862
BRD7	bromodomain containing 7(BRD7)	NM_013263	111.9	104.4	0.01868	0.878
SOX4	SRY-box 4(SOX4)	NM_003107	227.9	498.5	0.01876	1.891
HIF3A	hypoxia inducible factor 3 alpha subunit(HIF3A)	NM_022462	114.3	139.9	0.01887	1.166

		XM_001715696	116.8	111	0.01896	0.91
MAFF	MAF bZIP transcription factor F(MAFF)	NM_012323	183.4	173.6	0.01903	0.855
TRIM47	tripartite motif containing 47(TRIM47)	NM_033452	104.5	123.2	0.01921	1.118
ADCY7	adenylate cyclase 7(ADCY7)	NM_001114	260.2	480.8	0.01934	1.625
ADCY6	adenylate cyclase 6(ADCY6)	NM_020983	173	239.1	0.01934	1.625
MAP3K4	mitogen-activated protein kinase kinase kinase 4(MAP3K4)	NM_005922	157	140.3	0.01935	0.822
		XM_933836	122.2	115.4	0.01944	0.907
HLA-DQB2	major histocompatibility complex, class II, DQ beta 2(HLA-DQB2)	NM_182549	147.6	137.5	0.01945	0.88
		XR_017689	128.7	124.7	0.01946	0.914
ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2(ASAP2)	NM_003887	112.3	100	0.01946	0.869
ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2(ASAP2)	NM_003887	280.6	369.1	0.01946	0.869

ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2(ASAP2)	NM_003887	293	451.6	0.01946	0.869
		AW088717	87.6	105.6	0.01956	1.168
FOXO4	forkhead box O4(FOXO4)	NM_005938	273	450.4	0.0196	1.44
FOXO3	forkhead box O3(FOXO3)	NM_201559	197.9	344.8	0.0196	1.44
ACER3	alkaline ceramidase 3(ACER3)	NM_018367	123.9	121.4	0.01965	0.699
ACHE	acetylcholinesterase (Cartwright blood group)(ACHE)	NM_015831	213.5	160	0.01965	0.699
HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)(HNRNPH1)	NM_005520	144.4	155.1	0.01969	1.357
HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)(HNRNPH1)	NM_005520	144.8	200.9	0.01969	1.357
HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)(HNRNPH1)	NM_005520	1152.8	1768.4	0.01969	1.357
CCNK	cyclin K(CCNK)	NM_003858	93.5	110.5	0.01975	1.141
DEFA1B	defensin alpha 1B(DEFA1B)	NM_001042500	92.5	114.2	0.01976	1.177
OR2B6	olfactory receptor family 2 subfamily B member 6(OR2B6)	NM_012367	113.9	108.7	0.01984	0.919

BRD9	bromodomain containing 9(BRD9)	NM_023924	387.8	306.3	0.01987	0.71
BRD8	bromodomain containing 8(BRD8)	NM_183359	205.6	261.6	0.01987	0.71
PRPF40B	pre-mRNA processing factor 40 homolog B(PRPF40B)	NM_001031698	113.8	138.2	0.01988	1.165
CTAG2	cancer/testis antigen 2(CTAG2)	NM_020994	119.5	107	0.02006	0.879
ATL3	atlastin GTPase 3(ATL3)	NM_015459	88.8	106.2	0.02007	1.169
ZFHX3	zinc finger homeobox 3(ZFHX3)	NM_006885	161.7	298.1	0.02023	1.591
		XM_926073	121.5	115.3	0.02028	0.903
		XM_001125745	102.8	105.3	0.02028	0.861
		XM_001125745	104.3	94.6	0.02028	0.861
TCTE3	t-complex-associated-testis-expressed 3(TCTE3)	NM_174910	95.5	117.8	0.02032	1.186
		XM_928619	177.5	168.5	0.02033	0.882
ACSS2	acyl-CoA synthetase short-chain family member 2(ACSS2)	NM_001076552	116.3	101.8	0.0204	0.822
ACSS2	acyl-CoA synthetase short-chain family member 2(ACSS2)	NM_018677	1898.7	1215.1	0.0204	0.822

ITGB2	integrin subunit beta 2(ITGB2)	NM_000211	717.3	1190.7	0.02047	1.437
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	NM_181676	96.8	121.6	0.0205	1.224
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	NM_181676	165.8	336	0.0205	1.224
ZNF451	zinc finger protein 451(ZNF451)	NM_001031623	101.2	112.8	0.02055	1.245
ZNF451	zinc finger protein 451(ZNF451)	NM_001031623	105.3	136.7	0.02055	1.245
		XM_940726	110.2	98.1	0.02058	0.847
		XM_940726	136.9	138.7	0.02058	0.847
f2rl2	coagulation factor II thrombin receptor like 2(F2RL2)	NM_004101	16746	19918.8	0.02059	1.189
		XM_927957	130.6	118.9	0.02066	0.856
GUF1	GUF1 homolog, GTPase(GUF1)	NM_021927	109	151.7	0.02068	1.295
or8g1	olfactory receptor family 8 subfamily G member 1 (gene/pseudogene)(OR8G1)	NM_001002905	111.3	102.1	0.02076	0.875
ADD1	adducin 1(ADD1)	NM_001119	135.1	102.5	0.02083	0.732

LOC102724002	uncharacterized LOC102724002(LOC102724002)	AK025166	110.4	127.3	0.02097	1.116			
TOR2A	torsin family 2 member A(TOR2A)	NM_130459	93	122.1	0.02099	1.263			
		XM_001133423	98.7	115.5	0.02112	1.112			
LRRN4CL	LRRN4 C-terminal like(LRRN4CL)	NM_203422	176.6	309.6	0.02115	1.57			
SERTAD1	SERTA domain containing 1(SERTAD1)	NM_013376	288.4	483.5	0.02118	1.464			
RSBN1L	round spermatid basic protein 1 like(RSBN1L)	NM_198467	107.1	132.8	0.02119	1.186			
c14orf166	chromosome 14 open reading frame 166(C14orf166)	NM_016039	185.8	441.1	0.02125	2.099			
SAFB2	scaffold attachment factor B2(SAFB2)	NM_014649	125.4	127.8	0.0213	0.788			
SAFB2	scaffold attachment factor B2(SAFB2)	NM_014649	758.5	683	0.0213	0.788			
		CK299443	149.4	135.7	0.02132	0.864			
ELAVL1	ELAV like RNA binding protein 1(ELAVL1)	NM_001419	1332.8	1198.1	0.02133	0.763	NM_144744	0.11	40.01
DKKL1	dickkopf like acrosomal protein 1(DKKL1)	NM_014419	847.9	2015.2	0.02142	2.089			
DPH3	diphthamide biosynthesis 3(DPH3)	NM_001047434	422.9	685.1	0.02147	1.426			

AIMP2	aminoacyl tRNA synthetase complex interacting multifunctional protein 2(AIMP2)	NM_006303	125.2	114.1	0.02159	0.878
		XM_379378	108.6	127.6	0.0216	1.113
ILK	integrin linked kinase(ILK)	NM_004517	200.8	295	0.02166	1.285
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	166.4	241.1	0.02168	1.307
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	182.9	208.1	0.02168	1.307
C1orf74	chromosome 1 open reading frame 74(C1orf74)	NM_152485	117.9	107.9	0.02172	0.873
		XM_001721243	92.6	110.3	0.02172	1.146
SNORA2C	small nucleolar RNA, H/ACA box 2C(SNORA2C)	NR_002968	100.9	119.4	0.02172	1.125
		XM_001716887	115.4	154.2	0.02184	1.268
		XM_940353	114.2	106.7	0.02191	0.894
TAGLN	transgelin(TAGLN)	NM_003186	343.4	753.9	0.02196	1.675

TAGLN	transgelin(TAGLN)	NM_003186	1523	2874.1	0.02196	1.675
CEPT1	choline/ethanolamine phosphotransferase 1(CEPT1)	NM_006090	139.7	130.3	0.02205	0.872
MYL9	myosin light chain 9(MYL9)	NM_006097	185.8	203.6	0.02227	1.349
MYL9	myosin light chain 9(MYL9)	NM_006097	222	341.8	0.02227	1.349
		XM_927196	109.4	103.7	0.02243	0.892
S100A13	S100 calcium binding protein A13(S100A13)	NM_001024211	122.2	200.3	0.02246	1.49
S100A13	S100 calcium binding protein A13(S100A13)	NM_001024211	170.6	178	0.02246	1.49
PDGFA	platelet derived growth factor subunit A(PDGFA)	NM_033023	123.1	166.8	0.02255	1.263
SIDT2	SID1 transmembrane family member 2(SIDT2)	NM_001040455	350.6	349.9	0.02287	0.87
SEPT4	septin 4(SEPT4)	NM_080415	1066.6	1678.5	0.02295	1.379
TGIF1	TGFB induced factor homeobox 1(TGIF1)	NM_170695	197.5	302.5	0.02298	1.35
TGIF1	TGFB induced factor homeobox 1(TGIF1)	NM_170695	284.3	451.6	0.02298	1.35
		XM_498969	203.5	155.4	0.02308	0.718

ATG4A	autophagy related 4A cysteine peptidase(ATG4A)	NM_178270	100.5	93.6	0.02313	0.877
ORC3	origin recognition complex subunit 3(ORC3)	NM_181837	100.3	134.1	0.02325	1.267
ZFX	zinc finger protein, X-linked(ZFX)	NM_003410	95.7	116.2	0.02342	1.16
		XR_037203	378	584.7	0.02343	1.362
		AI005586	101	122.5	0.02367	1.144
NIPAL1	NIPA like domain containing 1(NIPAL1)	NM_207330	127.6	148.1	0.02372	1.113
		XM_928722	125.3	118.7	0.02373	0.911
C1orf87	chromosome 1 open reading frame 87(C1orf87)	NM_152377	94.1	109.7	0.02376	1.141
C1QA	complement C1q A chain(C1QA)	NM_015991	104.5	115.3	0.02376	1.141
AMZ2P1	archaelysin family metallopeptidase 2 pseudogene 1(AMZ2P1)	NM_153032	302.1	551.9	0.02377	1.58
PIGV	phosphatidylinositol glycan anchor biosynthesis class V(PIGV)	NM_017837	112	104.2	0.02381	0.875

TMEM158	transmembrane protein 158 (gene/pseudogene)(TMEM158)	NM_015444	224.3	1619.8	0.02384	6.279
scaf8	SR-related CTD associated factor 8(SCAF8)	NM_014892	144.7	214	0.02396	1.296
APCS	amyloid P component, serum(APCS)	NM_001639	130.2	304.7	0.02396	2.035
		XM_001716882	119.4	187.4	0.02399	1.452
DCP1A	decapping mRNA 1A(DCP1A)	NM_018403	433.8	1278.5	0.02402	2.633
		BC035064	95	108.8	0.02409	1.105
setmar	SET domain and mariner transposase fusion gene(SETMAR)	NM_006515	201	301.3	0.02416	1.305
GDF9	growth differentiation factor 9(GDF9)	NM_005260	89.5	107.5	0.02425	1.163
SGCE	sarcoglycan epsilon(SGCE)	NM_001099400	391.5	695.5	0.02436	1.536
ZNF789	zinc finger protein 789(ZNF789)	NM_001013258	112.3	154.8	0.02438	1.284
		XM_941746	101.5	130.2	0.02441	1.219
KIAA1429	KIAA1429(KIAA1429)	NM_183009	93.6	111.7	0.02442	1.152
PTK2	protein tyrosine kinase 2(PTK2)	NM_005607	1002.1	1702.9	0.02444	1.484

PDX1	pancreatic and duodenal homeobox 1(PDX1)	NM_000209	150.3	142	0.02458	0.886
MYLK	myosin light chain kinase(MYLK)	NM_053032	239.3	559.1	0.02464	1.993
		XR_017001	118.2	108.6	0.02469	0.868
		XR_017364	236.8	160.9	0.02471	0.62
DNM3	dynamin 3(DNM3)	NM_015569	132	123.2	0.02486	0.878
		XR_018230	90.2	109.7	0.02487	1.179
		XM_001713713	101.5	116.1	0.02491	1.1
RPS6KA3	ribosomal protein S6 kinase A3(RPS6KA3)	NM_004586	99.5	115	0.02507	1.236
RPS6KA3	ribosomal protein S6 kinase A3(RPS6KA3)	NM_004586	127.2	176.7	0.02507	1.236
HOXC10	homeobox C10(HOXC10)	NM_017409	343.8	869.4	0.02507	2.234
CBL	Cbl proto-oncogene(CBL)	NM_005188	171.7	142.1	0.02513	0.799
GPN1	GPN-loop GTPase 1(GPN1)	NM_007266	129.6	315.4	0.0252	1.183
GPM6B	glycoprotein M6B(GPM6B)	NM_001001995	96.8	119.1	0.0252	1.183
		XM_370711	108.5	100.6	0.02535	0.885

ORMDL1	ORMDL sphingolipid biosynthesis regulator 1(ORMDL1)	NM_016467	107.8	129.3	0.02553	1.158
IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)(IFNGR2)	NM_005534	79.7	98.7	0.02557	1.218
SLC13A2	solute carrier family 13 member 2(SLC13A2)	NM_003984	281.3	207.6	0.02559	0.68
FAM98B	family with sequence similarity 98 member B(FAM98B)	NM_001042429	347.8	311	0.02568	0.795
CEACAM21	carcinoembryonic antigen related cell adhesion molecule 21(CEACAM21)	NM_001098506	106.4	130.3	0.02569	1.163
RUFY3	RUN and FYVE domain containing 3(RUFY3)	NM_001037442	104	121.5	0.02572	1.124
RUFY3	RUN and FYVE domain containing 3(RUFY3)	NM_001037442	349.3	465.4	0.02572	1.124
OSGEPL1	O-sialoglycoprotein endopeptidase like 1(OSGEPL1)	NM_022353	107.6	116.1	0.02575	0.911
OSGEPL1	O-sialoglycoprotein endopeptidase like 1(OSGEPL1)	NM_022353	111.9	105.9	0.02575	0.911
		CD242195	119.9	113.3	0.02585	0.896
GOLGB1	golgin B1(GOLGB1)	NM_004487	767	1093.7	0.026	1.244

FKBP8	FK506 binding protein 8(FKBP8)	NM_012181	194.9	170.1	0.02609	0.813
HTR3A	5-hydroxytryptamine receptor 3A(HTR3A)	NM_000869	109.4	162.8	0.02612	1.411
PRR4	proline rich 4 (lacrimal)(PRR4)	NM_001098538	116.9	108.1	0.02613	0.858
OGFOD3	2-oxoglutarate and iron dependent oxygenase domain containing 3(OGFOD3)	NM_175902	108.8	99	0.02616	0.867
		XM_001725354	119.8	108.9	0.02617	0.865
VWA1	von Willebrand factor A domain containing 1(VWA1)	NM_022834	101.9	125.3	0.02625	1.189
fcrl2	Fc receptor like 2(FCRL2)	NM_030764	187.4	135.9	0.02637	0.675
PSEN1	presenilin 1(PSEN1)	NM_007318	111.6	130.4	0.02646	1.108
Dgcr5	DiGeorge syndrome critical region gene 5 (non-protein coding)(DGCR5)	NR_002733	98.8	122.5	0.02684	1.163
TUBGCP4	tubulin gamma complex associated protein 4(TUBGCP4)	NM_014444	96.3	114.7	0.02686	1.148
PCP4	Purkinje cell protein 4(PCP4)	NM_006198	96.1	159.9	0.02691	1.528
PSMA7	proteasome subunit alpha 7(PSMA7)	NM_152255	114.1	103	0.02694	0.857

TPP1	tripeptidyl peptidase 1(TPP1)	NM_000391	1257	865.7	0.02701	0.592
UTRN	utrophin(UTRN)	NM_007124	106.4	147.9	0.02706	1.298
MYO1C	myosin IC(MYO1C)	NM_033375	146.8	136.1	0.02711	0.886
CDK4	cyclin dependent kinase 4(CDK4)	NM_000075	1229.8	2746.6	0.02714	2.031
		AA484800	107.6	93.7	0.02724	0.846
TARBP2	TARBP2, RISC loading complex RNA binding subunit(TARBP2)	NM_134323	100	119.5	0.02734	1.137
XRRA1	X-ray radiation resistance associated 1(XRRA1)	NM_182969	134.2	125.3	0.02735	0.889
CRK	CRK proto-oncogene, adaptor protein(CRK)	NM_016823	128.2	168.4	0.02736	1.209
CRK	CRK proto-oncogene, adaptor protein(CRK)	NM_016823	147.1	173	0.02736	1.209
CRK	CRK proto-oncogene, adaptor protein(CRK)	NM_016823	250.1	347.5	0.02736	1.209
		XM_001713654	6200.5	6337.7	0.02746	0.888
VCL	vinculin(VCL)	NM_014000	1068	1829.8	0.02752	1.505
PLPP2	phospholipid phosphatase 2(PLPP2)	NM_177526	102.4	119.2	0.02753	1.123
AMOTL2	angiomotin like 2(AMOTL2)	NM_016201	284.1	233.1	0.02772	0.729
LCE1B	late cornified envelope 1B(LCE1B)	NM_178349	131.2	120	0.02772	0.875

		AW341257	126.1	117.1	0.02774	0.848
GPX5	glutathione peroxidase 5(GPX5)	NM_001509	124.2	106.9	0.02786	0.784
GPX8	glutathione peroxidase 8 (putative)(GPX8)	NM_001008397	135.3	109.9	0.02786	0.784
SCN7A	sodium voltage-gated channel alpha subunit 7(SCN7A)	NM_002976	143.4	125.8	0.02787	0.838
ZNF691	zinc finger protein 691(ZNF691)	NM_015911	146.1	131.7	0.02793	0.838
		XM_001126896	121.5	113.4	0.02794	0.9
c1orf116	chromosome 1 open reading frame 116(C1orf116)	NM_023938	249.6	190.8	0.02798	0.674
		CD514751	111.1	106.3	0.028	0.917
		XM_001713613	100.5	93.9	0.02801	0.878
ccdc15	coiled-coil domain containing 15(CCDC15)	NM_025004	94.6	99.7	0.02803	1.132
CCDC150	coiled-coil domain containing 150(CCDC150)	NM_173646	107.3	128.6	0.02803	1.132
		XR_015544	218.2	193	0.02813	0.808
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_006745	144.3	246.1	0.0282	1.452

POGZ	pogo transposable element with ZNF domain(POGZ)	NM_015100	112.2	150.6	0.02825	1.248			
SERTAD4-AS1	SERTAD4 antisense RNA 1(SERTAD4-AS1)	NR_024337	112.5	153.9	0.02827	1.291			
		XM_937676	143.9	135.7	0.02827	0.89			
FERD3L	Fer3 like bHLH transcription factor(FERD3L)	NM_152898	249.8	267	0.02837	0.86			
FER1L5	fer-1 like family member 5(FER1L5)	NM_001077400	167.4	152.7	0.02837	0.86			
FGF13	fibroblast growth factor 13(FGF13)	NM_033642	95.8	111	0.02843	1.118			
		XM_001715647	137.4	129.6	0.02845	0.89			
NGDN	neuroguidin(NGDN)	NM_015514	125	127.8	0.02871	1.31	NM_017196	14.73	0.69
NGDN	neuroguidin(NGDN)	NM_015514	160.8	240	0.02871	1.31	NM_017196	14.73	0.69
ITGA2	integrin subunit alpha 2(ITGA2)	NM_002203	693.2	1187.6	0.02886	1.504			
HNRNPU	heterogeneous nuclear ribonucleoprotein U(HNRNPU)	NM_004501	475.3	1009.4	0.02894	1.854	NM_017196	14.73	0.69
HNRNPR	heterogeneous nuclear ribonucleoprotein R(HNRNPR)	NM_005826	402.4	867.3	0.02894	1.854			
LOC441666	zinc finger protein 91 pseudogene(LOC441666)	NR_024380	122.9	112.8	0.02896	0.875			

		XM_001128586	95.5	121.3	0.029	1.186			
NETO1	neuropilin and tolloid like 1(NETO1)	AK123319	118.2	111.3	0.02906	0.889	NM_031356	5.43	24.53
AVP	arginine vasopressin(AVP)	NM_000490	133.2	124.1	0.02907	0.894	NM_031356	5.43	24.53
AVPI1	arginine vasopressin induced 1(AVPI1)	NM_021732	139.9	163.5	0.02907	0.894			
		XM_001718145	94.8	113.1	0.02919	1.145			
ZC2HC1A	zinc finger C2HC-type containing 1A(ZC2HC1A)	NM_016010	101.2	108.9	0.0292	1.306			
ZC2HC1A	zinc finger C2HC-type containing 1A(ZC2HC1A)	NM_016010	126.1	180	0.0292	1.306			
HVCN1	hydrogen voltage gated channel 1(HVCN1)	NM_001040107	120.9	111.6	0.02928	0.871			
DIXDC1	DIX domain containing 1(DIXDC1)	NM_001037954	117	163.8	0.02932	1.305			
DKC1	dyskerin pseudouridine synthase 1(DKC1)	NM_001363	154.8	168.3	0.02932	1.305			
CD36	CD36 molecule(CD36)	NM_000072	536.7	1163.6	0.02933	1.957			
CD34	CD34 molecule(CD34)	NM_001773	157.2	158.6	0.02933	1.957			
CD34	CD34 molecule(CD34)	NM_001773	408.5	908.2	0.02933	1.957			
LINC01132	long intergenic non-protein coding RNA 1132(LINC01132)	AK125357	112.3	105	0.02951	0.883			

SSBP4	single stranded DNA binding protein 4(SSBP4)	NM_032627	124.6	189.1	0.02955	1.401			
RPL36	ribosomal protein L36(RPL36)	NM_015414	95.5	115.4	0.02965	1.161			
		XM_001713717	162	255.8	0.0297	1.381			
		XM_001717999	174.3	148.6	0.0297	0.797	NM_017135	41.45	2.88
HIF1A	hypoxia inducible factor 1 alpha subunit(HIF1A)	NM_001530	97.6	121.3	0.02976	1.203	NM_017135	41.45	2.88
HIF1A	hypoxia inducible factor 1 alpha subunit(HIF1A)	NM_181054	116.8	189.3	0.02976	1.203	NM_017135	41.45	2.88
		XM_001719745	104.4	149.5	0.02976	1.313	NM_017135	41.45	2.88
AGO3	argonaute 3, RISC catalytic component(AGO3)	NM_177422	159	149	0.02976	0.857	NM_017135	41.45	2.88
FKBP1A	FK506 binding protein 1A(FKBP1A)	NM_054014	147.4	154.1	0.02979	1.329			
FKBP1A	FK506 binding protein 1A(FKBP1A)	NM_054014	368.7	566.7	0.02979	1.329			
FKBP1A	FK506 binding protein 1A(FKBP1A)	NM_054014	412.5	668	0.02979	1.329			
ZNF177	zinc finger protein 177(ZNF177)	NM_003451	170.1	215.6	0.02983	1.139			
DYNLRB1	dynein light chain roadblock-type 1(DYNLRB1)	NM_014183	112.6	121.7	0.02987	1.216			

DYNLRB1	dynein light chain roadblock-type 1(DYNLRB1)	NM_014183	125.6	164.1	0.02987	1.216			
DYNLRB1	dynein light chain roadblock-type 1(DYNLRB1)	NM_014183	214.3	285.7	0.02987	1.216			
DYNLRB1	dynein light chain roadblock-type 1(DYNLRB1)	NM_014183	899.2	1510.4	0.02987	1.216	NM_001033653	43.46	1.56
		XM_932276	98.7	115.2	0.0299	1.112			
ROR2	receptor tyrosine kinase like orphan receptor 2(ROR2)	NM_004560	97.2	124.8	0.02991	1.234			
GOLGA6B	golgin A6 family member B(GOLGA6B)	NM_018652	193.4	265.4	0.02996	1.204			
WSB1	WD repeat and SOCS box containing 1(WSB1)	NM_134264	187.5	351	0.02996	1.625			
ECM2	extracellular matrix protein 2(ECM2)	NM_001393	119.7	152	0.02998	1.191			
FAM131A	family with sequence similarity 131 member A(FAM131A)	NM_144635	200.9	487.4	0.03022	2.11			
		XM_938232	106.2	97.7	0.03028	0.871			
FAM160B2	family with sequence similarity 160 member B2(FAM160B2)	NM_022749	114.1	121	0.03036	1.137			

FAM161A	family with sequence similarity 161 member A(FAM161A)	NM_032180	124.6	151.9	0.03036	1.137
TRIL	TLR4 interactor with leucine rich repeats(TRIL)	NM_014817	318.2	748.9	0.03036	2.049
BAK1	BCL2 antagonist/killer 1(BAK1)	NM_001188	306.1	198.8	0.03038	0.597
NRXN2	neurexin 2(NRXN2)	NM_138734	127.5	125.9	0.03055	0.877
NRXN2	neurexin 2(NRXN2)	NM_138734	159.3	148	0.03055	0.877
taf7	TATA-box binding protein associated factor 7(TAF7)	NM_005642	167.2	279.4	0.03059	1.448
Hist2h2aa3	histone cluster 2 H2A family member a3(HIST2H2AA3)	NM_003516	99.5	120.8	0.03063	1.178
P4HA1	prolyl 4-hydroxylase subunit alpha 1(P4HA1)	NM_000917	98.8	118.6	0.03064	1.136
		AA883754	111.4	102.9	0.03065	0.876
SELENOM	selenoprotein M(SELENOM)	NM_080430	137.8	236	0.03069	1.523
arfip1	ADP ribosylation factor interacting protein 1(ARFIP1)	NM_001025595	99.4	121.9	0.03071	1.19
B4GALT3	beta-1,4-galactosyltransferase 3(B4GALT3)	NM_003779	118.7	106.1	0.03077	0.874

SRSF3	serine and arginine rich splicing factor 3(SRSF3)	NM_003017	160.3	248.6	0.03078	1.312			
CD34	CD34 molecule(CD34)	NM_001773	157.2	158.6	0.03083	1.913			
CD34	CD34 molecule(CD34)	NM_001773	408.5	908.2	0.03083	1.913			
CD34	CD34 molecule(CD34)	NM_001773	536.7	1163.6	0.03083	1.913	NM_134407	50.47	11.16
TCF12	transcription factor 12(TCF12)	NM_207038	163.4	248	0.03084	1.308			
STAT5B	signal transducer and activator of transcription 5B(STAT5B)	NM_012448	206.4	175.5	0.03084	0.777			
		XM_373547	101.1	116.1	0.03085	1.111			
ATP6V1C1	ATPase H+ transporting V1 subunit C1(ATP6V1C1)	NM_001695	101.3	102.8	0.03087	0.858			
ATP6V1C2	ATPase H+ transporting V1 subunit C2(ATP6V1C2)	NM_144583	130.8	121.1	0.03087	0.858			
ERF	ETS2 repressor factor(ERF)	NM_006494	116.7	136.3	0.03088	1.118			
MOSPD2	motile sperm domain containing 2(MOSPD2)	NM_152581	122.9	116.4	0.03089	0.903			
MOSPD2	motile sperm domain containing 2(MOSPD2)	NM_152581	151.1	152.7	0.03089	0.903			
FAM65C	family with sequence similarity 65 member C(FAM65C)	NM_080829	453.2	344.6	0.03096	0.669			

		XM_936382	138.4	126.5	0.03096	0.867			
		XM_001716660	116	103.6	0.03107	0.85			
MBIP	MAP3K12 binding inhibitory protein 1(MBIP)	NM_016586	97.4	117.6	0.03129	1.358			
MBIP	MAP3K12 binding inhibitory protein 1(MBIP)	NM_016586	168.4	261.3	0.03129	1.358			
ZNF777	zinc finger protein 777(ZNF777)	NM_015694	122.1	125.8	0.03145	1.213			
ZNF777	zinc finger protein 777(ZNF777)	NM_015694	141.1	183.9	0.03145	1.213			
ZRANB2	zinc finger RANBP2-type containing 2(ZRANB2)	NM_005455	117.1	148.5	0.03154	1.191			
ZRANB2	zinc finger RANBP2-type containing 2(ZRANB2)	NM_005455	155.9	197.1	0.03154	1.191			
RCN1	reticulocalbin 1(RCN1)	NM_002901	116.1	167.2	0.03157	1.345			
QPRT	quinolinate phosphoribosyltransferase(QPRT)	NM_014298	1274.1	671.9	0.03159	0.45			
MRO	maestro(MRO)	NM_031939	127.7	109	0.03161	0.799	NM_001033706	2.42	10.86
		XM_929740	115.6	110.6	0.03163	0.91			

WRNIP1	Werner helicase interacting protein 1(WRNIP1)	NM_020135	148.8	203.6	0.03164	1.226			
		XM_926143	107.9	100.7	0.03167	0.879			
BEND6	BEN domain containing 6(BEND6)	NM_152731	93.3	110.4	0.03181	1.152			
BEND7	BEN domain containing 7(BEND7)	NM_152751	98.5	110.8	0.03181	1.152			
MOCS1	molybdenum cofactor synthesis 1(MOCS1)	NM_005943	221.3	192.3	0.03183	0.786	NM_153300	0.14	61.17
Miat	myocardial infarction associated transcript (non-protein coding)(MIAT)	NR_003491	110.1	138	0.03188	1.197			
EFNA4	ephrin A4(EFNA4)	NM_182689	149.9	139.8	0.03197	0.878	NM_032416	108.51	1.87
EXT2	exostosin glycosyltransferase 2(EXT2)	NM_000401	242.3	383.3	0.03198	1.364			
NSMCE1	NSE1 homolog, SMC5-SMC6 complex component(NSMCE1)	NM_145080	243.5	237	0.03205	0.849			
HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	103	115.2	0.03205	0.868			
HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	112.7	118.8	0.03205	0.868			

HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	137.8	124	0.03205	0.868		
HYDIN	HYDIN, axonemal central pair apparatus protein(HYDIN)	NM_032821	150.8	144.1	0.03205	0.868		
N4BP2L2	NEDD4 binding protein 2 like 2(N4BP2L2)	NM_014887	242.5	324.2	0.0321	1.183		
SMAGP	small cell adhesion glycoprotein(SMAGP)	NM_001031628	112.3	133.5	0.0321	1.139		
RCN3	reticulocalbin 3(RCN3)	NM_020650	151.3	142.6	0.03212	0.886		
DYNLL2	dynein light chain LC8-type 2(DYNLL2)	NM_080677	265.3	487.6	0.03212	1.593		
		XR_038018	343.3	292.2	0.03218	0.75		
C6orf136	chromosome 6 open reading frame 136(C6orf136)	NM_145029	226.6	175.9	0.03234	0.719		
c6orf106	chromosome 6 open reading frame 106(C6orf106)	NM_024294	102.6	107.1	0.03234	0.719		
PTGS2	prostaglandin-endoperoxide synthase 2(PTGS2)	NM_000963	114.5	293.7	0.0324	2.188		
ADAMTSL2	ADAMTS like 2(ADAMTSL2)	NM_014694	100.9	116.1	0.03243	1.104	NM_001191088	10.07	0.03
SETBP1	SET binding protein 1(SETBP1)	NM_015559	176	271.4	0.03246	1.362	NM_001191088	10.07	0.03

H3f3c	H3 histone family member 3C(H3F3C)	NM_001013699	100.1	119.8	0.03247	1.156	NM_001191088	10.07	0.03
H6PD	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase(H6PD)	NM_004285	103.7	114.7	0.03247	1.156			
PCBP3	poly(rC) binding protein 3(PCBP3)	NM_020528	148.1	134.5	0.0325	0.867			
SLC10A7	solute carrier family 10 member 7(SLC10A7)	NM_001029998	103.4	112.9	0.03264	1.15			
SLC10A7	solute carrier family 10 member 7(SLC10A7)	NM_001029998	125.2	152.1	0.03264	1.15	NM_012496	1095.39	8.76
		XM_001125904	126.9	168.5	0.03274	1.239			
		XM_927568	118.9	112	0.03275	0.891			
SNORA14B	small nucleolar RNA, H/ACA box 14B(SNORA14B)	NR_002956	106.5	124.6	0.03278	1.103			
		XM_926372	112.8	102.5	0.03282	0.871			
APPBP2	amyloid beta precursor protein binding protein 2(APPBP2)	NM_006380	977.2	2039.5	0.03291	1.862			
APP	amyloid beta precursor protein(APP)	NM_201414	658.1	1613.9	0.03291	1.862			
ARMCX3	armadillo repeat containing, X-linked 3(ARMCX3)	NM_177947	278.8	350	0.03296	1.32			

ARMCX3	armadillo repeat containing, X-linked 3(ARMCX3)	NM_177948	343.6	527.9	0.03296	1.32
TUBB4A	tubulin beta 4A class IVa(TUBB4A)	NM_006087	171.7	154.1	0.03321	0.84
PASK	PAS domain containing serine/threonine kinase(PASK)	NM_015148	114	137.2	0.03337	1.143
PASK	PAS domain containing serine/threonine kinase(PASK)	NM_015148	160	181.6	0.03337	1.143
CLSTN1	calsyntenin 1(CLSTN1)	NM_001009566	107.6	129.2	0.03337	1.142
CLSTN1	calsyntenin 1(CLSTN1)	NM_001009566	123.5	152.2	0.03337	1.142
CLSTN1	calsyntenin 1(CLSTN1)	NM_001009566	2058	2595.3	0.03337	1.142
		XM_930029	348.7	287.2	0.03353	0.73
NUMBL	NUMB like, endocytic adaptor protein(NUMBL)	NM_004756	94.2	109.7	0.03374	1.124
APRT	adenine phosphoribosyltransferase(APRT)	NM_000485	265.9	407.6	0.03376	1.315
NPIPB13	nuclear pore complex interacting protein family, member B13(NPIPB13)	NR_002555	209	172.2	0.03407	0.769
DDX5	DEAD-box helicase 5(DDX5)	NM_004396	217.9	303.9	0.03409	1.215

SELENOS	selenoprotein S(SELENOS)	NM_018445	167.6	266.4	0.03411	1.38
SELENOS	selenoprotein S(SELENOS)	NM_018445	911.9	1149.3	0.03411	1.38
CCDC25	coiled-coil domain containing 25(CCDC25)	NM_018246	117	176.1	0.03412	1.34
CCDC28A	coiled-coil domain containing 28A(CCDC28A)	NM_015439	280.8	296.2	0.03412	1.34
		XM_933277	112	105.3	0.03414	0.896
		XM_937706	375.2	306.2	0.03416	0.724
		XM_001129527	218.6	388.6	0.03418	1.568
INHBC	inhibin beta C subunit(INHBC)	NM_005538	109.7	133.3	0.03419	1.173
ANO1	anoctamin 1(ANO1)	NM_018043	112.4	167.9	0.03426	1.329
ANO10	anoctamin 10(ANO10)	NM_018075	116.6	168.9	0.03426	1.329
SNHG3	small nucleolar RNA host gene 3(SNHG3)	NR_002909	120.3	112.3	0.0343	0.897
LINC00950	long intergenic non-protein coding RNA 950(LINC00950)	NR_024006	122.7	112.3	0.03435	0.87
SUPT3H	SPT3 homolog, SAGA and STAGA complex component(SUPT3H)	NM_181356	105.8	132.3	0.03445	1.191

PLA2G2D	phospholipase A2 group IID(PLA2G2D)	NM_012400	103.8	98.5	0.03448	0.902			
PLA2G2D	phospholipase A2 group IID(PLA2G2D)	NM_012400	457.9	475.7	0.03448	0.902			
AAMDC	adipogenesis associated Mth938 domain containing(AAMDC)	NM_024684	122.9	125.6	0.0346	1.123			
AAK1	AP2 associated kinase 1(AAK1)	NM_014911	104.7	123.6	0.0346	1.123			
SSBP2	single stranded DNA binding protein 2(SSBP2)	NM_012446	312.9	513.6	0.03464	1.437			
SPTY2D1	SPT2 chromatin protein domain containing 1(SPTY2D1)	NM_194285	111.3	140.2	0.03469	1.191			
C1orf162	chromosome 1 open reading frame 162(C1orf162)	NM_174896	142.2	129	0.03471	0.866			
THOC7	THO complex 7(THOC7)	NM_025075	495.7	685	0.03473	1.198			
PCDHGA10	protocadherin gamma subfamily A, 10(PCDHGA10)	NM_032090	117.9	141.5	0.03496	1.149			
		NM_058183	97.7	115.6	0.03498	1.127			
		XM_942687	128.6	164.4	0.03501	1.218	NM_013059	21.02	0.11
		XM_942687	160.6	189.5	0.03501	1.218			

SLC7A8	solute carrier family 7 member 8(SLC7A8)	NM_182728	87.1	101.3	0.03503	1.126
SLC7A8	solute carrier family 7 member 8(SLC7A8)	NM_182728	295.1	183.7	0.03503	1.126
MAP2K3	mitogen-activated protein kinase kinase 3(MAP2K3)	NM_002756	118.9	101.4	0.03505	0.846
		XM_932354	142.7	130.1	0.03512	0.874
MLXIPL	MLX interacting protein like(MLXIPL)	NM_032953	1590.4	709.9	0.03513	0.394
FBXO11	F-box protein 11(FBXO11)	NM_025133	351.7	461.9	0.03518	1.215
FBXO15	F-box protein 15(FBXO15)	NM_152676	514.1	726.3	0.03518	1.215
BRINP3	BMP/retinoic acid inducible neural specific 3(BRINP3)	NM_199051	102.6	173.8	0.03519	1.557
PLEKHH2	pleckstrin homology, MyTH4 and FERM domain containing H2(PLEKHH2)	NM_172069	146.6	195.1	0.03523	1.261
DNAJC10	DnaJ heat shock protein family (Hsp40) member C10(DNAJC10)	NM_018981	146.3	185	0.03526	1.163
		NM_001013840	122.3	145.6	0.03533	1.127
		NM_001013840	130.5	147.3	0.03533	1.127

NECAB3	N-terminal EF-hand calcium binding protein 3(NECAB3)	NM_031231	124	115	0.03539	0.868	NM_012816	19.78	2.28
FAM30A	family with sequence similarity 30, member A(FAM30A)	NM_014792	95	112.5	0.0354	1.134	NM_012816	19.78	2.28
		AW664435	110.1	103.1	0.03543	0.864			
		XM_001715935	426.2	210.4	0.03552	0.451			
MT1IP	metallothionein 1I, pseudogene(MT1IP)	NM_175621	1855.3	812.8	0.03556	0.385			
ABAT	4-aminobutyrate aminotransferase(ABAT)	NM_000663	131.5	137.6	0.03556	0.888			
AATK	apoptosis associated tyrosine kinase(AATK)	NM_001080395	121.1	112.4	0.03556	0.888			
HOXA5	homeobox A5(HOXA5)	NM_019102	124.7	164.9	0.03566	1.234			
MVB12B	multivesicular body subunit 12B(MVB12B)	NM_033446	108.1	145.9	0.03576	1.257			
TAGLN3	transgelin 3(TAGLN3)	NM_001008273	116.1	108.1	0.03579	0.903			
DECR1	2,4-dienoyl-CoA reductase 1, mitochondrial(DECR1)	NM_001359	121.4	155	0.03583	1.194			
SLC5A3	solute carrier family 5 member 3(SLC5A3)	AK055913	98.8	128.4	0.03587	1.247			
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	101	96.7	0.03593	1.309			

RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	125.9	182.1	0.03593	1.309			
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	137.5	227.6	0.03593	1.309			
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	142.1	189.9	0.03593	1.309			
APOD	apolipoprotein D(APOD)	NM_001647	105.5	125.9	0.03605	1.134			
JUP	junction plakoglobin(JUP)	NM_002230	106.2	155.1	0.03606	1.387			
ALPPL2	alkaline phosphatase, placental like 2(ALPPL2)	NM_031313	2121.6	1017.4	0.03611	0.405			
SNTA1	syntrophin alpha 1(SNTA1)	NM_003098	221.5	198	0.03626	0.821			
FAM124A	family with sequence similarity 124 member A(FAM124A)	NM_145019	118.4	112.8	0.03626	0.92			
		XR_038380	532	436	0.03629	0.714			
		XM_927136	104.8	123	0.03638	1.117	NM_031544	4.79	38.59
C11ORF49	chromosome 11 open reading frame 49(C11orf49)	NM_024113	105.1	98	0.0366	0.889	NM_031544	4.79	38.59
ANGPTL3	angiopoietin like 3(ANGPTL3)	NM_014495	91.2	132.8	0.03662	1.391			
RABGGTA	Rab geranylgeranyltransferase alpha subunit(RABGGTA)	NM_182836	93.8	112.5	0.03674	1.173			

		XM_378876	127.6	120.8	0.03679	0.892
		AW051978	132.7	126.6	0.03685	0.903
c16orf52	chromosome 16 open reading frame 52(C16orf52)	NM_173501	108.6	125.1	0.03687	1.121
ATP8B4	ATPase phospholipid transporting 8B4 (putative)(ATP8B4)	NM_024837	139	130.6	0.03691	0.877
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	NM_001895	133.1	194.4	0.03697	1.316
CSNK2A2	casein kinase 2 alpha 2(CSNK2A2)	NM_001896	270	294.8	0.03697	1.316
NUCKS1	nuclear casein kinase and cyclin dependent kinase substrate 1(NUCKS1)	AK095855	1253.8	1798.2	0.03699	1.26
		XM_001723239	13523.8	16849.9	0.03706	1.176
DUSP22	dual specificity phosphatase 22(DUSP22)	NM_020185	118.8	173	0.03711	1.35
DUSP23	dual specificity phosphatase 23(DUSP23)	NM_017823	177.7	290.6	0.03711	1.35
ILF3	interleukin enhancer binding factor 3(ILF3)	NM_012218	307.4	481.7	0.03712	1.378
PCGF1	polycomb group ring finger 1(PCGF1)	NM_032673	144.5	182.6	0.03728	1.136

DYNLRB1	dynein light chain roadblock-type 1(DYNLRB1)	NM_014183	1232.5	2157.6	0.0373	1.567
SYTL2	synaptotagmin like 2(SYTL2)	NM_206928	149.7	221.5	0.0373	1.32
STXBP4	syntaxin binding protein 4(STXBP4)	NM_178509	104.3	137.7	0.03735	1.232
SPTLC1	serine palmitoyltransferase long chain base subunit 1(SPTLC1)	NM_006415	120	150.5	0.03752	1.193
TNC	tenascin C(TNC)	NM_002160	118.4	248.5	0.03754	1.897
TNC	tenascin C(TNC)	NM_002160	128.4	274.8	0.03754	1.897
RAB11FIP2	RAB11 family interacting protein 2(RAB11FIP2)	NM_014904	202.9	342.1	0.03765	1.378
RAB11FIP2	RAB11 family interacting protein 2(RAB11FIP2)	NM_014904	250.6	399.4	0.03765	1.378
LOC105372028	uncharacterized LOC105372028(LOC105372028)	DA128369	111.1	102.8	0.03765	0.893
		BQ021435	121.2	113.1	0.03773	0.89
SIRT6	sirtuin 6(SIRT6)	NM_016539	142.2	123.1	0.03774	0.826
CNIH2	cornichon family AMPA receptor auxiliary protein 2(CNIH2)	NM_182553	260.4	346.5	0.03775	1.302

CNIH1	cornichon family AMPA receptor auxiliary protein 1(CNIH1)	NM_005776	202.1	301.9	0.03775	1.302
VWA1	von Willebrand factor A domain containing 1(VWA1)	NM_199121	106.7	100.5	0.03777	0.886
TPM1	tropomyosin 1 (alpha)(TPM1)	NM_001018008	108.4	139	0.0378	1.199
TPM1	tropomyosin 1 (alpha)(TPM1)	NM_001018008	109.7	138.8	0.0378	1.199
CD14	CD14 molecule(CD14)	NM_001040021	116.6	145.8	0.03783	1.17
		XR_017376	95.8	117.6	0.03787	1.202
		XR_017376	127.2	134.8	0.03787	1.202
PKM	pyruvate kinase, muscle(PKM)	NM_182470	180.2	326.4	0.03789	1.586
DHCR7	7-dehydrocholesterol reductase(DHCR7)	NM_001360	105.3	134	0.03791	1.205
DHDDS	dehydrodolichyl diphosphate synthase subunit(DHDDS)	NM_024887	164	196.9	0.03791	1.205
FGG	fibrinogen gamma chain(FGG)	NM_000509	385.4	236.6	0.03808	0.551
ZFAT	zinc finger and AT-hook domain containing(ZFAT)	NM_001029939	133.6	116.7	0.03809	0.818

map4k4	mitogen-activated protein kinase kinase kinase kinase 4(MAP4K4)	NM_145687	212.7	330.9	0.03818	1.324
SMOX	spermine oxidase(SMOX)	NM_175842	108.9	121.2	0.03821	0.769
SMOX	spermine oxidase(SMOX)	NM_175842	204.4	168.1	0.03821	0.769
ARHGAP28	Rho GTPase activating protein 28(ARHGAP28)	NM_030672	116.5	106.3	0.03831	0.874
CHMP5	charged multivesicular body protein 5(CHMP5)	NM_016410	217.8	321.6	0.03832	1.439
CHMP5	charged multivesicular body protein 5(CHMP5)	NM_016410	369.6	623.7	0.03832	1.439
CHMP5	charged multivesicular body protein 5(CHMP5)	NM_016410	1042.1	1140.5	0.03832	1.439
		AW294430	121.2	109.9	0.03833	0.874
SORCS2	sortilin related VPS10 domain containing receptor 2(SORCS2)	NM_020777	92.2	141.6	0.0384	1.451
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	119.7	160.1	0.03841	1.498
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	133.1	132.3	0.03841	1.498
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	401.5	695.6	0.03841	1.498
UBA3	ubiquitin like modifier activating enzyme 3(UBA3)	NM_198197	147.6	189.4	0.03843	1.192

PCYT2	phosphate cytidylyltransferase 2, ethanolamine(PCYT2)	NM_002861	161.6	142.2	0.03852	0.821
EFS	embryonal Fyn-associated substrate(EFS)	NM_032459	87	108.4	0.03855	1.219
HYLS1	HYLS1, centriolar and ciliogenesis associated(HYLS1)	NM_145014	242.1	208.1	0.03856	0.771
c12orf73	chromosome 12 open reading frame 73(C12orf73)	NM_001135570	99.3	115.3	0.03857	1.112
CFH	complement factor H(CFH)	NM_001014975	98.3	116.7	0.03872	1.512
CFH	complement factor H(CFH)	NM_001014975	109.6	183.6	0.03872	1.512
CFH	complement factor H(CFH)	NM_001014975	111.8	131.7	0.03872	1.512
MAP1A	microtubule associated protein 1A(MAP1A)	NM_002373	117.1	159.4	0.0388	1.248
		BU622756	122.1	118.7	0.03894	0.903
MTFMT	mitochondrial methionyl-tRNA formyltransferase(MTFMT)	NM_139242	136.7	124.5	0.03904	0.865
MTFMT	mitochondrial methionyl-tRNA formyltransferase(MTFMT)	NM_139242	184	212.3	0.03904	0.865

MOAP1	modulator of apoptosis 1(MOAP1)	NM_022151	116.8	149.8	0.0391	1.191
		XM_941861	259.1	350.4	0.03912	1.18
		XM_935575	104.3	129.7	0.0393	1.202
MKRN2	makorin ring finger protein 2(MKRN2)	NM_014160	227.6	334.8	0.03931	1.298
VCL	vinculin(VCL)	NM_003373	139.4	198.9	0.03935	1.298
TH	tyrosine hydroxylase(TH)	NM_199293	96.2	113.9	0.03936	1.145
bcam	basal cell adhesion molecule (Lutheran blood group)(BCAM)	NM_005581	112	119.4	0.03939	1.197
BCAP29	B-cell receptor associated protein 29(BCAP29)	NM_001008405	120.5	152.8	0.03939	1.197
ORC1	origin recognition complex subunit 1(ORC1)	NM_004153	118.4	141.4	0.03942	1.142
CFAP69	cilia and flagella associated protein 69(CFAP69)	NM_001039706	109.5	105.8	0.03943	0.912
RREB1	ras responsive element binding protein 1(RREB1)	NM_001003699	113.2	108	0.03947	0.898
RREB1	ras responsive element binding protein 1(RREB1)	NM_001003699	116.1	114.1	0.03947	0.898

RREB1	ras responsive element binding protein 1(RREB1)	NM_001003699	118.3	138.9	0.03947	0.898
RREB1	ras responsive element binding protein 1(RREB1)	NM_001003699	144.7	152.1	0.03947	0.898
EIF5	eukaryotic translation initiation factor 5(EIF5)	NM_001969	200.8	318.6	0.0395	1.387
MMS19	MMS19 homolog, cytosolic iron-sulfur assembly component(MMS19)	NM_022362	309.1	420.5	0.03954	1.28
MMS19	MMS19 homolog, cytosolic iron-sulfur assembly component(MMS19)	NM_022362	351.4	516.4	0.03954	1.28
FXYD1	FXYD domain containing ion transport regulator 1(FXYD1)	NM_021902	148.8	122.1	0.03956	0.786
FXYD1	FXYD domain containing ion transport regulator 1(FXYD1)	NM_005031	103.2	102.9	0.03956	0.786
		XM_001714161	145.7	133.1	0.03964	0.862
ERCC8	ERCC excision repair 8, CSA ubiquitin ligase complex subunit(ERCC8)	NM_000082	127.1	151.5	0.03993	1.138

ERCC4	ERCC excision repair 4, endonuclease catalytic subunit(ERCC4)	NM_005236	91.9	107.8	0.03993	1.138
		XM_001126750	93.7	107.4	0.03996	1.116
		XM_001126750	116.2	172	0.03996	1.116
DZANK1	double zinc ribbon and ankyrin repeat domains 1(DZANK1)	NM_001099407	102.2	126.3	0.04004	1.181
		BM705347	108.7	98.5	0.04007	0.865
AKT1	AKT serine/threonine kinase 1(AKT1)	NM_001014432	7980.7	3741.1	0.0401	0.397
TMEM219	transmembrane protein 219(TMEM219)	NM_001083613	448.4	433	0.04012	0.833
		CN283269	135	131	0.04023	0.925
ACTL6A	actin like 6A(ACTL6A)	NM_004301	697.6	1184.4	0.04033	1.478
		XM_943472	96.5	112.8	0.04063	1.104
		BX441478	90.2	106.8	0.04063	1.155
TMEM64	transmembrane protein 64(TMEM64)	AK095472	126.3	167.1	0.04065	1.211
SORL1	sortilin related receptor 1(SORL1)	NM_003105	152	340.2	0.04066	1.952
ODF2	outer dense fiber of sperm tails 2(ODF2)	NM_002540	93.2	113.4	0.04071	1.178

ODF2	outer dense fiber of sperm tails 2(ODF2)	NM_002540	170.7	226.7	0.04071	1.178			
cyp4f3	cytochrome P450 family 4 subfamily F member 3(CYP4F3)	NM_000896	1010.8	413.5	0.04089	0.351			
		XM_001725366	122.9	156.8	0.04093	1.188			
RBP1	retinol binding protein 1(RBP1)	NM_002899	169.5	313.5	0.04103	1.598			
		XR_017130	1504	2336.1	0.04106	1.365			
PTK7	protein tyrosine kinase 7 (inactive)(PTK7)	NM_152880	129.3	206.9	0.04107	1.45			
UBQLN1	ubiquilin 1(UBQLN1)	NM_053067	140.8	183.7	0.04107	1.189			
UBQLN1	ubiquilin 1(UBQLN1)	NM_053067	268.7	364.1	0.04107	1.189			
EXOC7	exocyst complex component 7(EXOC7)	NM_001013839	175.7	251.2	0.0411	1.26	NM_031012	19.39	0.85
		XR_001336	121.5	110.1	0.04112	0.876			
CDKL1	cyclin dependent kinase like 1(CDKL1)	NM_004196	105	127.6	0.04113	1.137			
SCRT1	scratch family transcriptional repressor 1(SCRT1)	NM_031309	152	142.7	0.04125	0.891			
MAU2	MAU2 sister chromatid cohesion factor(MAU2)	NM_015329	119.3	115.2	0.04125	0.925	NM_012904	10.16	55.22
PRMT6	protein arginine methyltransferase 6(PRMT6)	NM_018137	159.9	211	0.04125	1.188			

PRMT6	protein arginine methyltransferase 6(PRMT6)	NM_018137	217.9	271.8	0.04125	1.188			
COPRS	coordinator of PRMT5 and differentiation stimulator(COPRS)	NM_018405	104.3	122	0.04128	1.129			
CUL7	cullin 7(CUL7)	NM_014780	374.7	374.2	0.04129	0.867			
ecd	ecdysoneless cell cycle regulator(ECD)	NM_007265	106.6	133.6	0.04145	1.156			
ECEL1	endothelin converting enzyme like 1(ECEL1)	NM_004826	106.8	133.1	0.04145	1.156			
KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2(KCNMB2)	NM_181361	117.7	109.4	0.0415	0.85			
KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2(KCNMB2)	NM_005832	107.7	106.4	0.0415	0.85			
TBC1D8B	TBC1 domain family member 8B(TBC1D8B)	NM_017752	111.7	114	0.04165	1.176			
TBC1D8B	TBC1 domain family member 8B(TBC1D8B)	NM_017752	129.1	166.3	0.04165	1.176			
		XM_927939	129.4	155	0.04183	1.142			
		XM_934270	103.3	121.2	0.04184	1.132	NM_012823	17.52	0.04

		NM_178230	2370.4	3782.8	0.04191	1.398
VENTXP1	VENT homeobox pseudogene 1(VENTXP1)	NR_001559	112.7	119.1	0.04199	0.889
VENTXP1	VENT homeobox pseudogene 1(VENTXP1)	NR_001559	118.7	111.3	0.04199	0.889
MYADM	myeloid associated differentiation marker(MYADM)	NM_001020820	623.5	1205.7	0.04203	1.735
SLC5A10	solute carrier family 5 member 10(SLC5A10)	NM_152351	131.7	109.5	0.04208	0.552
SLC5A10	solute carrier family 5 member 10(SLC5A10)	NM_152351	244.8	147.2	0.04208	0.552
PPT2	palmitoyl-protein thioesterase 2(PPT2)	NM_138717	97.6	115	0.0421	1.156
PPT2	palmitoyl-protein thioesterase 2(PPT2)	NM_138717	172.1	220.5	0.0421	1.156
		XM_001716173	134.1	114.2	0.0421	0.784
		XM_001722148	130.6	117.1	0.04219	0.861
ZNF423	zinc finger protein 423(ZNF423)	NM_015069	105	118.2	0.04221	1.274
ZNF423	zinc finger protein 423(ZNF423)	NM_015069	128.5	177.2	0.04221	1.274
		XM_113971	141.6	208.4	0.04226	1.312

WIPI2	WD repeat domain, phosphoinositide interacting 2(WIPI2)	NM_016003	258.2	199.3	0.04226	0.689
		XM_0011126128	117.8	108.1	0.04231	0.884
EWSR1	EWS RNA binding protein 1(EWSR1)	NM_013986	765.4	1037	0.04238	1.34
EWSR1	EWS RNA binding protein 1(EWSR1)	NM_005243	464.8	719.9	0.04238	1.34
ZMYM5	zinc finger MYM-type containing 5(ZMYM5)	NM_001039650	113.5	135	0.04239	1.143
CALML3-AS1	CALML3 antisense RNA 1(CALML3-AS1)	AL831877	3392.2	2742.2	0.04246	0.697
F7	coagulation factor VII(F7)	NM_000131	92.9	107.1	0.04254	1.124
bola2	bolA family member 2(BOLA2)	NM_001031827	107	130.3	0.04255	1.161
bola2	bolA family member 2(BOLA2)	NM_001031827	108.1	112.6	0.04255	1.161
bola2	bolA family member 2(BOLA2)	NM_001031827	197.4	255.1	0.04255	1.161
bola2	bolA family member 2(BOLA2)	NM_001031827	539.5	624.5	0.04255	1.161
		XM_927256	113.3	102	0.04261	0.876
		XM_0017245 30	116.3	110.4	0.04266	0.899
CRY1	cryptochrome circadian clock 1(CRY1)	NM_004075	105.8	116.6	0.04272	1.26
cryaa	crystallin alpha A(CRYAA)	NM_000394	121.6	166.5	0.04272	1.26

PRMT1	protein arginine methyltransferase 1(PRMT1)	NM_198319	451.8	726.2	0.04292	1.378
ACOT2	acyl-CoA thioesterase 2(ACOT2)	NM_006821	259.5	193.4	0.04295	0.682
RASEF	RAS and EF-hand domain containing(RASEF)	NM_152573	133.6	229.4	0.04299	1.569
ICA1	islet cell autoantigen 1(ICA1)	NM_004968	108.4	101.2	0.04299	0.886
KITLG	KIT ligand(KITLG)	NM_000899	136.5	148.7	0.04309	1.289
KLB	klotho beta(KLB)	NM_175737	179.8	265.7	0.04309	1.289
MRFAP1L1	Morf4 family associated protein 1 like 1(MRFAP1L1)	NM_203462	454.5	751.2	0.04315	1.416
ANKRD17	ankyrin repeat domain 17(ANKRD17)	NM_198889	98.6	125.5	0.04317	1.202
MAVS	mitochondrial antiviral signaling protein(MAVS)	NM_020746	104	126.3	0.0432	1.134
DLX6	distal-less homeobox 6(DLX6)	NM_005222	187.9	167	0.04327	0.831
DTNA	dystrobrevin alpha(DTNA)	NM_032980	105.6	127.8	0.04331	1.158
IER2	immediate early response 2(IER2)	NM_004907	99.8	111.9	0.04342	1.088
		XM_929291	103.2	96.4	0.04361	0.897

TM2D3	TM2 domain containing 3(TM2D3)	NM_078474	144.6	210.6	0.0437	1.311
zswim5	zinc finger SWIM-type containing 5(ZSWIM5)	NM_020883	105.2	134.2	0.04386	1.21
CCDC115	coiled-coil domain containing 115(CCDC115)	NM_032357	104.5	123.2	0.04389	1.125
ZNF548	zinc finger protein 548(ZNF548)	NM_152909	144.8	176.6	0.04393	1.115
RP2	retinitis pigmentosa 2 (X-linked recessive)(RP2)	NM_006915	108.5	133.8	0.04406	1.166
FAM167B	family with sequence similarity 167 member B(FAM167B)	NM_032648	100.7	117.6	0.04406	1.118
RASSF4	Ras association domain family member 4(RASSF4)	NM_032023	267.4	209.6	0.04414	0.712
DSCAM	DS cell adhesion molecule(DSCAM)	NM_001389	105.3	120.2	0.04416	1.084
		XR_039278	1398	2010.8	0.04419	1.281
LOC284009	uncharacterized LOC284009(LOC284009)	NM_001025459	134.1	123.9	0.0443	0.871
RHOT1	ras homolog family member T1(RHOT1)	NM_001033566	192.4	280.1	0.04439	1.266
RHOT1	ras homolog family member T1(RHOT1)	NM_001033566	316.4	379.3	0.04439	1.266
		XM_001133534	544.4	1026.9	0.04448	1.65

		XM_001133534	742.4	1375.2	0.04448	1.65			
PFN2	profilin 2(PFN2)	NM_053024	631.9	1133.6	0.0445	1.57			
PHF6	PHD finger protein 6(PHF6)	NM_001015877	113.8	149.1	0.04466	1.232	NM_017170	13.37	0.05
PTK7	protein tyrosine kinase 7 (inactive)(PTK7)	NM_152882	134.6	210.4	0.04466	1.422			
		BF194881	131.1	124.9	0.04474	0.876			
		DB337588	118.9	112.8	0.04487	0.908			
ZHX1	zinc fingers and homeoboxes 1(ZHX1)	NM_007222	98.1	121	0.04493	1.171			
		XM_933543	123.3	117.8	0.04501	0.89			
GAGE4	G antigen 4(GAGE4)	NM_001474	145.7	227	0.04506	1.382			
SORD	sorbitol dehydrogenase(SORD)	NM_003104	145.7	111.7	0.04511	0.696			
MOBP	myelin-associated oligodendrocyte basic protein(MOBP)	NM_182935	115.1	106.7	0.04511	0.89			
HCG4B	HLA complex group 4B (non-protein coding)(HCG4B)	NR_001317	110.7	130.6	0.04511	1.11	NM_001106492	2.61	10.85
SUGP2	SURP and G-patch domain containing 2(SUGP2)	NM_001017392	140.4	227.5	0.04513	1.443	NM_001106492	2.61	10.85

ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta(ACTR1B)	NM_005735	387.6	517.3	0.04519	1.156	NM_001106492	2.61	10.85
IRF2BP2	interferon regulatory factor 2 binding protein 2(IRF2BP2)	NM_182972	147.5	139.7	0.04519	0.895			
PURB	purine rich element binding protein B(PURB)	NM_033224	536.6	838.9	0.0452	1.356			
ABCC4	ATP binding cassette subfamily C member 4(ABCC4)	NM_005845	90.7	102.9	0.04522	1.425			
ABCC5	ATP binding cassette subfamily C member 5(ABCC5)	NM_001023587	229.1	379.6	0.04522	1.425			
DLAT	dihydrolipoamide S-acetyltransferase(DLAT)	NM_001931	531.2	1140.2	0.04524	1.862			
GPN2	GPN-loop GTPase 2(GPN2)	NM_018066	129.6	315.4	0.04528	2.074			
		XR_015609	111.5	108.6	0.04529	0.927			
C9orf72	chromosome 9 open reading frame 72(C9orf72)	NM_018325	175.1	223.9	0.0453	1.183			
		BQ185080	121.5	115.2	0.04532	0.9			
		XM_940079	126.1	169.1	0.0454	1.227			

OR4F21	olfactory receptor family 4 subfamily F member 21(OR4F21)	NM_001005504	144.4	131.2	0.04541	0.851			
NOTCH3	notch 3(NOTCH3)	NM_000435	196.5	302.7	0.04549	1.365			
LCOR	ligand dependent nuclear receptor corepressor(LCOR)	NM_032440	89.9	110.8	0.04553	1.196			
UBR2	ubiquitin protein ligase E3 component n-recognin 2(UBR2)	NM_015255	205.4	204.3	0.04571	0.897			
		XR_017963	101	117.5	0.0458	1.101			
MARK2	microtubule affinity regulating kinase 2(MARK2)	NM_004954	121.8	155.8	0.04583	1.227			
MPRIP	myosin phosphatase Rho interacting protein(MPRIP)	NM_015134	428.3	655.7	0.04591	1.341			
CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1(CEACAM1)	NM_001712	98.8	127.4	0.04593	1.221			
ANG	angiogenin(ANG)	NM_001097577	131.7	176.3	0.04596	1.203	NM_001270681	26.79	0.09
ARMCX3	armadillo repeat containing, X-linked 3(ARMCX3)	NM_177947	275.7	414	0.04596	1.282			
PAPOLG	poly(A) polymerase gamma(PAPOLG)	NM_022894	122.7	113.7	0.04608	0.904			

HECTD2	HECT domain E3 ubiquitin protein ligase 2(HECTD2)	NM_182765	499.3	744.7	0.04616	1.298			
XRCC5	X-ray repair cross complementing 5(XRCC5)	NM_021141	116.8	140.3	0.04621	1.154			
STAG1	stromal antigen 1(STAG1)	NM_005862	104	130.1	0.0463	1.302			
STAG1	stromal antigen 1(STAG1)	NM_005862	136.5	199.9	0.0463	1.302			
TSPYL5	TSPY like 5(TSPYL5)	NM_033512	110.9	144.3	0.0463	1.232	NM_019373	263.23	1.01
HPD	4-hydroxyphenylpyruvate dioxygenase(HPD)	NM_002150	705.6	634.9	0.04632	0.773			
DUSP27	dual specificity phosphatase 27 (putative)(DUSP27)	NM_001080426	177.7	290.6	0.04634	1.441			
PML	promyelocytic leukemia(PML)	NM_033238	142.1	132.7	0.04635	0.889			
MT2A	metallothionein 2A(MT2A)	NM_005953	1687.2	886	0.04637	0.474			
POFUT2	protein O-fucosyltransferase 2(POFUT2)	NM_133635	175.3	253.2	0.04637	1.325			
POFUT2	protein O-fucosyltransferase 2(POFUT2)	NM_133635	210	324	0.04637	1.325			
		XM_001717507	150.8	134.5	0.04639	0.844			

NAT14	N-acetyltransferase 14 (putative)(NAT14)	NM_020378	109.4	133.7	0.04646	1.166			
		XM_001130428	130.9	122.2	0.04651	0.897			
ZNF112	zinc finger protein 112(ZNF112)	NM_001083335	124	121.6	0.04658	0.921			
		XM_0017188435	1858.9	3170.4	0.04663	1.506			
CTNS	cystinosin, lysosomal cystine transporter(CTNS)	NM_004937	92.9	109.1	0.04668	1.131			
SLC12A1	solute carrier family 12 member 1(SLC12A1)	NM_000338	354.4	919.4	0.04678	2.317	NM_012778	744.78	0.71
		XM_0017211828	127.3	114.6	0.0468	0.874	NM_012778	744.78	0.71
AMDHD2	amidohydrolase domain containing 2(AMDHD2)	NM_015944	208.4	387.2	0.04693	1.585	NM_012778	744.78	0.71
ACYP2	acylphosphatase 2(ACYP2)	NM_138448	331	583.4	0.0471	1.561			
ACYP1	acylphosphatase 1(ACYP1)	NM_001107	111.4	116.1	0.0471	1.561			
		XM_374200	110.6	105.2	0.0472	0.914	NM_012909	6.73	5427.66
		XR_018889	161.9	252.8	0.04754	1.368	NM_022181	0.40	160.77
		XM_944079	145	137.5	0.04756	0.884	NM_019157	14.48	0.05
PLPP5	phospholipid phosphatase 5(PLPP5)	NM_032483	234.8	413.3	0.04771	1.501			

SLC30A5	solute carrier family 30 member 5(SLC30A5)	NM_022902	155.6	204.1	0.04776	1.197
SLC30A5	solute carrier family 30 member 5(SLC30A5)	NM_022902	186.1	251.5	0.04776	1.197
RAI1	retinoic acid induced 1(RAI1)	NM_030665	166.5	224.9	0.04791	1.139
RAI1	retinoic acid induced 1(RAI1)	NM_030665	168.9	210.7	0.04791	1.139
PALLD	palladin, cytoskeletal associated protein(PALLD)	NM_016081	289	670.3	0.04805	1.988
HLA-DQB1	major histocompatibility complex, class II, DQ beta 1(HLA-DQB1)	NM_002123	116.5	106.6	0.04807	0.894
BCHE	butyrylcholinesterase(BCHE)	NM_000055	194.8	271.6	0.04814	1.219
PRSS12	protease, serine 12(PRSS12)	NM_003619	100.3	122.6	0.0482	1.17
UNC50	unc-50 inner nuclear membrane RNA binding protein(UNC50)	NM_014044	564.2	849.1	0.04823	1.295
CAPRIN1	cell cycle associated protein 1(CAPRIN1)	NM_005898	351.4	546.6	0.04829	1.359
DCP2	decapping mRNA 2(DCP2)	NM_152624	142	130.8	0.0483	0.871
DDX24	DEAD-box helicase 24(DDX24)	NM_020414	165.4	253.2	0.04831	1.363
		XM_001723486	116.7	107.4	0.04842	0.861

CSK	c-src tyrosine kinase(CSK)	NM_004383	93.3	112.9	0.04845	1.16			
KAT2B	lysine acetyltransferase 2B(KAT2B)	NM_003884	132.2	120.9	0.04847	0.865			
URGCP	upregulator of cell proliferation(URGCP)	NM_017920	459.2	428.6	0.0485	0.826			
UBE2E3	ubiquitin conjugating enzyme E2 E3(UBE2E3)	NM_006357	127.3	131.4	0.04859	1.312			
UBE2E3	ubiquitin conjugating enzyme E2 E3(UBE2E3)	NM_006357	157.4	234.2	0.04859	1.312			
UBE2E3	ubiquitin conjugating enzyme E2 E3(UBE2E3)	NM_006357	431	760.1	0.04859	1.312			
CYP4A11	cytochrome P450 family 4 subfamily A member 11(CYP4A11)	NM_000778	124.5	120.8	0.0486	0.927			
SOCS5	suppressor of cytokine signaling 5(SOCS5)	NM_014011	149.1	221.4	0.04864	1.291			
LRIG3	leucine rich repeats and immunoglobulin like domains 3(LRIG3)	NM_153377	107.3	127.8	0.04864	1.161			
DOK1	docking protein 1(DOK1)	NM_001381	241.9	393.2	0.04874	1.434			
		XM_929565	217.9	198.6	0.04874	0.84			
		XR_038768	140.2	126.6	0.04876	0.848	NM_019168	8.26	61.49
		AA454665	119.9	113.6	0.04878	0.894			

hyal3	hyaluronoglucosaminidase 3(HYAL3)	NM_003549	1365.7	1085.5	0.04886	0.695
MT1A	metallothionein 1A(MT1A)	NM_005946	11240.4	5630.1	0.04894	0.441
DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic(DPM1)	NM_003859	167.3	214.6	0.04898	1.208
DPM2	dolichyl-phosphate mannosyltransferase subunit 2, regulatory(DPM2)	NM_003863	463.5	648.1	0.04898	1.208
TGM5	transglutaminase 5(TGM5)	NM_201631	110.8	106.2	0.04898	0.915
ACTR5	ARP5 actin-related protein 5 homolog(ACTR5)	NM_024855	106.5	117.3	0.04901	1.071
ZNF616	zinc finger protein 616(ZNF616)	NM_178523	166.8	234	0.04903	1.24
FGF18	fibroblast growth factor 18(FGF18)	NM_003862	90.5	114.3	0.04906	1.216
FBXO11	F-box protein 11(FBXO11)	NM_018693	113.5	102.8	0.04911	0.876
FBXO11	F-box protein 11(FBXO11)	NM_025133	124.4	118.9	0.04911	0.876
ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)(ST13)	NM_003932	272.3	206.7	0.04912	0.675

TTC3	tetratricopeptide repeat domain 3(TTC3)	NM_003316	282.6	435.8	0.04931	1.339
MYH10	myosin heavy chain 10(MYH10)	NM_005964	999.3	1734.4	0.04936	1.546
		XM_498859	118.2	110.8	0.04938	0.898
UGT1A6	UDP glucuronosyltransferase family 1 member A6(UGT1A6)	NM_001072	146.1	129	0.0496	0.714
UGT1A6	UDP glucuronosyltransferase family 1 member A6(UGT1A6)	NM_001072	161.1	128.8	0.0496	0.714
ZNF567	zinc finger protein 567(ZNF567)	NM_152603	100.2	117.6	0.04961	1.128
ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle(ATP5A1)	NM_004046	164.7	291.5	0.04966	1.527
FAM131C	family with sequence similarity 131 member C(FAM131C)	NM_182623	108.1	131.4	0.04966	1.167
FAM132A	family with sequence similarity 132 member A(FAM132A)	NM_001014980	173.9	170.2	0.04966	1.167
RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1(RAP1GDS1)	NM_021159	152.2	196.2	0.04973	1.197

sdc1	syndecan 1(SDC1)	NM_001006946	449.1	285.7	0.04975	0.562
ARMC8	armadillo repeat containing 8(ARMC8)	NM_015396	106.4	125.8	0.04976	1.106
ARMC8	armadillo repeat containing 8(ARMC8)	NM_213654	108.6	128.3	0.04976	1.106
DEFB123	defensin beta 123(DEFB123)	NM_153324	102.3	126.3	0.04976	1.152
AGPS	alkylglycerone phosphate synthase(AGPS)	NM_003659	153.7	145	0.04978	0.884
SNORD3A	small nucleolar RNA, C/D box 3A(SNORD3A)	NR_006880	173.2	158.3	0.04979	0.841
MMGT1	membrane magnesium transporter 1(MMGT1)	NM_173470	182.1	208.7	0.04979	1.271
MMGT1	membrane magnesium transporter 1(MMGT1)	NM_173470	605.3	897.2	0.04979	1.271
OR2B2	olfactory receptor family 2 subfamily B member 2(OR2B2)	NM_033057	129.6	118	0.04984	0.839
STX12	syntaxin 12(STX12)	NM_177424	188.3	246.2	0.04986	1.168
fosl1	FOS like 1, AP-1 transcription factor subunit(FOSL1)	NM_005438	194.5	2066.5	0.0499	10.276
TBX3	T-box 3(TBX3)	NM_005996	111.7	132.8	0.04995	1.121
CHMP2A	charged multivesicular body protein 2A(CHMP2A)	NM_014453	130	152.2	0.05	1.116

Gene Symbol	Gene Name	Accession No.	IUGR Chow M Mean	IUGR HFHS M Mean	p-val IUGR M HFHS vs. CON M HFHS	Ratio IUGR M HFHS vs. CON M HFHS	REFSEQ ID	NEPHRON (MEAN RPKM)	COLLECTING DUCT (MEAN RPKM)
		XM_927511	92.1	101.9	0.00001	1.219			
VRK3	vaccinia related kinase 3(VRK3)	NM_001025778	96.8	95.2	0.00003	1.28			
VRK3	vaccinia related kinase 3(VRK3)	NM_001025778	180.3	150.5	0.00003	1.28			
MPHOSPH10	M-phase phosphoprotein 10(MPHOSPH10)	NM_005791	409.1	391.6	0.00005	1.389			
		XM_927848	101.2	99	0.00007	0.784			
fam134b	family with sequence similarity 134 member B(FAM134B)	NM_001034850	368.5	320.8	0.0001	1.602			
RPS26	ribosomal protein S26(RPS26)	NM_001029	93	82.7	0.00011	0.838			
RPS26	ribosomal protein S26(RPS26)	NM_001029	1438.4	1055.6	0.00011	0.838			
TMEM184C	transmembrane protein 184C(TMEM184C)	NM_018241	103.1	104.8	0.00017	1.194	NM_017193	356.13	8.18
TMEM184C	transmembrane protein 184C(TMEM184C)	NM_018241	256.8	245.8	0.00017	1.194	NM_017193	356.13	8.18
		XM_001133500	129.3	163.1	0.00018	1.458	NM_017193	356.13	8.18
		XM_934672	104.5	101	0.00019	1.15	NM_017193	356.13	8.18

		XM_001723164	122.5	137.8	0.0002	1.153
SEZ6L2	seizure related 6 homolog like 2(SEZ6L2)	NM_201575	102	87.2	0.0002	0.84
RAI1	retinoic acid induced 1(RAI1)	NM_030665	142.8	121.4	0.00025	0.733
RAI1	retinoic acid induced 1(RAI1)	NM_030665	164.3	172	0.00025	0.733
		AI350600	97.7	103.8	0.00025	1.154
		XM_001717043	129.2	145.6	0.00032	1.42
TTLL9	tubulin tyrosine ligase like 9(TTLL9)	NM_001008409	92.1	100.1	0.00035	1.257
CCND1	cyclin D1(CCND1)	NM_053056	138.6	148.6	0.00039	1.304
CCNC	cyclin C(CCNC)	NM_005190	126.3	128.5	0.00039	1.304
RRAGB	Ras related GTP binding B(RRAGB)	NM_006064	91.4	89	0.00041	0.653
RRAGB	Ras related GTP binding B(RRAGB)	NM_006064	110.8	119.2	0.00041	0.653
EIF6	eukaryotic translation initiation factor 6(EIF6)	NM_181466	457.4	426.8	0.00046	1.382
LOC101927421	uncharacterized LOC101927421(LOC101927421)	BU517015	104.6	127.7	0.00048	1.322
OR52N5	olfactory receptor family 52 subfamily N member 5(OR52N5)	NM_001001922	99.9	106	0.0005	1.172

		XM_001714678	99.8	102.5	0.00053	1.178
RORA	RAR related orphan receptor A(RORA)	NM_134261	96.1	108.6	0.00054	1.188
		XM_936101	168.2	178.1	0.00061	1.303
		XR_039453	109.9	102.4	0.00064	1.167
		XR_039453	203.3	176	0.00064	1.167
TIGD1	tigger transposable element derived 1(TIGD1)	NM_145702	97.5	100.2	0.0007	1.191
		BX111977	101.4	93.1	0.00072	0.846
		XM_942158	98.7	101.1	0.00074	1.201
ATCAY	ATCAY, caytaxin(ATCAY)	NM_033064	114.3	93.6	0.00081	0.801
ZNF137P	zinc finger protein 137, pseudogene(ZNF137P)	NM_003438	123.9	107.3	0.00083	0.786
RPN2	ribophorin II(RPN2)	NM_002951	330.9	310.2	0.00087	1.341
		XM_927344	101.3	113.6	0.00091	1.175
		NM_000648	93.4	90.3	0.00092	1.291
		NM_000648	96.7	108.6	0.00092	1.291
		BX103136	108.4	96.7	0.00101	0.822
MBP	myelin basic protein(MBP)	NM_001025090	252.9	264.5	0.00114	1.672

PPARA	peroxisome proliferator activated receptor alpha(PPARA)	NM_001001928	121.6	125.4	0.00131	1.312
C3orf84	chromosome 3 open reading frame 84(C3orf84)	NM_001080528	110.3	112.1	0.00132	1.229
TRIM51EP	tripartite motif-containing 51E, pseudogene(TRIM51EP)	NM_001136118	115.4	121.1	0.0015	1.191
		XM_936103	158.8	169.6	0.00153	1.502
NAA25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit(NAA25)	NM_024953	193.6	203.3	0.00155	1.316
SFTA2	surfactant associated 2(SFTA2)	NM_205854	100.1	91.9	0.00165	0.839
PCDH18	protocadherin 18(PCDH18)	NM_019035	117.6	102.5	0.00171	0.774
PCDH18	protocadherin 18(PCDH18)	NM_019035	223.4	162.3	0.00171	0.774
CYP4X1	cytochrome P450 family 4 subfamily X member 1(CYP4X1)	NM_178033	97.2	104.4	0.00191	1.245
LRBA	LPS responsive beige-like anchor protein(LRBA)	NM_006726	99.3	92.8	0.00204	0.828
GPM6B	glycoprotein M6B(GPM6B)	NM_001001995	130.7	142.1	0.00205	1.341

		XM_944653	98.1	113.5	0.00211	1.177
MCTS1	MCTS1, re-initiation and release factor(MCTS1)	NM_014060	184.6	192.4	0.00215	1.407
TBC1D7	TBC1 domain family member 7(TBC1D7)	NM_016495	183.5	141.2	0.00227	0.768
AAMDC	adipogenesis associated Mth938 domain containing(AAMDC)	NM_024684	111	113.1	0.00236	0.829
AAK1	AP2 associated kinase 1(AAK1)	NM_014911	100.8	89	0.00236	0.829
		BM930795	105.8	117.8	0.00236	1.192
ARMCX2	armadillo repeat containing, X-linked 2(ARMCX2)	NM_177949	95.7	103	0.00247	1.19
		BU587445	101.9	95.2	0.0025	0.887
RORA	RAR related orphan receptor A(RORA)	AK055969	134.3	125.8	0.0025	1.384
MEG8	maternally expressed 8 (non-protein coding)(MEG8)	NR_024149	93.2	98.6	0.00251	1.234
TRIM36	tripartite motif containing 36(TRIM36)	NM_001017397	87.1	88.5	0.00253	0.842
		XM_001717551	103.1	100.8	0.00256	1.155
		XM_001715747	91.4	102.4	0.00263	1.195

RSRC2	arginine and serine rich coiled-coil 2(RSRC2)	NM_023012	112.4	102.5	0.00269	0.743			
RSRC2	arginine and serine rich coiled-coil 2(RSRC2)	NM_023012	607.3	465.3	0.00269	0.743			
OPRM1	opioid receptor mu 1(OPRM1)	NM_001008505	105.6	96.1	0.0027	0.889			
OPRM1	opioid receptor mu 1(OPRM1)	NM_001008505	143.3	135.2	0.0027	0.889			
		XR_017376	105.2	92.8	0.00277	0.809			
		XR_017376	108.1	99.5	0.00277	0.809			
HAGH	hydroxyacylglutathione hydrolase(HAGH)	NM_005326	92.2	99.8	0.00277	1.247			
SPRN	shadow of prion protein homolog (zebrafish)(SPRN)	NM_001012508	91.6	90.4	0.0028	1.152			
SPRN	shadow of prion protein homolog (zebrafish)(SPRN)	NM_001012508	98.1	105.9	0.0028	1.152	NM_053502	4.02	18.01
BTLA	B and T lymphocyte associated(BTLA)	NM_181780	92.2	98.4	0.00283	1.179	NM_053502	4.02	18.01
PDGFRL	platelet derived growth factor receptor like(PDGFRL)	NM_006207	109.9	95.1	0.00285	0.793	NM_053502	4.02	18.01
SPAG6	sperm associated antigen 6(SPAG6)	NM_172242	130.5	101.6	0.00289	0.775	NM_053502	4.02	18.01
Amy1a	amylase, alpha 1A (salivary)(AMY1A)	NM_001008221	90.5	87.3	0.00292	0.839			

TMTC3	transmembrane and tetratricopeptide repeat containing 3(TMTC3)	NM_181783	139.4	161.3	0.00292	1.292			
ABCF1	ATP binding cassette subfamily F member 1(ABCF1)	NM_001025091	107.1	94.8	0.00295	0.859			
		XM_001725241	102.1	85.2	0.00296	0.862			
HEPACAM2	HEPACAM family member 2(HEPACAM2)	NM_198151	123.5	128.7	0.00299	1.295			
KALRN	kalirin, RhoGEF kinase(KALRN)	NM_003947	3377.9	2800.3	0.003	0.724			
		XM_944999	114.1	125	0.00301	1.21	NM_001009670	33.30	2.04
DCTN2	dynactin subunit 2(DCTN2)	NM_006400	139.4	129	0.00302	1.179			
DCTN1	dynactin subunit 1(DCTN1)	NM_004082	91	99	0.00302	1.179			
GORASP2	golgi reassembly stacking protein 2(GORASP2)	NM_015530	103.5	98.9	0.00303	0.888			
PPTC7	PTC7 protein phosphatase homolog(PPTC7)	NM_139283	238.9	261.2	0.00311	1.449			
ZNF548	zinc finger protein 548(ZNF548)	NM_152909	137.1	117.4	0.00315	0.836			
MYO19	myosin XIX(MYO19)	NM_025109	91.7	86.7	0.00317	0.851			
		XM_939706	106.9	107.8	0.00318	1.244			

ATG4A	autophagy related 4A cysteine peptidase(ATG4A)	NM_178270	91.3	96.8	0.00324	1.193
KCTD10	potassium channel tetramerization domain containing 10(KCTD10)	NM_031954	96.8	82.7	0.00325	0.836
SCN2B	sodium voltage-gated channel beta subunit 2(SCN2B)	NM_004588	96.5	101.2	0.00338	1.215
BAG5	BCL2 associated athanogene 5(BAG5)	NM_004873	152.1	151.7	0.00339	1.297
JMJD1C	jumonji domain containing 1C(JMJD1C)	NM_032776	103	95.9	0.00346	0.854
JMJD1C	jumonji domain containing 1C(JMJD1C)	NM_032776	238.7	158.7	0.00346	0.854
JMJD1C	jumonji domain containing 1C(JMJD1C)	NM_032776	396.4	291.5	0.00346	0.854
RRP1B	ribosomal RNA processing 1B(RRP1B)	NM_015056	97.9	98.3	0.0035	1.236
CRHBP	corticotropin releasing hormone binding protein(CRHBP)	NM_001882	93.8	101	0.00351	1.189
		BX109970	104.8	100.8	0.00353	0.753
		XR_017532	214.7	191.6	0.00358	1.368
		XR_037047	96.6	100.5	0.00376	1.149

ZNF177	zinc finger protein 177(ZNF177)	NM_003451	153.2	134.3	0.00385	0.827
UBTF	upstream binding transcription factor, RNA polymerase I(UBTF)	NM_014233	95.9	97.8	0.00398	0.818
UBTF	upstream binding transcription factor, RNA polymerase I(UBTF)	NM_014233	102.9	88.1	0.00398	0.818
ZNF436	zinc finger protein 436(ZNF436)	NM_030634	90.6	95.1	0.00409	0.798
ZNF436	zinc finger protein 436(ZNF436)	NM_030634	108.6	93.7	0.00409	0.798
ABHD12	abhydrolase domain containing 12(ABHD12)	NM_001042472	93.2	98.9	0.00415	1.155
		AA722034	102.7	109.3	0.00422	1.199
FZD1	frizzled class receptor 1(FZD1)	NM_003505	119.8	108.1	0.00423	1.169
FZD2	frizzled class receptor 2(FZD2)	NM_001466	149.7	143.3	0.00423	1.169
PHF12	PHD finger protein 12(PHF12)	NM_020889	103.9	97.8	0.0043	0.845
		XM_930798	105.9	90.4	0.00433	0.825
RBCK1	RANBP2-type and C3HC4-type zinc finger containing 1(RBCK1)	NM_006462	152.4	132.4	0.00437	1.12
		XM_942469	105	111.7	0.00445	1.271

		XM_942469	150.9	128.9	0.00445	1.271
ZNF138	zinc finger protein 138(ZNF138)	NM_006524	93.5	98.2	0.00447	1.177
GMCL1	germ cell-less, spermatogenesis associated 1(GMCL1)	NM_178439	95.1	106.3	0.00451	1.207
GMDS	GDP-mannose 4,6-dehydratase(GMDS)	NM_001500	160.1	135.5	0.00451	1.207
		XR_038119	100.7	111.4	0.00456	1.277
LETMD1	LETM1 domain containing 1(LETMD1)	NM_015416	125.2	116.1	0.0046	1.177
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(LFNG)	NM_001040167	130.4	136.3	0.0046	1.177
		XM_929701	102.4	108.8	0.00463	1.149
SEL1L3	SEL1L family member 3(SEL1L3)	NM_015187	116	113.6	0.00485	1.243
		XR_018424	113.2	115.5	0.00494	1.206
c12orf4	chromosome 12 open reading frame 4(C12orf4)	NM_020374	107.1	105	0.00496	1.165
SH3GL1	SH3 domain containing GRB2 like 1, endophilin A2(SH3GL1)	NM_003025	113	120.5	0.00499	1.234

ZBTB43	zinc finger and BTB domain containing 43(ZBTB43)	NM_014007	139.1	120.8	0.00505	1.24
ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3(ST3GAL3)	NM_174970	113.1	99.8	0.00511	0.864
LST1	leukocyte specific transcript 1(LST1)	NM_205840	100.3	103.6	0.00513	1.151
		BM681626	92.4	97.7	0.00513	1.18
C11ORF49	chromosome 11 open reading frame 49(C11orf49)	NM_024113	90.6	99.6	0.00514	1.177
slc26a6	solute carrier family 26 member 6(SLC26A6)	NM_001040454	88.9	84.6	0.00515	0.834
EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1(EEPD1)	NM_030636	112.2	118	0.00522	0.683
HEATR3	HEAT repeat containing 3(HEATR3)	NM_182922	121.4	125.9	0.00526	1.24
		XR_040021	101.4	102.6	0.00532	1.129
		XR_015689	130.6	110.2	0.00547	0.802
		XM_001720837	102.1	103.9	0.00549	1.146
		AA705831	100.3	93.9	0.00551	0.88
CCNL1	cyclin L1(CCNL1)	NM_020307	105.6	109.2	0.00556	1.195

ASB8	ankyrin repeat and SOCS box containing 8(ASB8)	NM_024095	104.7	99.3	0.00562	0.891
ASB9	ankyrin repeat and SOCS box containing 9(ASB9)	NM_024087	106.7	92.9	0.00562	0.891
PIGN	phosphatidylinositol glycan anchor biosynthesis class N(PIGN)	NM_176787	95.4	94	0.00566	0.839
PIGN	phosphatidylinositol glycan anchor biosynthesis class N(PIGN)	NM_176787	97.6	94.8	0.00566	0.839
		XM_940199	96.9	103.1	0.00573	1.14
RORA	RAR related orphan receptor A(RORA)	NM_002943	97.5	98.3	0.00574	1.262
RORA	RAR related orphan receptor A(RORA)	NM_002943	127.3	119.3	0.00574	1.262
SS18	SS18, nBAF chromatin remodeling complex subunit(SS18)	NM_005637	109	123	0.00577	1.326
SS18	SS18, nBAF chromatin remodeling complex subunit(SS18)	NM_005637	214.4	178.5	0.00577	1.326
SS18	SS18, nBAF chromatin remodeling complex subunit(SS18)	NM_005637	285.2	259.8	0.00577	1.326

MRGPRD	MAS related GPR family member D(MRGPRD)	NM_198923	106.7	99.2	0.00594	0.815			
CAPN10	calpain 10(CAPN10)	NM_023083	88.4	99.8	0.00597	1.207			
CAPN11	calpain 11(CAPN11)	NM_007058	101	104	0.00597	1.207			
CAMK1	calcium/calmodulin dependent protein kinase I(CAMK1)	NM_003656	175.8	166	0.00599	1.243			
GCSH	glycine cleavage system protein H(GCSH)	NM_004483	110.2	89.6	0.00601	0.785			
RAB2B	RAB2B, member RAS oncogene family(RAB2B)	NM_032846	348.1	310	0.00607	1.399			
E2F4	E2F transcription factor 4(E2F4)	NM_001950	110.4	95.9	0.00616	0.871			
STMN3	stathmin 3(STMN3)	NM_015894	378.9	410.6	0.00632	1.407	NM_001107943	0.63	112.77
		XR_017962	98.1	108.7	0.00633	1.189			
		XR_017962	99.9	105.9	0.00633	1.189			
		XM_001133686	91.8	104.2	0.00634	1.215			
map4k4	mitogen-activated protein kinase kinase kinase kinase 4(MAP4K4)	NM_145687	185.9	156.6	0.00636	0.66			

		XM_928495	95.6	91.9	0.00637	0.845			
TMEM161A	transmembrane protein 161A(TMEM161A)	NM_017814	112.1	112.7	0.00638	1.182			
KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2(KCNMB2)	NM_181361	106.3	103.7	0.00644	1.136			
KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2(KCNMB2)	NM_005832	92.5	103	0.00644	1.136			
MIR33B	microRNA 33b(MIR33B)	NR_030361	84.7	81.6	0.00664	0.845			
PLXND1	plexin D1(PLXND1)	NM_015103	104.3	84.3	0.00664	0.768			
		XM_932032	103.6	94.2	0.00665	0.839			
		XM_001716372	89.9	94.9	0.00667	1.185			
MRO	maestro(MRO)	NM_031939	106.5	115.8	0.00679	1.332			
SPINT1	serine peptidase inhibitor, Kunitz type 1(SPINT1)	NM_003710	114.2	110.7	0.00698	0.604	NM_134372	22.51	0.03
RNA5S9	RNA, 5S ribosomal 9(RNA5S9)	NR_023371	218.1	182.1	0.00698	1.316			

c16orf58	chromosome 16 open reading frame 58(C16orf58)	NM_022744	100.8	107.7	0.00706	1.175
RBBP8	RB binding protein 8, endonuclease(RBBP8)	NM_002894	107.6	103.9	0.00709	1.126
NUGGC	nuclear GTPase, germinal center associated(NUGGC)	NM_001010906	98.3	86.8	0.0071	0.824
		XM_001721670	98	103.6	0.0071	1.301
NECTIN1	nectin cell adhesion molecule 1(NECTIN1)	NM_203285	113.8	120.3	0.00713	1.223
GSKIP	GSK3B interacting protein(GSKIP)	NM_016472	93.2	93.3	0.00721	1.216
CT47A1	cancer/testis antigen family 47, member A1(CT47A1)	NM_001080146	101.6	99.8	0.00721	1.167
EMC4	ER membrane protein complex subunit 4(EMC4)	NM_016454	95.5	105.9	0.00722	1.269
ZNF398	zinc finger protein 398(ZNF398)	NM_170686	99.8	106.7	0.00723	1.208
ARL5B	ADP ribosylation factor like GTPase 5B(ARL5B)	NM_178815	128.4	140	0.0073	1.332
DNHD1	dynein heavy chain domain 1(DNHD1)	NM_173589	91.4	111	0.00735	1.379
PRPF40A	pre-mRNA processing factor 40 homolog A(PRPF40A)	NM_017892	102.9	107	0.00735	1.175

UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)(UPF3A)	NM_023011	347.5	270.1	0.00755	1.418			
NCDN	neurochondrin(NCDN)	NM_001014839	127.3	126.2	0.00756	1.143			
OR8J3	olfactory receptor family 8 subfamily J member 3(OR8J3)	NM_001004064	100.5	104.1	0.00756	1.113			
		XM_928281	118.5	117.2	0.00765	1.163			
DLGAP4	DLG associated protein 4(DLGAP4)	NM_001042486	116	92.9	0.00777	0.799			
SNORA12	small nucleolar RNA, H/ACA box 12(SNORA12)	NR_002954	110.3	100.7	0.0079	1.243			
OVGP1	oviductal glycoprotein 1(OVGP1)	NM_002557	102.4	101.3	0.00794	1.153			
EIF1B	eukaryotic translation initiation factor 1B(EIF1B)	NM_005875	139.4	162.7	0.00795	1.232			
EIF1AX	eukaryotic translation initiation factor 1A, X-linked(EIF1AX)	NM_001412	122.6	127	0.00795	1.232			
TSPAN1	tetraspanin 1(TSPAN1)	NM_005727	100.8	94.6	0.00802	0.835	NM_001031645	1.93	10.04
RHOT1	ras homolog family member T1(RHOT1)	NM_001033566	196.7	172.1	0.00818	1.273			
RHOT1	ras homolog family member T1(RHOT1)	NM_001033566	316.1	331.4	0.00818	1.273			

IP6K1	inositol hexakisphosphate kinase 1(IP6K1)	NM_153273	100.8	89.3	0.00819	1.358
IP6K2	inositol hexakisphosphate kinase 2(IP6K2)	NM_001005909	320.9	350.1	0.00819	1.358
Snora47	small nucleolar RNA, H/ACA box 47(SNORA47)	NR_003014	102.4	101.7	0.00826	1.14
SCARNA12	small Cajal body-specific RNA 12(SCARNA12)	NR_003010	115.5	112.6	0.00831	0.849
CX3CR1	C-X3-C motif chemokine receptor 1(CX3CR1)	NM_001337	94.9	106.3	0.00831	1.225
CXCL10	C-X-C motif chemokine ligand 10(CXCL10)	NM_001565	108.3	103.4	0.00831	1.225
MIR21	microRNA 21(MIR21)	NR_029493	98.3	100.3	0.00846	0.671
ASCL2	achaete-scute family bHLH transcription factor 2(ASCL2)	NM_005170	97.6	89.5	0.0085	0.858
		XM_934471	108.4	115.5	0.00856	1.181
fxyd7	FXYD domain containing ion transport regulator 7(FXYD7)	NM_022006	180.9	96.4	0.00857	1.136
FXYD5	FXYD domain containing ion transport regulator 5(FXYD5)	NM_144779	113	107.7	0.00857	1.136

EIF2A	eukaryotic translation initiation factor 2A(EIF2A)	NM_032025	139.4	162.7	0.00872	1.352			
IL21R	interleukin 21 receptor(IL21R)	NM_181078	106.5	115.5	0.00873	1.166	NM_144748	66.99	0.14
IL21R	interleukin 21 receptor(IL21R)	NM_181079	114.3	113.8	0.00873	1.166			
DDX19B	DEAD-box helicase 19B(DDX19B)	NM_001014449	219.8	201.5	0.00874	0.834			
DDX19A	DEAD-box helicase 19A(DDX19A)	NM_018332	109	114.6	0.00874	0.834			
ZNF326	zinc finger protein 326(ZNF326)	NM_182976	108.7	111.9	0.00881	1.218			
ZNF326	zinc finger protein 326(ZNF326)	NM_182976	120.3	125.4	0.00881	1.218			
		BX441478	85.8	80.2	0.00884	0.821			
ADGRG3	adhesion G protein-coupled receptor G3(ADGRG3)	NM_170776	103.4	102.1	0.00884	1.145			
LINC01559	long intergenic non-protein coding RNA 1559(LINC01559)	NM_182558	103.4	108	0.00886	1.171			
bcam	basal cell adhesion molecule (Lutheran blood group)(BCAM)	NM_005581	373.6	360.4	0.00888	1.394	NM_001107793	77.29	6.85
C8orf59	chromosome 8 open reading frame 59(C8orf59)	NM_001099672	258	258.8	0.00891	0.535	NM_001107793	77.29	6.85
		XM_001715215	111.6	98.5	0.00899	0.854	NM_001107793	77.29	6.85

CEP41	centrosomal protein 41(CEP41)	NM_018718	119.8	126.7	0.00906	1.205	NM_001107793	77.29	6.85
CEP55	centrosomal protein 55(CEP55)	NM_018131	140.2	129.6	0.00906	1.205			
CREBRF	CREB3 regulatory factor(CREBRF)	NM_153607	260.6	211.6	0.00906	1.385			
CREBZF	CREB/ATF bZIP transcription factor(CREBZF)	NM_001039618	332	231.8	0.00906	1.385			
		XM_939026	102.8	97.1	0.00912	0.857			
TONSL	tonsoku-like, DNA repair protein(TONSL)	NM_013432	143.4	132.6	0.00919	0.779			
trak1	trafficking kinesin protein 1(TRAK1)	NM_001042646	114.6	114.2	0.00922	1.176			
trak1	trafficking kinesin protein 1(TRAK1)	NM_001042646	131.9	136.7	0.00922	1.176			
TGM5	transglutaminase 5(TGM5)	NM_201631	99.9	102	0.00932	1.129			
CHD4	chromodomain helicase DNA binding protein 4(CHD4)	NM_001273	398.3	351	0.00936	0.761			
CHD6	chromodomain helicase DNA binding protein 6(CHD6)	NM_032221	566.9	433.9	0.00936	0.761			
ELK3	ELK3, ETS transcription factor(ELK3)	NM_005230	95.7	99.3	0.00939	1.149			
CPLX2	complexin 2(CPLX2)	NM_001008220	101.5	105.4	0.00941	1.122			

RRBP1	ribosome binding protein 1(RRBP1)	NM_001042576	165.2	144.5	0.00948	1.276
RRBP1	ribosome binding protein 1(RRBP1)	NM_001042576	314.1	310.3	0.00948	1.276
FBLN1	fibulin 1(FBLN1)	NM_006486	95.7	104.7	0.00954	1.175
ADCK1	aarF domain containing kinase 1(ADCK1)	NM_020421	93.2	97.5	0.00963	1.205
		XM_927939	121.1	106.6	0.00977	0.835
TENM2	teneurin transmembrane protein 2(TENM2)	NM_001080428	108.7	106.2	0.00979	1.127
IL1R2	interleukin 1 receptor type 2(IL1R2)	NM_173343	88.6	97.1	0.00982	1.254
TCP10L	t-complex 10-like(TCP10L)	NM_018277	93.8	88.8	0.00984	0.841
c6orf106	chromosome 6 open reading frame 106(C6orf106)	NM_024294	117.8	106.5	0.00985	0.906
PTP4A1	protein tyrosine phosphatase type IVA, member 1(PTP4A1)	NM_003463	101.6	106.9	0.0099	1.142
RPL37A	ribosomal protein L37a(RPL37A)	NM_000998	4299.1	3407.7	0.00991	0.783
SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3(SMARCD3)	NM_003078	93.2	100.2	0.00993	1.137

FREM2	FRAS1 related extracellular matrix protein 2(FREM2)	NM_207361	94.1	101.8	0.01002	1.153			
		XM_930292	114.3	97.8	0.01016	0.849			
		DR980429	95.6	90.7	0.01018	0.842			
		XM_941821	100.1	107.3	0.01025	1.086			
		XR_019567	104.9	106.3	0.01035	1.185			
TTLL11	tubulin tyrosine ligase like 11(TTLL11)	NM_194252	110.2	96.6	0.01037	0.855			
AGAP3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3(AGAP3)	NM_001042535	106	126.3	0.01043	1.231			
L3HYPDH	trans-L-3-hydroxyproline dehydratase(L3HYPDH)	NM_144581	116.3	116.2	0.01044	1.189			
L3MBTL2	L3MBTL2 polycomb repressive complex 1 subunit(L3MBTL2)	NM_031488	121	118.6	0.01044	1.189			
UBE3A	ubiquitin protein ligase E3A(UBE3A)	NM_000462	219.6	191.4	0.01045	1.246			
UBE3A	ubiquitin protein ligase E3A(UBE3A)	NM_000462	504.6	507.7	0.01045	1.246			
C1QTNF6	C1q and tumor necrosis factor related protein 6(C1QTNF6)	NM_031910	99.7	105	0.01046	1.112	NM_001009603	28.32	0.90

C1QTNF6	C1q and tumor necrosis factor related protein 6(C1QTNF6)	NM_182486	110.2	93.5	0.01046	1.112
RSPH9	radial spoke head 9 homolog(RSPH9)	NM_152732	98.3	93.2	0.01049	0.828
RDH10	retinol dehydrogenase 10 (all-trans)(RDH10)	NM_172037	197.6	344	0.01056	1.664
SNRPD3	small nuclear ribonucleoprotein D3 polypeptide(SNRPD3)	NM_004175	207.8	217.9	0.01057	1.603
RAB13	RAB13, member RAS oncogene family(RAB13)	NM_002870	113	113	0.01059	1.16
DBT	dihydrolipoamide branched chain transacylase E2(DBT)	NM_001918	94.8	99.7	0.0106	1.173
DCAF1	DDB1 and CUL4 associated factor 1(DCAF1)	NM_014703	527	473.7	0.0106	1.173
		BX114974	99.5	104	0.01064	1.196
		XM_938867	97.7	91.2	0.01069	0.881
BZW1	basic leucine zipper and W2 domains 1(BZW1)	NM_014670	97.8	104.5	0.01076	1.195
BZW2	basic leucine zipper and W2 domains 2(BZW2)	NM_014038	109.2	104.1	0.01076	1.195
GPN1	GPN-loop GTPase 1(GPN1)	NM_007266	137.4	156.4	0.01078	0.819

GPM6B	glycoprotein M6B(GPM6B)	NM_001001995	91.1	87.2	0.01078	0.819
MMP19	matrix metallopeptidase 19(MMP19)	NM_002429	98.9	88.4	0.01079	0.881
TUBG1	tubulin gamma 1(TUBG1)	NM_001070	102.4	109.8	0.01092	0.756
TUBG1	tubulin gamma 1(TUBG1)	NM_001070	129.5	109.9	0.01092	0.756
TUBG1	tubulin gamma 1(TUBG1)	NM_001070	164.4	186.6	0.01092	0.756
SIM1	single-minded family bHLH transcription factor 1(SIM1)	NM_005068	104.1	95.8	0.01096	0.791
slc26a6	solute carrier family 26 member 6(SLC26A6)	NM_134426	99.6	106.9	0.011	1.275
slc26a6	solute carrier family 26 member 6(SLC26A6)	NM_134426	112.5	122.8	0.011	1.275
prb1	proline rich protein BstNI subfamily 1(PRB1)	NM_199354	94.5	102.6	0.01106	1.151
CTNNB1	catenin beta 1(CTNNB1)	NM_001098209	96.5	96.4	0.01106	1.239
CTNNB1	catenin beta 1(CTNNB1)	NM_001098209	148.2	145.9	0.01106	1.239
CTNNBIP1	catenin beta interacting protein 1(CTNNBIP1)	NM_020248	154	164.5	0.01106	1.239
C6orf1	chromosome 6 open reading frame 1(C6orf1)	NM_001008704	107.5	105.3	0.01112	1.242
		AW182385	95	81.2	0.01119	0.821

BAGE2	B melanoma antigen family member 2(BAGE2)	NM_182482	170.4	172.4	0.01119	1.245
TTC16	tetratricopeptide repeat domain 16(TTC16)	NM_144965	109.5	105.2	0.0112	1.156
PIGM	phosphatidylinositol glycan anchor biosynthesis class M(PIGM)	NM_145167	112.7	92.8	0.01129	0.797
KDM5D	lysine demethylase 5D(KDM5D)	NM_004653	241	203.4	0.01132	1.415
CCPG1	cell cycle progression 1(CCPG1)	NM_020739	272.5	284.1	0.01138	1.444
lrch4	leucine rich repeats and calponin homology domain containing 4(LRCH4)	NM_002319	99.8	86.4	0.01141	0.856
		XM_938802	108.6	109.8	0.01146	1.222
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2(UGGT2)	NM_020121	139.4	123.4	0.01154	0.84
c5orf30	chromosome 5 open reading frame 30(C5orf30)	NM_033211	129.9	119.6	0.01179	0.877
MAPK7	mitogen-activated protein kinase 7(MAPK7)	NM_139032	107.2	99.7	0.01189	0.85

MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1(MAPK8IP1)	NM_005456	126.5	107.4	0.01189	0.85
		XM_927142	112.5	105.4	0.01196	1.174
		CR748464	100	101.4	0.01198	1.13
MBP	myelin basic protein(MBP)	NM_001025101	158	179.2	0.01202	1.301
CAB39L	calcium binding protein 39 like(CAB39L)	NM_001079670	96.5	98.9	0.01209	1.176
		XM_938374	85.8	98.5	0.01209	1.231
TBRG4	transforming growth factor beta regulator 4(TBRG4)	NM_004749	117	101	0.0121	0.866
EGF	epidermal growth factor(EGF)	NM_001963	119.3	109.3	0.01217	0.816
SQLE	squalene epoxidase(SQLE)	NM_003129	91.9	95.3	0.01224	0.779
SQLE	squalene epoxidase(SQLE)	NM_003129	99.5	94.2	0.01224	0.779
		XM_001713809	664.9	830.1	0.01224	2.787
Hist1h2bk	histone cluster 1 H2B family member k(HIST1H2BK)	NM_080593	97.5	102	0.01226	1.157

UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1(UAP1L1)	NM_207309	109.2	112.3	0.01228	1.172
		XM_001723218	92.1	88.6	0.01229	0.87
NUFIP2	NUFIP2, FMR1 interacting protein 2(NUFIP2)	NM_020772	158.4	138.3	0.0123	1.382
NUFIP2	NUFIP2, FMR1 interacting protein 2(NUFIP2)	NM_020772	341.6	290.4	0.0123	1.382
IVNS1ABP	influenza virus NS1A binding protein(IVNS1ABP)	NM_006469	100.2	106	0.01234	1.172
ADGRL2	adhesion G protein-coupled receptor L2(ADGRL2)	NM_012302	96.7	104.6	0.01237	1.182
ALX3	ALX homeobox 3(ALX3)	NM_006492	110.5	116.8	0.01242	0.513
ALX1	ALX homeobox 1(ALX1)	NM_006982	98.4	99.8	0.01242	0.513
MATN4	matrilin 4(MATN4)	NM_030592	85.9	85.7	0.01245	0.817
MATN4	matrilin 4(MATN4)	NM_030592	89	88.4	0.01245	0.817
TNFRSF10B	TNF receptor superfamily member 10b(TNFRSF10B)	NM_003842	90	103.7	0.01247	1.21

TNFRSF10B	TNF receptor superfamily member 10b(TNFRSF10B)	NM_003842	98.4	95	0.01247	1.21
ITM2A	integral membrane protein 2A(ITM2A)	NM_004867	84.9	92.9	0.01249	1.152
MRPL35	mitochondrial ribosomal protein L35(MRPL35)	NM_145644	498.9	558.5	0.01249	1.371
GSTM1	glutathione S-transferase mu 1(GSTM1)	NM_000561	98.3	90.7	0.01251	0.89
SMIM10L2B	small integral membrane protein 10 like 2B(SMIM10L2B)	NR_024493	98.7	102.4	0.01253	1.142
		XM_944438	93.3	96	0.01258	1.187
PCYOX1L	prenylcysteine oxidase 1 like(PCYOX1L)	NM_024028	96	92.3	0.01264	0.885
Snora2b	small nucleolar RNA, H/ACA box 2B(SNORA2B)	NR_002951	136	122.9	0.01265	1.285
		XR_018309	94.4	87.4	0.01274	0.758
		NM_001004302	96.2	94.7	0.01278	0.831
		XR_015695	104.4	93.5	0.01282	0.862
		XR_001498	97.8	105	0.01286	1.243
		XM_931141	96.3	100.6	0.01286	1.149

DNMT3L	DNA methyltransferase 3 like(DNMT3L)	NM_013369	114.9	114.2	0.01288	1.141
DNMT3B	DNA methyltransferase 3 beta(DNMT3B)	NM_006892	86.8	90.6	0.01288	1.141
		XR_039041	3488.4	2355.4	0.01288	0.812
		DA572372	92.6	101.7	0.01293	1.163
EIF2AK1	eukaryotic translation initiation factor 2 alpha kinase 1(EIF2AK1)	NM_014413	522.9	441.4	0.01296	0.753
ZSCAN32	zinc finger and SCAN domain containing 32(ZSCAN32)	NM_017810	111.9	107.1	0.01299	1.171
NFASC	neurofascin(NFASC)	NM_001005387	98.2	92.2	0.01303	0.902
CSMD1	CUB and Sushi multiple domains 1(CSMD1)	NM_033225	127.1	119.8	0.01306	0.804
		XR_037583	100.9	103.8	0.01316	1.08
MAVS	mitochondrial antiviral signaling protein(MAVS)	NM_020746	108.1	92.9	0.01321	0.85
		AW297854	97.9	93.4	0.01335	0.879
SLC35F1	solute carrier family 35 member F1(SLC35F1)	NM_001029858	96.2	105.8	0.01344	1.163
		AI873192	127.3	108.1	0.01344	0.64
MRPL53	mitochondrial ribosomal protein L53(MRPL53)	NM_053050	155.2	157.6	0.01346	1.285

		BX116001	97.4	106.1	0.01352	1.171			
LOC102724002	uncharacterized LOC102724002(LOC102724002)	AK025166	99.7	96.9	0.01354	0.887			
		XM_370758	115.6	105.4	0.01357	0.913			
DCUN1D4	defective in cullin neddylation 1 domain containing 4(DCUN1D4)	NM_015115	177.1	187.7	0.01363	1.296			
		NM_001015047	100.2	108.3	0.01365	1.154			
SNORA2C	small nucleolar RNA, H/ACA box 2C(SNORA2C)	NR_002968	102.5	91.1	0.01367	0.879	NM_144744	0.11	40.01
		XM_930670	122.4	128.8	0.01372	1.364			
Mir574	microRNA 574(MIR574)	NR_030300	102.3	94.5	0.01377	0.783			
DENR	density regulated re-initiation and release factor(DENR)	NM_003677	155.7	149.2	0.01383	1.226			
DEPDC5	DEP domain containing 5(DEPDC5)	NM_001007188	843.8	567.2	0.01383	1.226			
ARL17A	ADP ribosylation factor like GTPase 17A(ARL17A)	NM_016632	163.2	163.5	0.01388	1.274			
		XM_928111	92.5	99.8	0.01393	1.106			
SLFN11	schlafen family member 11(SLFN11)	NM_152270	102.7	95.7	0.01394	0.876			

SLFN11	schlafen family member 11(SLFN11)	NM_152270	108.1	107.6	0.01394	0.876
SMN1	survival of motor neuron 1, telomeric(SMN1)	NM_000344	98	105.1	0.01394	1.181
PTPN23	protein tyrosine phosphatase, non-receptor type 23(PTPN23)	NM_015466	106.7	107.7	0.01397	1.191
OFD1	OFD1, centriole and centriolar satellite protein(OFD1)	NM_003611	105.5	108.9	0.01399	1.156
HSCB	HscB mitochondrial iron-sulfur cluster cochaperone(HSCB)	NM_172002	95.2	92.9	0.01421	0.877
NEDD8	neural precursor cell expressed, developmentally down-regulated 8(NEDD8)	NM_006156	231.6	239.3	0.01424	0.742
NEDD8	neural precursor cell expressed, developmentally down-regulated 8(NEDD8)	NM_006156	1873.4	1679.1	0.01424	0.742
ARID4B	AT-rich interaction domain 4B(ARID4B)	NM_016374	127.9	108.8	0.01428	1.674
ARID4B	AT-rich interaction domain 4B(ARID4B)	NM_016374	210.3	153.7	0.01428	1.674
ARID4B	AT-rich interaction domain 4B(ARID4B)	NM_016374	430.2	318.2	0.01428	1.674

ERO1B	endoplasmic reticulum oxidoreductase 1 beta(ERO1B)	NM_019891	108.7	92.1	0.01431	0.832
RHBDL3	rhomboid like 3(RHBDL3)	NM_138328	141.9	115.2	0.01436	0.808
GON7	GON7, KEOPS complex subunit homolog(GON7)	NM_032490	97.7	103.8	0.01446	1.223
ANGPTL7	angiopoietin like 7(ANGPTL7)	NM_021146	109.6	97.3	0.01447	0.873
PHLDA1	pleckstrin homology like domain family A member 1(PHLDA1)	NM_007350	99.5	105.4	0.01451	0.745
PHLDA1	pleckstrin homology like domain family A member 1(PHLDA1)	NM_007350	157.6	155.9	0.01451	0.745
MOS	v-mos Moloney murine sarcoma viral oncogene homolog(MOS)	NM_005372	92.4	89.7	0.01457	0.899
		XM_001130102	122.6	117.7	0.01466	1.189
CSRP2	cysteine and glycine rich protein 2(CSRP2)	NM_001321	102.3	91.5	0.01466	0.903
NECTIN3	nectin cell adhesion molecule 3(NECTIN3)	NM_015480	145.6	166.7	0.0148	1.412
NECTIN3	nectin cell adhesion molecule 3(NECTIN3)	NM_015480	179.6	197.3	0.0148	1.412
		XM_001720754	96.1	102.4	0.01485	1.108

LOC105372672	uncharacterized LOC105372672(LOC105372672)	AW661821	113.6	99.2	0.01499	0.821
		BX107471	92.6	90.4	0.01502	0.863
KIF5C	kinesin family member 5C(KIF5C)	NM_004522	111.7	110.1	0.01506	0.881
mri1	methylthioribose-1-phosphate isomerase 1(MRI1)	NM_001031727	118.3	118.3	0.01512	1.33
mri1	methylthioribose-1-phosphate isomerase 1(MRI1)	NM_001031727	126.3	142.2	0.01512	1.33
		XR_039704	100.4	90.1	0.01516	0.84
LENG8	leukocyte receptor cluster member 8(LENG8)	NM_052925	125.4	100.3	0.01521	0.779
FRS3	fibroblast growth factor receptor substrate 3(FRS3)	NM_006653	187.5	189.9	0.01526	1.243
MIR657	microRNA 657(MIR657)	NR_030394	91.8	97.2	0.01527	1.278
		XM_001726567	139.6	137	0.01529	0.795
C1QTNF1	C1q and tumor necrosis factor related protein 1(C1QTNF1)	NM_198593	101	105.7	0.01536	1.14
C1QTNF1	C1q and tumor necrosis factor related protein 1(C1QTNF1)	NM_198594	139	133.4	0.01536	1.14

DAPL1	death associated protein like 1(DAPL1)	NM_001017920	159.5	127.5	0.01541	0.71
RBM6	RNA binding motif protein 6(RBM6)	NM_005777	123.5	101.2	0.01542	0.864
ARSB	arylsulfatase B(ARSB)	NM_000046	118.4	123.1	0.01544	1.227
UBN2	ubinuclein 2(UBN2)	NM_173569	153.5	130.9	0.01546	0.853
UBN2	ubinuclein 2(UBN2)	NM_173569	242.7	199.3	0.01546	0.853
EPS8L3	EPS8 like 3(EPS8L3)	NM_139053	91	83.7	0.01554	0.862
MAPT	microtubule associated protein tau(MAPT)	NM_016834	148.3	128.8	0.01556	0.786
AGFG2	ArfGAP with FG repeats 2(AGFG2)	NM_006076	183.1	177.2	0.0156	1.351
MIR571	microRNA 571(MIR571)	NR_030297	105.3	106.7	0.01567	1.114
SF3B1	splicing factor 3b subunit 1(SF3B1)	NM_012433	148.3	148.7	0.01586	1.302
SF3B1	splicing factor 3b subunit 1(SF3B1)	NM_012433	636.6	434.5	0.01586	1.302
GALE	UDP-galactose-4-epimerase(GALE)	NM_000403	98.9	102.7	0.0159	1.194
RANBP3	RAN binding protein 3(RANBP3)	NM_003624	101.5	97.4	0.01593	1.132
RANBP3	RAN binding protein 3(RANBP3)	NM_003624	102.5	105.1	0.01593	1.132
UBE2D3	ubiquitin conjugating enzyme E2 D3(UBE2D3)	NM_181890	1623.6	1372.6	0.01594	1.335

UBE2D3	ubiquitin conjugating enzyme E2 D3(UBE2D3)	NM_181890	2032.9	1807.8	0.01594	1.335
BPTF	bromodomain PHD finger transcription factor(BPTF)	NM_004459	93.9	96.4	0.01602	1.24
FAM220A	family with sequence similarity 220 member A(FAM220A)	NM_001037163	104	93.3	0.01602	0.894
LAIR1	leukocyte associated immunoglobulin like receptor 1(LAIR1)	NM_021706	118	114.2	0.01603	1.234
LAMA2	laminin subunit alpha 2(LAMA2)	NM_000426	17263.4	17310.7	0.01603	1.234
		AI341386	101.5	119	0.01616	1.28
TMEM217	transmembrane protein 217(TMEM217)	NM_145316	99.8	106.4	0.01617	1.149
TMEM217	transmembrane protein 217(TMEM217)	NM_145316	142.5	140.2	0.01617	1.149
PARP16	poly(ADP-ribose) polymerase family member 16(PARP16)	NM_017851	104.5	99.1	0.01623	0.851
TOP3A	topoisomerase (DNA) III alpha(TOP3A)	NM_004618	93.7	91.8	0.01623	0.799
TOP3A	topoisomerase (DNA) III alpha(TOP3A)	NM_004618	108.4	96.4	0.01623	0.799
BCL2L11	BCL2 like 11(BCL2L11)	NM_006538	98.4	103.9	0.0163	1.193
		BX097731	101.5	107.1	0.01631	1.172
		CR619250	95.1	99.3	0.01637	1.159

CNRIP1	cannabinoid receptor interacting protein 1(CNRIP1)	NM_015463	102.1	91.2	0.0164	0.87
RBM41	RNA binding motif protein 41(RBM41)	NM_018301	154.8	157.6	0.01644	1.28
SAMD9	sterile alpha motif domain containing 9(SAMD9)	NM_017654	91.4	87.8	0.01646	0.84
ZNF467	zinc finger protein 467(ZNF467)	NM_207336	185.3	202.1	0.01655	1.278
DDX10	DEAD-box helicase 10(DDX10)	NM_004398	101.9	87.7	0.0166	0.838
LUC7L	LUC7 like(LUC7L)	NM_018032	160.1	144.7	0.01666	0.858
POLR1B	RNA polymerase I subunit B(POLR1B)	NM_019014	103.4	92.7	0.01669	0.864
LGALS12	galectin 12(LGALS12)	NM_033101	100.6	105.3	0.01674	1.14
cyb5r3	cytochrome b5 reductase 3(CYB5R3)	NM_000398	113.2	106.6	0.01675	0.887
FAM86JP	family with sequence similarity 86, member A pseudogene(FAM86JP)	NR_024250	96.9	102.5	0.01686	1.163
DHX40	DEAH-box helicase 40(DHX40)	NM_024612	117.9	110.1	0.01687	0.864
DHX40	DEAH-box helicase 40(DHX40)	NM_024612	139	137.6	0.01687	0.864
DHX40	DEAH-box helicase 40(DHX40)	NM_024612	169.3	171.4	0.01687	0.864

EIF2S2	eukaryotic translation initiation factor 2 subunit beta(EIF2S2)	NM_003908	223.4	241	0.0169	1.26
XKR9	XK related 9(XKR9)	NM_001011720	109.2	93.9	0.01692	0.874
PDZD8	PDZ domain containing 8(PDZD8)	NM_173791	285.2	267.9	0.01699	1.213
NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147134	107.6	102.5	0.017	1.131
PHF14	PHD finger protein 14(PHF14)	NM_014660	100.5	101.6	0.01705	1.088
ZNF658B	zinc finger protein 658B (pseudogene)(ZNF658B)	NM_001032297	107.5	115.7	0.01713	1.186
		XM_001721880	101.2	98.2	0.0172	1.153
		XM_001721880	177.7	157.5	0.0172	1.153
FBXW4	F-box and WD repeat domain containing 4(FBXW4)	NM_022039	111.1	114.8	0.01739	1.195
Efcab13	EF-hand calcium binding domain 13(EFCAB13)	NM_152347	96.7	96.1	0.01742	1.122
LILRB3	leukocyte immunoglobulin like receptor B3(LILRB3)	NM_006864	129.4	93	0.01748	1.248
LILRB4	leukocyte immunoglobulin like receptor B4(LILRB4)	NM_001081438	14279.9	13030.4	0.01748	1.248

RNA28S5	RNA, 28S ribosomal 5(RNA28S5)	NR_003287	371.8	466.3	0.01766	2.305
RNA28S5	RNA, 28S ribosomal 5(RNA28S5)	NR_003287	769.5	878.2	0.01766	2.305
STRN	striatin(STRN)	NM_003162	118.2	110.9	0.01769	0.808
		AI239861	98.5	102.5	0.01771	1.116
CSNK1D	casein kinase 1 delta(CSNK1D)	NM_139062	256	242.1	0.01774	1.437
LINC01018	long intergenic non-protein coding RNA 1018(LINC01018)	NR_024424	106.9	97.3	0.01782	1.181
LINC01011	long intergenic non-protein coding RNA 1011(LINC01011)	NM_207495	99.4	104.9	0.01782	1.181
PSMD3	proteasome 26S subunit, non-ATPase 3(PSMD3)	NM_002809	106.3	90.9	0.01784	0.866
TMEM80	transmembrane protein 80(TMEM80)	NM_174940	135.9	123.3	0.01799	0.722
COG4	component of oligomeric golgi complex 4(COG4)	NM_015386	146.6	122	0.01803	0.77
COG3	component of oligomeric golgi complex 3(COG3)	NM_031431	137.6	123.3	0.01803	0.77
		XM_939521	105.4	106.4	0.01806	1.097
		DR980387	89.4	98.9	0.01823	1.166

GNB1L	G protein subunit beta 1 like(GNB1L)	NM_053004	100.1	93.4	0.01826	1.126
		XM_930349	85.2	82	0.0183	0.865
		XM_936804	109.4	104.4	0.01837	0.78
ALOX12B	arachidonate 12-lipoxygenase, 12R type(ALOX12B)	NM_001139	102.3	103	0.01837	1.172
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	94.7	96.7	0.01839	1.158
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	100	93.3	0.01839	1.158
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	101.7	99.2	0.01839	1.158
ZNF654	zinc finger protein 654(ZNF654)	NM_018293	105.3	110.3	0.01839	1.158
		XM_0017244542	109.3	131.8	0.0184	1.422
MIR939	microRNA 939(MIR939)	NR_030635	116.6	110.5	0.01851	0.874
		XR_017667	9770	7036.8	0.01851	0.742
E2F1	E2F transcription factor 1(E2F1)	NM_005225	171.1	168.6	0.01852	1.461
GADD45A	growth arrest and DNA damage inducible alpha(GADD45A)	NM_001924	104.9	99.7	0.01853	0.763
ITGB2	integrin subunit beta 2(ITGB2)	NM_000211	708.1	576.7	0.01855	0.69

CCL19	C-C motif chemokine ligand 19(CCL19)	NM_006274	110.3	112.8	0.01867	1.212	NM_017196	14.73	0.69
OR1K1	olfactory receptor family 1 subfamily K member 1(OR1K1)	NM_080859	100	94.1	0.01873	0.87	NM_017196	14.73	0.69
		XM_001130104	102	95.8	0.01878	0.881			
		XM_001126202	194.1	183	0.01883	1.428	NM_017196	14.73	0.69
		XM_929153	93.8	96.7	0.0189	0.859			
FANCE	Fanconi anemia complementation group E(FANCE)	NM_021922	177	154.6	0.01893	1.235			
		XM_944342	106.9	97.6	0.01896	0.875			
VARS	valyl-tRNA synthetase(VARS)	NM_006295	181.3	149	0.01902	0.727	NM_031356	5.43	24.53
		XM_001127768	99.9	104.9	0.01903	1.162	NM_031356	5.43	24.53
		XM_001725366	110.4	104.2	0.01904	0.815			
DTX2	deltex E3 ubiquitin ligase 2(DTX2)	NM_020892	109.1	113.2	0.01918	1.159			
DTX3	deltex E3 ubiquitin ligase 3(DTX3)	NM_178502	438	382.6	0.01918	1.159			
dhx37	DEAH-box helicase 37(DHX37)	NM_032656	133.3	112.5	0.0192	0.836			
		XM_940292	97	93.7	0.01925	0.888			

SLTM	SAFB like transcription modulator(SLTM)	NM_024755	132.4	131.2	0.01929	1.268			
SLTM	SAFB like transcription modulator(SLTM)	NM_024755	342.5	294.3	0.01929	1.268			
FIGN	fidgetin, microtubule severing factor(FIGN)	NM_018086	93.3	99.3	0.0193	1.132			
slx4ip	SLX4 interacting protein(SLX4IP)	NM_001009608	113.6	112	0.01934	1.119			
		XM_938977	116.5	111.7	0.01935	1.138			
SLC25A20	solute carrier family 25 member 20(SLC25A20)	NM_000387	95.2	103.1	0.0194	1.43			
SLC25A20	solute carrier family 25 member 20(SLC25A20)	NM_000387	212.9	290.9	0.0194	1.43			
TRAF1	TNF receptor associated factor 1(TRAF1)	NM_005658	104.5	114.2	0.01954	1.246			
ABTB1	ankyrin repeat and BTB domain containing 1(ABTB1)	NM_032548	114.2	97.5	0.01957	0.843			
CHAD	chondroadherin(CHAD)	NM_001267	96.4	91.9	0.01958	0.851	NM_017135	41.45	2.88
ZFP82	ZFP82 zinc finger protein(ZFP82)	NM_133466	115.8	106.4	0.01969	0.875	NM_017135	41.45	2.88
		XM_931238	108.5	104.2	0.01984	0.719	NM_017135	41.45	2.88
SHARPIN	SHANK associated RH domain interactor(SHARPIN)	NM_030974	116.9	108.1	0.01985	0.852	NM_017135	41.45	2.88
CALB2	calbindin 2(CALB2)	NM_007088	103.1	113.8	0.01986	1.279	NM_017135	41.45	2.88

		XM_944717	98.9	93.9	0.01987	0.858			
		AW168583	90.7	97.5	0.02005	1.164			
		XM_928447	97.7	102.2	0.02008	1.203			
		XM_0017199479	107.4	105.1	0.0201	1.136			
SERPINB7	serpin family B member 7(SERPINB7)	NM_003784	102.5	100	0.02011	0.85			
SERPINB7	serpin family B member 7(SERPINB7)	NM_003784	123.2	109.9	0.02011	0.85			
		XM_931877	98.6	103.2	0.02017	1.102			
		XR_039881	115.4	102.6	0.02022	1.218	NM_001033653	43.46	1.56
ARMCX3	armadillo repeat containing, X-linked 3(ARMCX3)	NM_177947	210.1	181.4	0.02027	0.708			
ARMCX3	armadillo repeat containing, X-linked 3(ARMCX3)	NM_177948	358.4	354.8	0.02027	0.708			
SYNE1	spectrin repeat containing nuclear envelope protein 1(SYNE1)	NM_033071	86.7	87.4	0.02027	0.74			
SEC63	SEC63 homolog, protein translocation regulator(SEC63)	NM_007214	103.2	112.3	0.02028	1.168			

TMEM57	transmembrane protein 57(TMEM57)	NM_018202	302.2	259	0.02049	1.361
		XR_019270	99.9	97.2	0.02052	0.878
PA2G4	proliferation-associated 2G4(PA2G4)	NM_006191	118.1	124.9	0.02056	1.19
		AI056317	98.3	91.3	0.02066	0.898
		XR_041761	99	104	0.02066	1.204
NOM1	nucleolar protein with MIF4G domain 1(NOM1)	NM_138400	99.5	90.9	0.02067	0.767
HS6ST2	heparan sulfate 6-O-sulfotransferase 2(HS6ST2)	NM_147175	107.9	109.4	0.02068	1.102
SRSF3	serine and arginine rich splicing factor 3(SRSF3)	NM_003017	140.1	138.1	0.02078	0.742
BTBD6	BTB domain containing 6(BTBD6)	NM_033271	124.3	116.8	0.02099	0.874
BTBD3	BTB domain containing 3(BTBD3)	NM_014962	92.5	88.5	0.02099	0.874
EP300	E1A binding protein p300(EP300)	NM_001429	104.5	106.6	0.02102	1.149
GSTTP2	glutathione S-transferase theta pseudogene 2(GSTTP2)	NR_003082	176.8	173.7	0.0211	1.158

GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)(GSTT2B)	NM_001080843	92.2	106.7	0.0211	1.158			
TM7SF3	transmembrane 7 superfamily member 3(TM7SF3)	NM_016551	131.8	120.2	0.02121	0.767			
RBM10	RNA binding motif protein 10(RBM10)	NM_152856	311.5	312.6	0.02124	1.256			
		XM_001713713	96.3	92.3	0.02127	0.907			
OBSL1	obscurin like 1(OBSL1)	NM_015311	104.6	114.2	0.02128	1.22			
cemip	cell migration inducing hyaluronan binding protein(CEMIP)	NM_018689	99.3	96.4	0.02131	0.883			
CCS	copper chaperone for superoxide dismutase(CCS)	NM_005125	104.2	111.5	0.02143	1.276			
CCSER2	coiled-coil serine rich protein 2(CCSER2)	NM_018999	117.4	111.4	0.02143	1.276	NM_134407	50.47	11.16
CSN1S1	casein alpha s1(CSN1S1)	NM_001890	98.7	102.3	0.02143	1.131			
FAHD1	fumarylacetoacetate hydrolase domain containing 1(FAHD1)	NM_001018104	318.4	348.8	0.02146	1.212			
ZFYVE28	zinc finger FYVE-type containing 28(ZFYVE28)	NM_020972	92.3	96.8	0.02152	1.133			
TNIP2	TNFAIP3 interacting protein 2(TNIP2)	NM_024309	108.2	102.8	0.02163	0.884			

OR11H1	olfactory receptor family 11 subfamily H member 1(OR11H1)	NM_001005239	98.6	95.5	0.02163	0.796
SPTBN5	spectrin beta, non-erythrocytic 5(SPTBN5)	NM_016642	131.5	123.8	0.02163	0.785
		XR_016400	98.2	93.9	0.02165	0.884
		XR_016218	114.4	112.6	0.0218	0.428
SKAP2	src kinase associated phosphoprotein 2(SKAP2)	NM_003930	95	93.7	0.02188	0.803
SKAP2	src kinase associated phosphoprotein 2(SKAP2)	NM_003930	210	162.9	0.02188	0.803
		XM_930512	95.6	100.7	0.02189	1.191
		XR_016302	83.5	92.6	0.02199	1.169
RAMP3	receptor activity modifying protein 3(RAMP3)	NM_005856	135.4	126.1	0.02208	1.338
RAMP3	receptor activity modifying protein 3(RAMP3)	NM_005856	155.8	125.8	0.02208	1.338
adgra3	adhesion G protein-coupled receptor A3(ADGRA3)	NM_145290	132.7	137.6	0.02213	1.561
BBS2	Bardet-Biedl syndrome 2(BBS2)	NM_031885	314.5	330.2	0.02224	0.766

BBS4	Bardet-Biedl syndrome 4(BBS4)	NM_033028	548.9	463.4	0.02224	0.766			
PPIL2	peptidylprolyl isomerase like 2(PPIL2)	NM_014337	106.2	112.2	0.02228	1.178			
PPIL2	peptidylprolyl isomerase like 2(PPIL2)	NM_014337	147.3	136.1	0.02228	1.178			
		XM_940079	121	108.1	0.02229	0.784	NM_001033706	2.42	10.86
C9orf85	chromosome 9 open reading frame 85(C9orf85)	NM_182505	95.9	100.4	0.02229	1.155			
TRAPPC4	trafficking protein particle complex 4(TRAPPC4)	NM_016146	351.4	304.6	0.0223	0.842			
PTK2	protein tyrosine kinase 2(PTK2)	NM_153831	103.7	106.5	0.0223	1.088			
		XM_937184	95.9	98.1	0.02234	1.158			
		XM_001713911	97	98.4	0.0224	1.166			
MS4A6A	membrane spanning 4-domains A6A(MS4A6A)	NM_022349	104.3	92	0.02245	0.891	NM_153300	0.14	61.17
		XM_001722445	109.3	92.3	0.02252	0.777			
setmar	SET domain and mariner transposase fusion gene(SETMAR)	NM_006515	184.2	161.7	0.02255	0.763	NM_032416	108.51	1.87

KCNJ14	potassium voltage-gated channel subfamily J member 14(KCNJ14)	NM_170720	97.9	101.8	0.02263	1.11
KRTAP12-1	keratin associated protein 12-1(KRTAP12-1)	NM_181686	101.8	102.5	0.02264	1.162
VPS13A	vacuolar protein sorting 13 homolog A(VPS13A)	NM_001018038	95.7	102.8	0.0227	1.183
VPS13A	vacuolar protein sorting 13 homolog A(VPS13A)	NM_001018038	100.6	97.6	0.0227	1.183
NUDT22	nudix hydrolase 22(NUDT22)	NM_032344	148.6	154.3	0.02273	1.244
KCNJ4	potassium voltage-gated channel subfamily J member 4(KCNJ4)	NM_152868	96.8	100.4	0.02275	1.124
BICDL2	BICD family like cargo adaptor 2(BICDL2)	NM_001103175	209.9	205.9	0.0228	1.275
		XM_001723741	96.8	106.1	0.02288	1.166
RPLP2	ribosomal protein lateral stalk subunit P2(RPLP2)	NM_001004	9850.2	8202.3	0.02299	1.4
BCORL1	BCL6 corepressor-like 1(BCORL1)	NM_021946	250.5	165.9	0.02302	0.737
PSMD5	proteasome 26S subunit, non-ATPase 5(PSMD5)	NM_005047	156.6	143.8	0.02303	0.834
TTLL3	tubulin tyrosine ligase like 3(TTLL3)	NM_015644	102.6	98.6	0.02307	0.901

TTLL3	tubulin tyrosine ligase like 3(TTLL3)	NM_015644	152.3	116	0.02307	0.901			
TAGLN	transgelin(TAGLN)	NM_003186	388.2	296.4	0.02309	0.565			
TAGLN	transgelin(TAGLN)	NM_003186	1629.7	1263	0.02309	0.565	NM_001191088	10.07	0.03
ZNF419	zinc finger protein 419(ZNF419)	NM_001098495	117.2	122.7	0.02311	1.195	NM_001191088	10.07	0.03
TBP	TATA-box binding protein(TBP)	NM_003194	176.5	138.7	0.02312	0.825	NM_001191088	10.07	0.03
		XM_944734	105.6	105.9	0.02315	1.137			
SDR16C5	short chain dehydrogenase/reductase family 16C, member 5(SDR16C5)	NM_138969	100.6	123	0.02318	1.399			
MANEA	mannosidase endo-alpha(MANEA)	NM_024641	284.5	258.2	0.0232	1.18			
MANBAL	mannosidase beta like(MANBAL)	NM_001003897	93.3	98	0.0232	1.18	NM_012496	1095.39	8.76
TMUB2	transmembrane and ubiquitin like domain containing 2(TMUB2)	NM_001076674	96.8	102.1	0.0232	1.093			
TAF8	TATA-box binding protein associated factor 8(TAF8)	NM_138572	106	117.7	0.02321	1.203			

TIMMDC1	translocase of inner mitochondrial membrane domain containing 1(TIMMDC1)	NM_016589	261.6	245.6	0.0234	1.756
OACYLP	O-acyltransferase like, pseudogene(OACYLP)	NR_024021	95.9	92.1	0.02342	0.881
ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif 17(ADAMTS17)	NM_139057	100.2	101.2	0.02354	1.182
FOXI3	forkhead box I3(FOXI3)	NM_001135649	125	122.7	0.02357	1.164
FOXI1	forkhead box I1(FOXI1)	NM_012188	95.4	100.1	0.02357	1.164
		BM674906	97.4	104.6	0.02358	1.129
ZNF839	zinc finger protein 839(ZNF839)	NM_018335	115.6	122.3	0.0236	1.15
		XM_936486	85.9	93.8	0.02362	1.19
RAMP2	receptor activity modifying protein 2(RAMP2)	NM_005854	120.2	108.4	0.02364	1.231
RAMP2	receptor activity modifying protein 2(RAMP2)	NM_005854	122.1	133.9	0.02364	1.231
MTMR1	myotubularin related protein 1(MTMR1)	NM_003828	103.1	96.4	0.02366	0.871
ANXA6	annexin A6(ANXA6)	NM_001155	97	97.9	0.02369	0.603

		XM_001130122	110.9	110.4	0.02369	0.899
		XM_001130122	119	109.5	0.02369	0.899
		XM_498608	95.9	94	0.0237	0.897
UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI(UQCR11)	NM_006830	102.6	110.8	0.02379	1.137
KRTAP13-3	keratin associated protein 13-3(KRTAP13-3)	NM_181622	106.2	101.1	0.02383	1.117
FAM76B	family with sequence similarity 76 member B(FAM76B)	NM_144664	101.8	111.2	0.02384	1.21
NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D(NAPEPLD)	NM_198990	109.8	105.8	0.02406	0.842
NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D(NAPEPLD)	NM_198990	136.7	129.8	0.02406	0.842
STAR	steroidogenic acute regulatory protein(STAR)	NM_001007243	107	91.7	0.02412	0.732
WDR4	WD repeat domain 4(WDR4)	NM_033661	100.8	100.2	0.02415	1.118
BPIFB3	BPI fold containing family B member 3(BPIFB3)	NM_182658	105	105.1	0.02418	1.174

		BX102609	97.7	94.7	0.02426	0.88
PRUNE2	prune homolog 2(PRUNE2)	NM_138818	101	109.8	0.02429	1.351
PRUNE2	prune homolog 2(PRUNE2)	NM_138818	101.6	102.3	0.02429	1.351
TRAPPC2	trafficking protein particle complex 2(TRAPPC2)	NM_014563	100.3	90.3	0.02438	0.846
TRAPPC2	trafficking protein particle complex 2(TRAPPC2)	NM_014563	204.2	161.1	0.02438	0.846
MLEC	malectin(MLEC)	NM_014730	226.4	205.3	0.02445	1.294
MLEC	malectin(MLEC)	NM_014730	530.9	526.3	0.02445	1.294
RNF215	ring finger protein 215(RNF215)	NM_001017981	101.8	89.7	0.0245	0.865
		XM_933836	104.9	105.5	0.02463	1.098
GALNT10	polypeptide N-acetylgalactosaminyltransferase 10(GALNT10)	NM_017540	144	142.8	0.02463	1.372
PCGF6	polycomb group ring finger 6(PCGF6)	NM_001011663	94.3	91.5	0.02464	0.859
KLHDC8B	kelch domain containing 8B(KLHDC8B)	NM_173546	99	101.9	0.02474	1.127
		XM_930350	121.4	116.3	0.02484	1.183

KANK3	KN motif and ankyrin repeat domains 3(KANK3)	NM_198471	92	96.5	0.02484	1.131			
BACH2	BTB domain and CNC homolog 2(BACH2)	NM_021813	95	99.7	0.02486	1.145			
BACH2	BTB domain and CNC homolog 2(BACH2)	NM_021813	110.5	88.8	0.02486	1.145			
BACH2	BTB domain and CNC homolog 2(BACH2)	NM_021813	125.9	97.7	0.02486	1.145			
HERPUD2	HERPUD family member 2(HERPUD2)	NM_022373	100.6	106.9	0.02489	1.125	NM_013059	21.02	0.11
HES1	hes family bHLH transcription factor 1(HES1)	NM_005524	110.3	105.6	0.02489	1.125			
MTIF2	mitochondrial translational initiation factor 2(MTIF2)	NM_001005369	724.5	656.1	0.02491	1.3			
TUSC3	tumor suppressor candidate 3(TUSC3)	NM_006765	92.7	97	0.02493	1.19			
TUSC3	tumor suppressor candidate 3(TUSC3)	NM_006765	162.1	190.1	0.02493	1.19			
		XM_001715936	109.1	107.4	0.02501	1.152			
DZANK1	double zinc ribbon and ankyrin repeat domains 1(DZANK1)	NM_001099407	99.6	91.5	0.02504	0.83			
ZNF471	zinc finger protein 471(ZNF471)	NM_020813	113.7	117.6	0.02504	1.249			
ZNF471	zinc finger protein 471(ZNF471)	NM_020813	131.7	127.7	0.02504	1.249			

		XM_001132307	95.6	94.6	0.02512	0.873			
mri1	methylthioribose-1-phosphate isomerase 1(MRI1)	NM_032285	138.6	130.6	0.02515	1.226			
		XR_019551	118.8	121.1	0.02526	1.225			
ABAT	4-aminobutyrate aminotransferase(ABAT)	NM_000663	114.2	120.3	0.02539	1.135			
AATK	apoptosis associated tyrosine kinase(AATK)	NM_001080395	107.4	106.4	0.02539	1.135			
THUMPD1	THUMP domain containing 1(THUMPD1)	NM_017736	141.6	149.7	0.02554	1.191	NM_012816	19.78	2.28
LASP1	LIM and SH3 protein 1(LASP1)	NM_006148	94.5	102	0.02565	1.111	NM_012816	19.78	2.28
		XM_0017177976	101.7	107.2	0.0257	1.106			
WWOX	WW domain containing oxidoreductase(WWOX)	NM_130791	117.4	101.4	0.02601	0.884			
Mt1f	metallothionein 1F(MT1F)	NM_005949	107.2	107.1	0.02606	1.153			
POTEE	POTE ankyrin domain family member E(POTEE)	NM_001083538	105.2	98.8	0.02607	0.867			
FLNC	filamin C(FLNC)	NM_001458	102.5	88.9	0.02607	0.81			
SNX29	sorting nexin 29(SNX29)	NM_001009607	122.6	117.5	0.02623	1.306			

GGT1	gamma-glutamyltransferase 1(GGT1)	NM_001032364	118.8	102.1	0.02633	0.846
HES5	hes family bHLH transcription factor 5(HES5)	NM_001010926	101.4	107.2	0.02635	1.16
EBAG9	estrogen receptor binding site associated, antigen, 9(EBAG9)	NM_198120	116.1	136.2	0.02635	1.35
		XR_037520	108.7	105	0.02637	0.903
MED7	mediator complex subunit 7(MED7)	NM_001100816	133.3	114.7	0.02641	0.797
MED7	mediator complex subunit 7(MED7)	NM_001100816	138.8	130.1	0.02641	0.797
		BX093647	97.4	103.2	0.02646	1.059
		BX111229	109.1	116.9	0.02648	1.194
		BX109868	124.8	118.1	0.02649	1.126
RINT1	RAD50 interactor 1(RINT1)	NM_021930	124.7	125.8	0.02653	1.177
		XR_019645	115.4	101.5	0.02655	0.864
SLC16A10	solute carrier family 16 member 10(SLC16A10)	NM_018593	238.6	234.4	0.02665	1.749
		XM_944489	251.6	275	0.02668	1.242
CAPZA1	capping actin protein of muscle Z-line alpha subunit 1(CAPZA1)	NM_006135	181.8	174.9	0.02672	1.272

AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase(AASDHPPT)	NM_015423	96.1	93.3	0.02681	0.881	NM_031544	4.79	38.59
PRSS3P2	protease, serine 3 pseudogene 2(PRSS3P2)	NR_001296	100.1	93.1	0.02683	1.142	NM_031544	4.79	38.59
C15orf56	chromosome 15 open reading frame 56(C15orf56)	NM_001039905	98.3	106.9	0.02686	1.146			
ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)(ST13)	NM_003932	217.8	232.6	0.02688	1.552			
Snora26	small nucleolar RNA, H/ACA box 26(SNORA26)	NR_003016	113.5	98.3	0.02695	0.84			
PSMD7	proteasome 26S subunit, non-ATPase 7(PSMD7)	NM_002811	152.8	133.6	0.02697	0.822			
MFSD14B	major facilitator superfamily domain containing 14B(MFSD14B)	NM_032558	95.4	95.9	0.02706	0.864			
MFSD14B	major facilitator superfamily domain containing 14B(MFSD14B)	NM_032558	101.3	95.5	0.02706	0.864			

MFSD14B	major facilitator superfamily domain containing 14B(MFSD14B)	NM_032558	101.7	94.1	0.02706	0.864
MFSD14B	major facilitator superfamily domain containing 14B(MFSD14B)	NM_032558	103	98.8	0.02706	0.864
JADE3	jade family PHD finger 3(JADE3)	NM_001077445	150.5	135.7	0.02712	0.817
SRCAP	Snf2 related CREBBP activator protein(SRCAP)	NM_006662	95.9	88.6	0.02716	0.886
		AL602970	93.8	101.5	0.02718	1.143
		XM_001716887	121.9	102.5	0.02723	0.798
folr1	folate receptor 1(FOLR1)	NM_016725	124.1	103.5	0.02737	0.781
NAE1	NEDD8 activating enzyme E1 subunit 1(NAE1)	NM_001018160	130.8	139.5	0.02747	0.661
NAE1	NEDD8 activating enzyme E1 subunit 1(NAE1)	NM_001018160	248.3	193.4	0.02747	0.661
LOC284009	uncharacterized LOC284009(LOC284009)	NM_001025459	110.2	117	0.02751	1.164
FAM99A	family with sequence similarity 99 member A (non-protein coding)(FAM99A)	NM_001014374	102.9	96	0.02757	1.139

		XM_001715669	90.3	96.4	0.02767	1.187
CD22	CD22 molecule(CD22)	NM_001771	94.4	98.4	0.02776	1.113
SLC25A26	solute carrier family 25 member 26(SLC25A26)	NM_001009938	101.1	98.5	0.02781	1.124
RASAL2	RAS protein activator like 2(RASAL2)	NM_170692	104.5	99.8	0.02782	1.156
STXBP1	syntaxin binding protein 1(STXBP1)	NM_001032221	100.5	104.6	0.02784	1.143
		AF009305	97.1	97.9	0.02795	1.177
ORC1	origin recognition complex subunit 1(ORC1)	NM_004153	115.9	102.3	0.02801	0.866
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	108.1	105.5	0.02802	0.644
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	111.3	104.6	0.02802	0.644
KLHL5	kelch like family member 5(KLHL5)	NM_001007075	351.6	304.8	0.02802	0.644
		XM_001131851	131.7	134.4	0.02806	1.163
		XM_929859	131.7	120.7	0.02807	0.809
MRPS2	mitochondrial ribosomal protein S2(MRPS2)	NM_016034	158.8	151.8	0.0281	1.263
		CV318379	116.5	109.4	0.02813	0.93

TIAM2	T-cell lymphoma invasion and metastasis 2(TIAM2)	NM_012454	90.2	83	0.02818	0.869
ZNF544	zinc finger protein 544(ZNF544)	NM_014480	139.9	139.6	0.02822	1.251
MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type(MMAA)	NM_172250	104.1	107.6	0.02831	1.107
HAX1	HCLS1 associated protein X-1(HAX1)	NM_006118	106.2	95.5	0.02836	0.896
NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147133	125.1	115	0.02839	1.188
NFX1	nuclear transcription factor, X-box binding 1(NFX1)	NM_147133	136.2	123.8	0.02839	1.188
MINOS1	mitochondrial inner membrane organizing system 1(MINOS1)	NM_001032363	107.5	100.1	0.0284	1.182
MINOS1	mitochondrial inner membrane organizing system 1(MINOS1)	NM_001032363	110.6	123.7	0.0284	1.182
c19orf60	chromosome 19 open reading frame 60(C19orf60)	NM_001100419	97.5	105.4	0.02846	1.138
LINC00161	long intergenic non-protein coding RNA 161(LINC00161)	NR_026552	94.1	102.4	0.02847	1.135
SLC9A8	solute carrier family 9 member A8(SLC9A8)	NM_015266	99	96.4	0.02853	0.878

POLR2H	RNA polymerase II subunit H(POLR2H)	NM_006232	160.7	168.4	0.0286	1.217
		BU734093	141.7	135.8	0.02871	1.192
lemd3	LEM domain containing 3(LEMD3)	NM_014319	213.3	209.3	0.02873	1.179
		XM_931518	88.3	82.8	0.02884	0.835
NFYA	nuclear transcription factor Y subunit alpha(NFYA)	NM_002505	105.6	91.6	0.02884	0.886
		AW150545	101.2	98.4	0.02887	1.115
PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1(PIN1)	NM_006221	324	338.9	0.02887	1.19
		XM_001723251	129.5	128.5	0.02892	1.16
RFESD	Rieske Fe-S domain containing(RFESD)	NM_001131066	96.8	87.2	0.02906	0.786
EXO5	exonuclease 5(EXO5)	NM_022774	98	94.6	0.02922	0.808
EXO5	exonuclease 5(EXO5)	NM_022774	99.5	94.6	0.02922	0.808
EXO5	exonuclease 5(EXO5)	NM_022774	1035.5	803	0.02922	0.808
SPDYE8P	speedy/RINGO cell cycle regulator family member E8, pseudogene(SPDYE8P)	NR_003664	106.3	92.3	0.02929	0.727

SPDYE8P	speedy/RINGO cell cycle regulator family member E8, pseudogene(SPDYE8P)	NR_003664	13009	11409.6	0.02929	0.727
TNRC6A	trinucleotide repeat containing 6A(TNRC6A)	NM_014494	128.5	121.8	0.0293	0.868
TNRC6A	trinucleotide repeat containing 6A(TNRC6A)	NM_014494	134.2	116.6	0.0293	0.868
TNRC6A	trinucleotide repeat containing 6A(TNRC6A)	NM_014494	310.9	258.5	0.0293	0.868
OR7C2	olfactory receptor family 7 subfamily C member 2(OR7C2)	NM_012377	108.8	107.4	0.0293	1.116
GPS1	G protein pathway suppressor 1(GPS1)	NM_212492	148.3	163.4	0.02938	0.897
GPS1	G protein pathway suppressor 1(GPS1)	NM_004127	103.2	98.9	0.02938	0.897
BRI3BP	BRI3 binding protein(BRI3BP)	NM_080626	117	118	0.02938	1.772
BRI3BP	BRI3 binding protein(BRI3BP)	NM_080626	124.8	116.6	0.02938	1.772
BRI3BP	BRI3 binding protein(BRI3BP)	NM_080626	305.1	288.1	0.02938	1.772
NPR3	natriuretic peptide receptor 3(NPR3)	NM_000908	116.2	124.6	0.02947	1.363
TBC1D9B	TBC1 domain family member 9B(TBC1D9B)	NM_015043	112.5	98.2	0.02948	0.814

		BQ021435	100.1	107.3	0.02951	1.131
		XM_001726935	113	104	0.02951	0.692
TMEM237	transmembrane protein 237(TMEM237)	NM_001044385	136.9	130.4	0.02976	0.758
CCT4	chaperonin containing TCP1 subunit 4(CCT4)	NM_006430	164.5	174.9	0.02979	1.323
KLHL28	kelch like family member 28(KLHL28)	NM_017658	145.5	125.2	0.02984	0.745
		XM_001132864	96	93.4	0.0299	0.844
SLC17A2	solute carrier family 17 member 2(SLC17A2)	NM_005835	94.3	100.6	0.02994	1.194
		XR_038252	103.7	111.8	0.03001	0.752
		XR_038252	610.6	508.9	0.03001	0.752
CD300LG	CD300 molecule like family member g(CD300LG)	NM_145273	99.2	93.7	0.03002	0.879
RTKN2	rhotekin 2(RTKN2)	NM_145307	101.3	92.8	0.03003	0.879
PCDHGA10	protocadherin gamma subfamily A, 10(PCDHGA10)	NM_032090	115.6	102.7	0.03005	0.866
		XM_941706	99.8	85.9	0.03012	0.849
SSRP1	structure specific recognition protein 1(SSRP1)	NM_003146	93	87.8	0.03019	0.886

		XM_001725293	258.1	171.5	0.03021	0.619
KHDRBS3	KH RNA binding domain containing, signal transduction associated 3(KHDRBS3)	NM_006558	536.6	500.8	0.03022	0.757
KDM4B	lysine demethylase 4B(KDM4B)	NM_015015	345.9	281.4	0.03044	0.792
HIKESHI	Hikeshi, heat shock protein nuclear import factor(HIKESHI)	NM_016401	177.8	214.5	0.03053	1.318
		XR_038706	360.2	335.1	0.0306	1.329
		AK021616	90.9	88.8	0.03065	0.832
ROM1	retinal outer segment membrane protein 1(ROM1)	NM_000327	124	142.3	0.03065	1.154
		AI263926	93.6	102.7	0.03068	1.217
SPO11	SPO11, initiator of meiotic double stranded breaks(SPO11)	NM_198265	103.7	99.5	0.03071	0.834
SPO11	SPO11, initiator of meiotic double stranded breaks(SPO11)	NM_198265	106.4	94.2	0.03071	0.834
JMJD8	jumonji domain containing 8(JMJD8)	NM_001005920	140.9	128.2	0.03073	1.24
ADD3	adducin 3(ADD3)	NM_001121	1598.4	1405.8	0.03086	0.847

PDE8B	phosphodiesterase 8B(PDE8B)	NM_001029851	93.6	97.1	0.03091	1.116
PDE8B	phosphodiesterase 8B(PDE8B)	NM_001029851	103.8	104.3	0.03091	1.116
TMED9	transmembrane p24 trafficking protein 9(TMED9)	NM_017510	187.4	172.8	0.03092	0.785
TDP1	tyrosyl-DNA phosphodiesterase 1(TDP1)	NM_018319	94.5	101.4	0.03101	1.125
TDP1	tyrosyl-DNA phosphodiesterase 1(TDP1)	NM_018319	97.8	100.2	0.03101	1.125
TDP1	tyrosyl-DNA phosphodiesterase 1(TDP1)	NM_018319	1550.9	1032.5	0.03101	1.125
FGF21	fibroblast growth factor 21(FGF21)	NM_019113	99.7	108	0.03104	1.098
SUZ12	SUZ12 polycomb repressive complex 2 subunit(SUZ12)	NM_015355	493.9	371.7	0.03109	1.517
		XR_037524	130.6	109.2	0.0311	0.819
CUL5	cullin 5(CUL5)	NM_003478	205.7	184.3	0.03112	0.826
ZNF549	zinc finger protein 549(ZNF549)	NM_153263	131.5	120.3	0.03118	0.862
ZNF549	zinc finger protein 549(ZNF549)	NM_153263	5630.6	3969.7	0.03118	0.862

ATP1B1	ATPase Na+/K+ transporting subunit beta 1(ATP1B1)	NM_001677	109.6	96.6	0.0312	0.878	NM_031012	19.39	0.85
		XM_936697	101.9	105.5	0.03128	1.112			
LOC613206	myeloproliferative disease associated tumor antigen 5(LOC613206)	NM_001033016	92.5	88	0.03131	0.876			
PUDP	pseudouridine 5'-phosphatase(PUDP)	NM_012080	99.4	110.4	0.03144	1.166			
PCBP2	poly(rC) binding protein 2(PCBP2)	NM_001098620	1075.5	729.4	0.03147	1.288	NM_012904	10.16	55.22
DCUN1D5	defective in cullin neddylation 1 domain containing 5(DCUN1D5)	NM_032299	109	105.9	0.03148	1.098			
		XM_001714155	100.1	99.8	0.03152	1.164			
GSKIP	GSK3B interacting protein(GSKIP)	NM_016472	260.7	206.5	0.03153	1.212			
CHIC2	cysteine rich hydrophobic domain 2(CHIC2)	NM_012110	97	109.6	0.03167	1.166			
PNMA1	paraneoplastic Ma antigen 1(PNMA1)	NM_006029	186.3	186.8	0.03178	0.762			
AKAP11	A-kinase anchoring protein 11(AKAP11)	NM_016248	271.4	236.4	0.03179	0.866			
AKAP12	A-kinase anchoring protein 12(AKAP12)	NM_144497	347.5	322.1	0.03179	0.866			

		DA266249	97.2	90.4	0.03191	0.864			
ADGRE5	adhesion G protein-coupled receptor E5(ADGRE5)	NM_078481	104.5	105.2	0.03199	1.093			
WDR44	WD repeat domain 44(WDR44)	NM_019045	114.7	111	0.03201	1.146			
WDR44	WD repeat domain 44(WDR44)	NM_019045	125.3	120.4	0.03201	1.146			
POLRMT	RNA polymerase mitochondrial(POLRMT)	NM_005035	202.6	175	0.03202	0.834	NM_012823	17.52	0.04
		XM_938965	93.5	103.4	0.03203	1.198			
SLC10A7	solute carrier family 10 member 7(SLC10A7)	NM_001029998	96.7	103	0.03204	0.869			
SLC10A7	solute carrier family 10 member 7(SLC10A7)	NM_001029998	115.6	108.9	0.03204	0.869			
		XR_017484	115.3	111.7	0.03211	0.457			
INTS6L	integrator complex subunit 6 like(INTS6L)	NM_182540	110.7	110.5	0.03221	1.206			
SOX18	SRY-box 18(SOX18)	NM_018419	256.5	228.1	0.0323	1.323			
		XM_0017133810	450.6	407.6	0.03235	1.904			
LATS2	large tumor suppressor kinase 2(LATS2)	NM_014572	101.1	100.5	0.0324	1.156			
		XM_929541	94.6	98.8	0.03246	1.115			

TMBIM1	transmembrane BAX inhibitor motif containing 1(TMBIM1)	NM_022152	229.2	278.1	0.03251	1.328
		XM_377725	111.5	114.1	0.03257	1.217
SUPV3L1	Suv3 like RNA helicase(SUPV3L1)	NM_003171	129.1	116.3	0.0326	0.894
PIKFYVE	phosphoinositide kinase, FYVE-type zinc finger containing(PIKFYVE)	NM_015040	90.8	96.9	0.03264	1.158
DCP2	decapping mRNA 2(DCP2)	NM_152624	111.9	122.2	0.0327	1.162
		XM_938181	7544.4	7392.2	0.0327	1.222
TH	tyrosine hydroxylase(TH)	NM_199293	94	88.2	0.03272	0.868
		AI732113	109.2	110.2	0.03273	1.11
TSPAN31	tetraspanin 31(TSPAN31)	NM_005981	280.4	249.8	0.03275	1.214
		BQ186959	100.2	97.5	0.03276	1.069
		XM_001723047	99.5	95	0.03278	0.878
		XM_937648	106.7	103.7	0.03278	0.879
TCEAL9	transcription elongation factor A like 9(TCEAL9)	NM_001006612	167.3	169.6	0.0328	1.264
RHBDD1	rhomboid domain containing 1(RHBDD1)	NM_032276	90.9	97	0.03282	1.129

RHBDD1	rhomboid domain containing 1(RHBDD1)	NM_032276	166.5	160.2	0.03282	1.129
POLH	DNA polymerase eta(POLH)	NM_006502	108	91.9	0.03282	0.775
		XM_499363	92.3	87	0.03283	0.895
H2AFJ	H2A histone family member J(H2AFJ)	NM_177925	129.8	116.1	0.0329	0.622
TAPT1-AS1	TAPT1 antisense RNA 1 (head to head)(TAPT1-AS1)	CA391675	112.2	98.4	0.03294	0.883
CLUAP1	clusterin associated protein 1(CLUAP1)	NM_015041	104.7	107.7	0.03295	0.869
CLUAP1	clusterin associated protein 1(CLUAP1)	NM_024793	110.9	104.1	0.03295	0.869
		XM_370557	98.3	90.5	0.03298	0.864
		XM_370557	111.8	105	0.03298	0.864
		XM_944469	90	79.1	0.03299	0.781
SLC35C2	solute carrier family 35 member C2(SLC35C2)	NM_173073	141.4	136.5	0.03302	1.131
arfip1	ADP ribosylation factor interacting protein 1(ARFIP1)	NM_001025595	95.4	90.7	0.03309	0.843
FHOD1	formin homology 2 domain containing 1(FHOD1)	NM_013241	220.4	322.4	0.03315	0.463

DISP2	dispatched RND transporter family member 2(DISP2)	NM_033510	112.2	113.2	0.03316	1.122
CSE1L	chromosome segregation 1 like(CSE1L)	NM_177436	412.3	329	0.03336	0.743
CSE1L	chromosome segregation 1 like(CSE1L)	NM_001316	378.1	277.6	0.03336	0.743
TRAPPC6B	trafficking protein particle complex 6B(TRAPPC6B)	NM_001079537	91.8	92.4	0.03336	0.777
TRAPPC6B	trafficking protein particle complex 6B(TRAPPC6B)	NM_001079537	109.7	102.2	0.03336	0.777
UFM1	ubiquitin fold modifier 1(UFM1)	NM_016617	209.1	185.6	0.03344	1.324
		AA454665	106.6	106.6	0.03356	1.13
SYNE4	spectrin repeat containing nuclear envelope family member 4(SYNE4)	NM_001039876	98.9	91.6	0.03363	0.903
PSRC1	proline and serine rich coiled-coil 1(PSRC1)	NM_001032290	107.7	106.5	0.03369	0.906
PPM1B	protein phosphatase, Mg2+/Mn2+ dependent 1B(PPM1B)	NM_177968	492.6	429.7	0.03382	1.302
PLAC9	placenta specific 9(PLAC9)	NM_001012973	137.1	135.9	0.03384	0.603

OR2A1	olfactory receptor family 2 subfamily A member 1(OR2A1)	NM_001005287	101.9	91.1	0.03389	0.87			
Uqcrh	ubiquinol-cytochrome c reductase hinge protein(UQCRH)	NM_006004	97.5	94.4	0.0339	0.839			
Uqcrh	ubiquinol-cytochrome c reductase hinge protein(UQCRH)	NM_006004	974.9	1252.9	0.0339	0.839			
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	NM_001895	136.4	143.1	0.03393	0.813			
CSNK2A2	casein kinase 2 alpha 2(CSNK2A2)	NM_001896	185.3	174	0.03393	0.813			
ADCY3	adenylate cyclase 3(ADCY3)	NM_004036	102.3	88.5	0.03401	0.898			
PTPA	protein phosphatase 2 phosphatase activator(PTPA)	NM_178003	108.9	110.5	0.03408	1.127			
		XR_001280	105.8	106.1	0.03411	1.125			
MAP3K4	mitogen-activated protein kinase kinase kinase 4(MAP3K4)	NM_005922	136.5	131	0.03415	1.193			
TRMT10A	tRNA methyltransferase 10A(TRMT10A)	NM_152292	101	96.3	0.03425	1.133	NM_017170	13.37	0.05
EIF4G2	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)	NM_001418	369.1	341.9	0.03434	0.827			
EIF4G2	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)	NM_001418	1858.1	1378.6	0.03434	0.827			

EIF4G2	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)	NM_001418	3468.8	2977.2	0.03434	0.827			
KDM2A	lysine demethylase 2A(KDM2A)	NM_012308	102.2	108.3	0.03439	0.91			
spdya	speedy/RINGO cell cycle regulator family member A(SPDYA)	NM_182756	94.9	100.2	0.0345	1.15			
MSLNL	mesothelin-like(MSLNL)	NM_001025190	96.1	102	0.03452	1.157			
MSLNL	mesothelin-like(MSLNL)	NM_001025190	101.8	99.3	0.03452	1.157			
CEP85L	centrosomal protein 85 like(CEP85L)	NM_206921	101.6	93.4	0.03455	0.873			
		XM_942374	106	96.4	0.03461	0.818	NM_001106492	2.61	10.85
NME2	NME/NM23 nucleoside diphosphate kinase 2(NME2)	NM_001018138	96.1	99.2	0.03465	1.129	NM_001106492	2.61	10.85
ELOVL3	ELOVL fatty acid elongase 3(ELOVL3)	NM_152310	109.3	98.8	0.03474	0.805	NM_001106492	2.61	10.85
LOC100996671	uncharacterized LOC100996671(LOC100996671)	BX111310	113.8	106.8	0.03476	0.834			
GNL3L	G protein nucleolar 3 like(GNL3L)	NM_019067	147.4	139.9	0.03477	0.771			
PUS7L	pseudouridylate synthase 7 like(PUS7L)	NM_001098615	107.1	97.3	0.03477	0.858			

		XM_944547	114.3	112	0.03477	1.202
		XM_929962	103.3	104.5	0.03483	1.131
DCAF10	DDB1 and CUL4 associated factor 10(DCAF10)	NM_024345	527	473.7	0.03486	1.6
RABL3	RAB, member of RAS oncogene family like 3(RABL3)	NM_173825	149.1	168.3	0.0349	1.267
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	93.6	90.3	0.03491	0.762
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	118	111.6	0.03491	0.762
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	119.8	142.3	0.03491	0.762
RSPH10B	radial spoke head 10 homolog B(RSPH10B)	NM_173565	120.8	133.7	0.03491	0.762
MTFMT	mitochondrial methionyl-tRNA formyltransferase(MTFMT)	NM_139242	120.9	116.6	0.03495	1.16
MTFMT	mitochondrial methionyl-tRNA formyltransferase(MTFMT)	NM_139242	166.5	161.6	0.03495	1.16
UTRN	utrophin(UTRN)	NM_007124	104.4	97.4	0.03497	0.782
NOL6	nucleolar protein 6(NOL6)	NM_139235	136.9	115.5	0.03505	0.772

CAPN10	calpain 10(CAPN10)	NM_023083	113.5	102.7	0.03514	1.132			
TBX19	T-box 19(TBX19)	NM_005149	98.5	104.3	0.03515	1.151			
TBX19	T-box 19(TBX19)	NM_005149	120.8	125.9	0.03515	1.151			
		CB858008	103.8	104.4	0.03516	1.155	NM_001270681	26.79	0.09
CRYL1	crystallin lambda 1(CRYL1)	NM_015974	95.5	89.6	0.03517	0.872			
KIAA0430	KIAA0430(KIAA0430)	NM_014647	99	110	0.03525	1.206			
CCDC114	coiled-coil domain containing 114(CCDC114)	NM_144577	131.9	119.5	0.03538	0.866			
		XM_937287	87.2	94.4	0.03544	1.17			
RSPRY1	ring finger and SPRY domain containing 1(RSPRY1)	NM_133368	294.2	256.2	0.03547	1.244			
RECQL5	RecQ like helicase 5(RECQL5)	NM_001003716	99.3	103	0.03559	1.086			
SLC37A3	solute carrier family 37 member 3(SLC37A3)	NM_207113	91.6	87.8	0.03569	0.91	NM_019373	263.23	1.01
ankrd40	ankyrin repeat domain 40(ANKRD40)	NM_052855	107.5	112.8	0.0357	0.719			
SRP14	signal recognition particle 14(SRP14)	NM_003134	236.8	255.8	0.03572	0.731			
SRP14	signal recognition particle 14(SRP14)	NM_003134	2418.6	2337.4	0.03572	0.731			

AKR1C4	aldo-keto reductase family 1 member C4(AKR1C4)	NM_001818	117.2	113.9	0.03575	1.309			
AKR1C8P	aldo-keto reductase family 1 member C8, pseudogene(AKR1C8P)	NM_001007536	222.7	203.9	0.03575	1.309			
NABP2	nucleic acid binding protein 2(NABP2)	NM_024068	122	106.8	0.03575	0.854			
ZBTB20	zinc finger and BTB domain containing 20(ZBTB20)	AK091904	536.2	613.9	0.03575	1.512			
EHBP1	EH domain binding protein 1(EHBP1)	NM_015252	117.5	122.8	0.03579	1.258			
SLC25A15	solute carrier family 25 member 15(SLC25A15)	NM_014252	109.6	106	0.03584	0.896			
		XR_038676	106	96.4	0.03588	0.887			
ZNF568	zinc finger protein 568(ZNF568)	NM_198539	101.6	101.2	0.03606	1.096			
ZNF568	zinc finger protein 568(ZNF568)	NM_198539	111.7	108.7	0.03606	1.096			
MAP3K3	mitogen-activated protein kinase kinase kinase 3(MAP3K3)	NM_203351	119.5	116.9	0.03609	1.197	NM_012778	744.78	0.71
PTPRA	protein tyrosine phosphatase, receptor type A(PTPRA)	NM_080840	157.4	134.9	0.03609	0.854	NM_012778	744.78	0.71
PTPRA	protein tyrosine phosphatase, receptor type A(PTPRA)	NM_080840	192.4	178.3	0.03609	0.854	NM_012778	744.78	0.71

		XM_374200	104	99.2	0.0361	1.1			
MPG	N-methylpurine DNA glycosylase(MPG)	NM_001015052	101.8	103.6	0.03621	1.109			
BBS2	Bardet-Biedl syndrome 2(BBS2)	NM_031885	124.6	112.4	0.03625	0.855	NM_012909	6.73	5427.66
		NM_001001700	99.8	101	0.03631	1.126	NM_022181	0.40	160.77
		NM_001001700	141.1	129.8	0.03631	1.126	NM_019157	14.48	0.05
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1(ENTPD1)	NM_001098175	178.6	209.8	0.03637	1.235			
C1orf168	chromosome 1 open reading frame 168(C1orf168)	NM_001004303	90.7	94.6	0.03637	1.191			
YY1	YY1 transcription factor(YY1)	NM_003403	282.3	279	0.03642	1.407			
YY1	YY1 transcription factor(YY1)	NM_003403	1066.2	1084	0.03642	1.407			
PREB	prolactin regulatory element binding(PREB)	NM_013388	138.7	150.5	0.03647	1.191			
		BX093763	102.8	95.7	0.03651	0.87			
		XM_001134421	104.6	104.5	0.03658	1.123			
MATR3	matrin 3(MATR3)	NM_199189	91.5	98.5	0.03663	1.115			
MATR3	matrin 3(MATR3)	NM_199189	107.2	96.5	0.03663	1.115			

MATR3	matrin 3(MATR3)	NM_199189	2099.5	1825.7	0.03663	1.115
CAPRIN1	cell cycle associated protein 1(CAPRIN1)	NM_005898	244.2	279.2	0.03664	0.718
aire	autoimmune regulator(AIRE)	NM_000658	95.7	99.7	0.03665	1.116
SMG6	SMG6, nonsense mediated mRNA decay factor(SMG6)	NM_017575	104.3	95.8	0.03668	0.846
KMT2C	lysine methyltransferase 2C(KMT2C)	NM_170606	111.9	101.8	0.03671	0.792
KMT2E	lysine methyltransferase 2E(KMT2E)	NM_018682	147.2	122	0.03671	0.792
GALT	galactose-1-phosphate uridylyltransferase(GALT)	NM_000155	111	102.9	0.03675	1.239
GAMT	guanidinoacetate N-methyltransferase(GAMT)	NM_000156	154	156.5	0.03675	1.239
AGBL5	ATP/GTP binding protein like 5(AGBL5)	NM_021831	109.3	97.6	0.03679	0.846
		BG216851	93.7	103.7	0.03681	1.164
		XM_933468	113.2	108.8	0.03689	1.105
HSF1	heat shock transcription factor 1(HSF1)	NM_005526	98.4	99.2	0.03691	1.128
FBXO48	F-box protein 48(FBXO48)	NM_001024680	103.6	105.1	0.03699	1.099

IFNA21	interferon alpha 21(IFNA21)	NM_002175	107.8	106.8	0.03715	0.875			
CAPS	calcyphosine(CAPS)	NM_004058	252.4	186.3	0.03722	0.833			
MED16	mediator complex subunit 16(MED16)	NM_005481	111.1	98.2	0.03728	1.192			
MED16	mediator complex subunit 16(MED16)	NM_005481	116.1	113.6	0.03728	1.192	NM_019168	8.26	61.49
PCBP2	poly(rC) binding protein 2(PCBP2)	NM_005016	2165.2	1520.7	0.03738	1.259			
SLC2A4RG	SLC2A4 regulator(SLC2A4RG)	NM_020062	150.6	159.9	0.03738	1.339			
		BF054947	99.1	94.1	0.03741	0.92			
		XR_037442	90	102	0.03752	1.168			
BEND3	BEN domain containing 3(BEND3)	NM_001080450	120.3	115.2	0.03753	1.102			
RUNX1T1	RUNX1 translocation partner 1(RUNX1T1)	NM_175636	95.3	99.8	0.03756	1.147			
RBM45	RNA binding motif protein 45(RBM45)	NM_152945	147.4	118.1	0.03758	0.822			
		DA804594	98.1	101.9	0.03767	1.112			
		XR_016054	156.9	180.8	0.03771	1.317			
CEP41	centrosomal protein 41(CEP41)	NM_018718	199.8	178.6	0.03777	1.191			
bag4	BCL2 associated athanogene 4(BAG4)	NM_004874	108.8	101.8	0.0378	1.117			
		AW975165	107.5	101.8	0.03783	1.119			

SLC22A7	solute carrier family 22 member 7(SLC22A7)	NM_153320	104.6	103	0.03789	1.119
SLC22A7	solute carrier family 22 member 7(SLC22A7)	NM_153320	350.2	461.9	0.03789	1.119
		XM_001716323	97	96.5	0.03792	0.872
		XM_001713618	119.8	134.3	0.03797	1.2
MARS	methionyl-tRNA synthetase(MARS)	NM_004990	96.4	98.5	0.03802	1.079
		BX098816	94.2	101.4	0.03807	1.113
CLCN1	chloride voltage-gated channel 1(CLCN1)	NM_000083	95.9	90.6	0.03813	0.908
C4orf3	chromosome 4 open reading frame 3(C4orf3)	NM_001001701	109.9	97.7	0.03819	0.716
C4orf32	chromosome 4 open reading frame 32(C4orf32)	NM_152400	182.1	169.5	0.03819	0.716
SCN7A	sodium voltage-gated channel alpha subunit 7(SCN7A)	NM_002976	127.2	117.9	0.03821	1.18
		XM_943579	104.4	92.2	0.03823	0.876
CTBP2	C-terminal binding protein 2(CTBP2)	NM_001329	137.8	117.4	0.03851	0.834
STX6	syntaxin 6(STX6)	NM_005819	171.4	158	0.03852	0.78
		XR_041454	100.6	101.4	0.03854	1.093

LRIF1	ligand dependent nuclear receptor interacting factor 1(LRIF1)	NM_018372	95.7	102.2	0.03856	1.112
RAB5C	RAB5C, member RAS oncogene family(RAB5C)	NM_201434	267.6	255.4	0.03861	1.26
		AV700714	130	115.3	0.03868	0.803
ABCC10	ATP binding cassette subfamily C member 10(ABCC10)	NM_033450	102.1	97.2	0.0387	0.877
TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)(TIMM17B)	NM_005834	181.2	193.7	0.03872	1.155
		XM_941677	99.8	104.6	0.03872	1.116
SHB	SH2 domain containing adaptor protein B(SHB)	NM_003028	125	132.2	0.03877	1.152
		XM_371901	96.9	94.7	0.03881	1.155
RACK1	receptor for activated C kinase 1(RACK1)	NM_006098	1944.8	1544.5	0.03882	1.319
CCDC122	coiled-coil domain containing 122(CCDC122)	NM_144974	112.6	119.8	0.039	1.183
GALNT16	polypeptide N-acetylgalactosaminyltransferase 16(GALNT16)	NM_020692	100.9	107	0.03902	1.171
FGF23	fibroblast growth factor 23(FGF23)	NM_020638	97.4	100.3	0.03903	1.145

PRNP	prion protein(PRNP)	NM_183079	94.5	99.9	0.03906	1.176
		XM_001726007	101.7	104.1	0.03917	1.142
DCP1A	decapping mRNA 1A(DCP1A)	NM_018403	442.3	405.3	0.03928	0.442
VPS28	VPS28, ESCRT-I subunit(VPS28)	NM_016208	257.1	224.2	0.03936	0.62
VPS28	VPS28, ESCRT-I subunit(VPS28)	NM_016208	445.5	357.9	0.03936	0.62
LAMTOR5	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5(LAMTOR5)	NM_006402	145.5	180.3	0.0395	1.251
DAZ4	deleted in azoospermia 4(DAZ4)	NM_020420	100.4	98.9	0.03952	0.903
ZNF626	zinc finger protein 626(ZNF626)	NM_001076675	105.2	101.2	0.03953	0.674
ZNF626	zinc finger protein 626(ZNF626)	NM_001076675	121.9	106.3	0.03953	0.674
EDF1	endothelial differentiation related factor 1(EDF1)	NM_003792	122.9	109.2	0.03956	0.661
		XM_930172	95	100.7	0.03963	1.136
		XM_937832	111	109.6	0.03963	1.13
SFXN3	sideroflexin 3(SFXN3)	NM_030971	113.2	115	0.03979	1.162

		XR_016984	90	85.9	0.03983	0.859			
AFTPH	aftiphilin(AFTPH)	NM_203437	105.4	106.4	0.03984	1.158			
AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1(AGAP1)	NM_014914	170.7	166.5	0.03984	1.158			
TRIM66	tripartite motif containing 66(TRIM66)	NM_014818	111.5	115.9	0.03989	1.121	NM_001106061	2.22	12.22
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	NM_181676	94.3	90	0.03992	0.841			
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	NM_181676	138.9	174.6	0.03992	0.841			
CCNL2	cyclin L2(CCNL2)	NM_030937	94.3	94.2	0.03993	1.207			
CCNO	cyclin O(CCNO)	NM_021147	148.9	146.1	0.03993	1.207			
		XM_001133393	99.7	91.2	0.03994	0.91			
		XM_001133393	136.5	124.6	0.03994	0.91			
GYS1	glycogen synthase 1(GYS1)	NM_002103	107	110	0.03994	1.226			
TRDMT1	tRNA aspartic acid methyltransferase 1(TRDMT1)	NM_176083	98.6	105.1	0.03995	1.126			

JPH4	junctophilin 4(JPH4)	NM_032452	123.1	111.4	0.03998	0.816
		XM_001713829	97.8	90.1	0.04012	0.863
LOC606724	coronin 1A pseudogene(LOC606724)	NR_002454	4102.1	2649.8	0.04015	0.694
		XM_929612	102.5	108	0.0402	1.135
		XM_927238	112	119.4	0.04032	1.122
CCT7	chaperonin containing TCP1 subunit 7(CCT7)	NM_001009570	99.2	98.7	0.04038	1.125
ICA1L	islet cell autoantigen 1 like(ICA1L)	NM_178231	98.2	100.6	0.04056	1.109
		AA704464	105	107.4	0.04058	1.163
		NM_001018158	116.3	120	0.04059	1.188
		XM_940033	97.7	100.7	0.04069	1.146
HNRNPDL	heterogeneous nuclear ribonucleoprotein D like(HNRNPDL)	NM_031372	1754	1190.2	0.0407	0.741
		XM_936861	104.2	102.6	0.04073	1.157
TMEM179B	transmembrane protein 179B(TMEM179B)	NM_199337	148.7	141.3	0.04075	1.215
TMEM179B	transmembrane protein 179B(TMEM179B)	NM_199337	371.3	310.8	0.04075	1.215
		XM_001715568	122.7	117.8	0.0408	1.106

RUNDC1	RUN domain containing 1(RUNDC1)	NM_173079	94.9	94.6	0.04083	0.851
		XM_0011128220	109.4	105.1	0.04087	1.095
CLDN14	claudin 14(CLDN14)	NM_012130	116.2	161.5	0.04089	0.554
		XR_018553	92.2	85.8	0.04089	0.842
		XR_018553	3382.9	2599.9	0.04089	0.842
SUMF1	sulfatase modifying factor 1(SUMF1)	NM_182760	184.7	201.5	0.04092	1.158
		XM_937666	98.6	96.9	0.04102	1.169
dguok	deoxyguanosine kinase(DGUOK)	NM_080916	93.7	98.1	0.04107	1.136
MPPE1	metallophosphoesterase 1(MPPE1)	NM_023075	194.9	191.8	0.04114	1.229
TAZ	tafazzin(TAZ)	NM_181312	130.4	114	0.04118	0.858
		XM_0017322883	99	104.1	0.04121	1.128
		XM_0011266665	104.3	104.4	0.04127	1.116
		AA909564	103.4	111.6	0.0414	1.19
osbpl6	oxysterol binding protein like 6(OSBPL6)	NM_032523	91.8	90.1	0.04142	1.222
osbpl6	oxysterol binding protein like 6(OSBPL6)	NM_032523	118.5	118.8	0.04142	1.222

PSMC6	proteasome 26S subunit, ATPase 6(PSMC6)	NM_002806	98.3	99.4	0.04143	1.24
PSMC6	proteasome 26S subunit, ATPase 6(PSMC6)	NM_002806	467.8	505.9	0.04143	1.24
HSD17B7	hydroxysteroid 17-beta dehydrogenase 7(HSD17B7)	NM_016371	88.7	96.3	0.04145	1.177
INPP5K	inositol polyphosphate-5-phosphatase K(INPP5K)	NM_130766	104	98.5	0.04166	0.914
INPPL1	inositol polyphosphate phosphatase like 1(INPPL1)	NM_001567	128.2	112.2	0.04166	0.914
HRG	histidine rich glycoprotein(HRG)	NM_000412	92.7	95.2	0.04169	1.117
		XM_941665	301.3	348.4	0.04175	0.695
GUSBP2	glucuronidase, beta pseudogene 2(GUSBP2)	NR_003504	96.1	106	0.04179	1.119
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2(CSGALNACT2)	NM_018590	86.5	94.4	0.04187	1.146
NMD3	NMD3 ribosome export adaptor(NMD3)	NM_015938	98.9	95.9	0.04188	0.874

SLC29A1	solute carrier family 29 member 1 (Augustine blood group)(SLC29A1)	NM_001078174	112.4	100	0.04192	0.854
SLC29A1	solute carrier family 29 member 1 (Augustine blood group)(SLC29A1)	NM_001078174	145.7	134.3	0.04192	0.854
LMBRD1	LMBR1 domain containing 1(LMBRD1)	NM_018368	118.5	119.1	0.04193	1.242
		XR_041507	95.3	106.8	0.04197	1.132
LHX6	LIM homeobox 6(LHX6)	NM_199160	90.8	86.1	0.04201	0.903
GINM1	glycoprotein integral membrane 1(GINM1)	NM_138785	122.3	102.7	0.04206	0.838
GIN1	gypsy retrotransposon integrase 1(GIN1)	NM_017676	101.3	100.6	0.04206	0.838
WDR83	WD repeat domain 83(WDR83)	NM_032332	123.2	113	0.04207	1.161
COL4A5	collagen type IV alpha 5 chain(COL4A5)	NM_000495	411.5	346.3	0.0421	1.547
COL4A3BP	collagen type IV alpha 3 binding protein(COL4A3BP)	NM_005713	127.5	110.4	0.0421	1.547
APOBEC3H	apolipoprotein B mRNA editing enzyme catalytic subunit 3H(APOBEC3H)	NM_181773	83.4	86.7	0.04211	0.859

UGGT1	UDP-glucose glycoprotein glucosyltransferase 1(UGGT1)	NM_020120	151.8	128.8	0.04211	1.303			
TAOK1	TAO kinase 1(TAOK1)	NM_020791	114	104.4	0.04226	1.121			
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3(HIVEP3)	BC080552	86.7	97	0.04229	1.182			
BCKDHB	branched chain keto acid dehydrogenase E1 subunit beta(BCKDHB)	NM_000056	134.2	153.7	0.04231	1.319	NM_001014273	3.32	15.01
BCKDHB	branched chain keto acid dehydrogenase E1 subunit beta(BCKDHB)	NM_183050	196	178.6	0.04231	1.319	NM_001014273	3.32	15.01
GRIA3	glutamate ionotropic receptor AMPA type subunit 3(GRIA3)	NM_007325	168.1	159.5	0.04234	1.452	NM_001014273	3.32	15.01
HSD17B12	hydroxysteroid 17-beta dehydrogenase 12(HSD17B12)	NM_016142	102	99.8	0.04238	0.899	NM_001014273	3.32	15.01
HSD17B13	hydroxysteroid 17-beta dehydrogenase 13(HSD17B13)	NM_178135	508.7	618.2	0.04238	0.899			
ZNF17	zinc finger protein 17(ZNF17)	NM_006959	103.4	94.5	0.04251	0.914			
RCCD1	RCC1 domain containing 1(RCCD1)	NM_033544	92.8	101.2	0.04252	1.135			
MYO18A	myosin XVIIIA(MYO18A)	NM_078471	162.4	161.7	0.04255	1.205			

LPCAT3	lysophosphatidylcholine acyltransferase 3(LPCAT3)	NM_005768	175.9	178.8	0.04258	1.344
jund	JunD proto-oncogene, AP-1 transcription factor subunit(JUND)	NM_005354	401	464.7	0.04266	0.375
ZNF621	zinc finger protein 621(ZNF621)	NM_001098414	116.4	117.1	0.04272	1.186
SGK3	serum/glucocorticoid regulated kinase family member 3(SGK3)	NM_170709	125.1	115.9	0.04284	1.314
SBSPON	somatomedin B and thrombospondin type 1 domain containing(SBSPON)	NM_153225	104.3	120.9	0.04286	1.18
RAD17	RAD17 checkpoint clamp loader component(RAD17)	NM_133340	138.7	125.1	0.04293	0.876
RAD17	RAD17 checkpoint clamp loader component(RAD17)	NM_133340	153.6	129.1	0.04293	0.876
SLC4A1	solute carrier family 4 member 1 (Diego blood group)(SLC4A1)	NM_000342	138.3	212.5	0.04306	1.716
		XR_016385	102.5	103.5	0.0431	0.612
		XM_926345	97	102.8	0.04316	1.121
		XM_496783	97.3	85.6	0.0432	0.597

CEPT1	choline/ethanolamine phosphotransferase 1(CEPT1)	NM_006090	114.9	117.1	0.04325	1.127
		XM_930777	126.2	108.9	0.04327	1.189
ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)(ENTPD6)	NM_001247	90.4	87.2	0.04337	1.117
ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7(ENTPD7)	NM_020354	100.4	101.5	0.04337	1.117
		XM_937442	119.2	128	0.04341	1.186
		XM_929297	103.1	101.2	0.04344	0.914
		AW135045	118.2	118.4	0.0435	1.096
VWA8	von Willebrand factor A domain containing 8(VWA8)	NM_015058	97.9	93.1	0.04351	0.874
NAIF1	nuclear apoptosis inducing factor 1(NAIF1)	NM_197956	105.6	107.1	0.04358	1.143
NAIF1	nuclear apoptosis inducing factor 1(NAIF1)	NM_197956	132.5	121.1	0.04358	1.143

WHAMM	WAS protein homolog associated with actin, golgi membranes and microtubules(WHAMM)	NM_001080435	145.8	127	0.0436	1.198
MAGEE1	MAGE family member E1(MAGEE1)	NM_020932	98.4	93.2	0.04365	0.889
MAGEF1	MAGE family member F1(MAGEF1)	NM_022149	108.8	104.2	0.04365	0.889
		XM_928267	103.8	109.4	0.04378	1.162
C11orf58	chromosome 11 open reading frame 58(C11orf58)	NM_001142705	142.5	149.8	0.04381	1.168
		AW082312	95.9	100.1	0.04392	1.109
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	96	95.8	0.04398	0.922
MSMO1	methylsterol monooxygenase 1(MSMO1)	NM_001017369	160.9	160.5	0.04398	0.922
YARS	tyrosyl-tRNA synthetase(YARS)	NM_003680	118.4	121.9	0.04401	1.132
KIAA0368	KIAA0368(KIAA0368)	NM_001080398	88.2	95.4	0.04438	1.149
		XM_001128895	111.7	109.7	0.04444	1.163
CLYBL	citrate lyase beta like(CLYBL)	NM_206808	106.2	108.2	0.04467	1.17
		XR_040448	93.4	84	0.04468	0.868

CNNM3	cyclin and CBS domain divalent metal cation transport mediator 3(CNNM3)	NM_017623	98.8	100.8	0.0447	1.101
STK40	serine/threonine kinase 40(STK40)	NM_032017	90.8	87.6	0.04476	1.385
STK40	serine/threonine kinase 40(STK40)	NM_032017	274	233.2	0.04476	1.385
		XM_211040	100.9	95.8	0.04476	0.887
SFTPA1	surfactant protein A1(SFTPA1)	NM_005411	86.4	94.9	0.04479	1.342
SOX4	SRY-box 4(SOX4)	NM_003107	180.4	215.5	0.04487	0.608
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	156.6	150.5	0.04489	1.18
MBTPS1	membrane bound transcription factor peptidase, site 1(MBTPS1)	NM_003791	195.8	179.5	0.04489	1.18
		XM_931458	97.7	95.7	0.04495	1.154
		XM_927506	90.8	94.8	0.045	1.16
NUTF2	nuclear transport factor 2(NUTF2)	NM_005796	137.9	126.8	0.04505	1.22
ERGIC3	ERGIC and golgi 3(ERGIC3)	NM_198398	196.6	157	0.04506	1.257

CPT1A	carnitine palmitoyltransferase 1A(CPT1A)	NM_001031847	94.2	85.4	0.04518	0.881
PEX7	peroxisomal biogenesis factor 7(PEX7)	NM_000288	201.8	164	0.04519	0.822
CTNNB1	catenin beta 1(CTNNB1)	NM_001098209	96.5	96.4	0.0452	0.697
CTNNB1	catenin beta 1(CTNNB1)	NM_001098209	148.2	145.9	0.0452	0.697
CTNNB1	catenin beta 1(CTNNB1)	NM_001098209	154	164.5	0.0452	0.697
		XR_039466	96.4	98.5	0.04521	1.169
MKRN2	makorin ring finger protein 2(MKRN2)	NM_014160	223.4	182.1	0.04524	0.778
RP1L1	retinitis pigmentosa 1 like 1(RP1L1)	NM_178857	97.9	91.9	0.04545	0.873
		XR_039516	92.6	93.2	0.04545	1.264
		XR_039516	188.3	171.5	0.04545	1.264
KCNJ15	potassium voltage-gated channel subfamily J member 15(KCNJ15)	NM_170736	99.7	90.2	0.04551	0.91
		XM_931506	101	97.5	0.04557	0.91
		CN283269	110.1	101.8	0.04559	0.921

MAPK3	mitogen-activated protein kinase 3(MAPK3)	NM_001040056	96.9	91.8	0.04562	0.908
TCL1B	T-cell leukemia/lymphoma 1B(TCL1B)	NM_004918	138.6	108.5	0.04562	1.148
THG1L	tRNA-histidine guanylyltransferase 1 like(THG1L)	NM_017872	103.1	99.4	0.04565	1.105
TPPP3	tubulin polymerization promoting protein family member 3(TPPP3)	NM_015964	98.7	89.8	0.04577	0.89
ANKRD33	ankyrin repeat domain 33(ANKRD33)	NM_182608	99	97.6	0.04587	0.781
MOB4	MOB family member 4, phocein(MOB4)	NM_001100819	105.6	104	0.04595	0.825
WASF3	WAS protein family member 3(WASF3)	NM_006646	108.2	124.8	0.04602	1.202
CTDSP1	CTD small phosphatase 1(CTDSP1)	NM_021198	90.5	93.2	0.04617	1.257
CTDSP2	CTD small phosphatase 2(CTDSP2)	NM_005730	287.9	256.9	0.04617	1.257
SLAMF6	SLAM family member 6(SLAMF6)	NM_052931	92.5	86.7	0.0462	0.841
SLAMF6	SLAM family member 6(SLAMF6)	NM_052931	120.4	96.9	0.0462	0.841
tcf20	transcription factor 20(TCF20)	NM_181492	101	100.8	0.04623	1.105

tcf20	transcription factor 20(TCF20)	NM_181492	304.4	258.7	0.04623	1.105
		BM679134	114.5	109	0.04623	1.144
TNFRSF11B	TNF receptor superfamily member 11b(TNFRSF11B)	NM_002546	176.2	176	0.04628	0.539
CHST4	carbohydrate sulfotransferase 4(CHST4)	NM_005769	95.6	92.2	0.04639	0.895
FAM162B	family with sequence similarity 162 member B(FAM162B)	NM_001085480	100.7	98.7	0.04639	1.108
STK25	serine/threonine kinase 25(STK25)	NM_006374	350.5	355.1	0.04641	1.298
		XM_926412	101	101	0.04651	1.127
		XM_001722392	100.1	91.8	0.04656	0.881
RASGRP4	RAS guanyl releasing protein 4(RASGRP4)	NM_052949	108.4	114.6	0.04659	1.118
BCKDHB	branched chain keto acid dehydrogenase E1 subunit beta(BCKDHB)	NM_000056	421.2	517.8	0.04661	1.682
PRDM15	PR/SET domain 15(PRDM15)	NM_001040424	98	90.2	0.04662	0.923
ZNF446	zinc finger protein 446(ZNF446)	NM_017908	159.2	134.1	0.04674	0.828
ZFP36L1	ZFP36 ring finger protein like 1(ZFP36L1)	NM_004926	943	789.9	0.04683	0.684

KIF2C	kinesin family member 2C(KIF2C)	NM_006845	104.9	104.8	0.04683	1.123
		XM_926130	141.1	123	0.04685	1.313
		BQ772469	115.1	95.4	0.04688	0.892
MED11	mediator complex subunit 11(MED11)	NM_001001683	92	100.3	0.04699	1.105
TMEM150B	transmembrane protein 150B(TMEM150B)	NM_001085488	108.7	112.9	0.04724	1.115
DENND2C	DENN domain containing 2C(DENND2C)	NM_198459	218.2	181.2	0.04726	1.251
MAMSTR	MEF2 activating motif and SAP domain containing transcriptional regulator(MAMSTR)	NM_182574	116.7	109.4	0.04729	0.833
		XR_015259	98.8	93.5	0.04738	0.697
		XR_017249	93.3	88.2	0.04739	0.829
		XM_930508	91.3	84	0.0474	0.773
MKNK2	MAP kinase interacting serine/threonine kinase 2(MKNK2)	NM_017572	579.1	427.2	0.04743	1.568
PBRM1	polybromo 1(PBRM1)	NM_181042	103.3	101	0.0475	0.877
PBRM1	polybromo 1(PBRM1)	NM_181042	113.7	94.4	0.0475	0.877

c21orf33	chromosome 21 open reading frame 33(C21orf33)	NM_004649	101.2	96.3	0.04761	0.886			
GHSR	growth hormone secretagogue receptor(GHSR)	NM_198407	92.6	97.5	0.04761	1.14			
		XM_001721744	122	128	0.04761	1.226	NM_145089	67.02	12.33
KLHL9	kelch like family member 9(KLHL9)	NM_018847	115.2	103	0.04767	1.121			
QKI	QKI, KH domain containing RNA binding(QKI)	NM_006775	98.2	93	0.04774	0.895	NM_013157	76.74	0.47
QKI	QKI, KH domain containing RNA binding(QKI)	NM_006775	102.4	106.3	0.04774	0.895	NM_013157	76.74	0.47
		XR_016047	102.3	97	0.04774	1.138	NM_013157	76.74	0.47
TRAPPC3	trafficking protein particle complex 3(TRAPPC3)	NM_014408	349	308.8	0.04783	1.167	NM_013157	76.74	0.47
IGFBP2	insulin like growth factor binding protein 2(IGFBP2)	NM_000597	88.8	101.1	0.04793	1.21			
COL18A1	collagen type XVIII alpha 1 chain(COL18A1)	NM_130445	233.3	218	0.04794	0.769			
		XM_925903	100.7	98.2	0.04795	0.875			
		XM_925903	103.1	90.2	0.04795	0.875			

LYNX1	Ly6/neurotoxin 1(LYNX1)	NM_177458	100.8	90.1	0.04813	0.905
ZC3H18-AS1	ZC3H18 antisense RNA 1 (head to head)(ZC3H18-AS1)	NM_001001682	101.8	94.3	0.04814	0.915
REV3L	REV3 like, DNA directed polymerase zeta catalytic subunit(REV3L)	NM_002912	100.2	94.6	0.04817	0.836
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)	NM_001040092	116	107.4	0.04824	1.141
		BQ771772	108.4	106.7	0.04828	1.121
		XR_039891	101.8	99.2	0.04833	1.078
ZNF80	zinc finger protein 80(ZNF80)	NM_007136	100.9	102.2	0.04834	1.112
EFEMP1	EGF containing fibulin like extracellular matrix protein 1(EFEMP1)	NM_001039348	98.8	108	0.0484	1.098
MPHOSPH6	M-phase phosphoprotein 6(MPHOSPH6)	NM_005792	120.3	140.9	0.04844	1.132
ZADH2	zinc binding alcohol dehydrogenase domain containing 2(ZADH2)	NM_175907	98.7	100.6	0.0485	1.095
RTN4RL1	reticulon 4 receptor like 1(RTN4RL1)	NM_178568	103.9	105	0.04862	1.097

SHANK2	SH3 and multiple ankyrin repeat domains 2(SHANK2)	NM_012309	165.9	212.4	0.04863	1.469
		XM_001726649	108.3	101.4	0.04868	0.858
		XR_015716	99.9	95.9	0.04877	0.869
AASDH	aminoadipate-semialdehyde dehydrogenase(AASDH)	NM_181806	148.8	131.2	0.04877	0.839
SNX22	sorting nexin 22(SNX22)	NM_024798	101.7	97.9	0.0488	0.83
C4BPA	complement component 4 binding protein alpha(C4BPA)	NM_000715	109.4	102.1	0.04887	0.887
RAD21	RAD21 cohesin complex component(RAD21)	NM_006265	296.7	266.7	0.0489	1.333
RAD21	RAD21 cohesin complex component(RAD21)	NM_006265	498	390.6	0.0489	1.333
OPN5	opsin 5(OPN5)	NM_001030051	120.6	108.4	0.04901	0.804
lsm11	LSM11, U7 small nuclear RNA associated(LSM11)	NM_173491	371	312.1	0.04901	1.17
		XR_041956	110.6	102.5	0.04909	0.852

COX16	COX16, cytochrome c oxidase assembly homolog(COX16)	NM_016468	110	105.3	0.04912	1.149
Cox15	COX15, cytochrome c oxidase assembly homolog(COX15)	NM_078470	100.1	103.9	0.04912	1.149
FRMD1	FERM domain containing 1(FRMD1)	NM_024919	109.2	100.4	0.04917	0.917
		XM_001725183	3889.8	2672	0.0492	0.763
LOC100996549	uncharacterized LOC100996549(LOC100996549)	AK094576	96.1	101.7	0.04925	1.137
SIGLEC7	sialic acid binding Ig like lectin 7(SIGLEC7)	NM_016543	98	96	0.04931	0.896
scaf8	SR-related CTD associated factor 8(SCAF8)	NM_014892	143.9	129.2	0.04939	0.805
		XM_925876	100.2	105.2	0.0494	1.148
KPNA3	karyopherin subunit alpha 3(KPNA3)	NM_002267	104.1	104.5	0.04953	0.871
YPEL2	yippee like 2(YPEL2)	NM_001005404	114.5	106.3	0.04958	0.869
C9orf72	chromosome 9 open reading frame 72(C9orf72)	NM_018325	135.7	142	0.0496	0.848
HERC2	HECT and RLD domain containing E3 ubiquitin protein ligase 2(HERC2)	NM_004667	110.6	108.6	0.0496	1.167

		XM_932019	98	107.3	0.04961	1.114			
		XM_941746	94.7	95.7	0.04968	0.846			
c16orf87	chromosome 16 open reading frame 87(C16orf87)	NM_001001436	226.8	267.9	0.04969	1.162			
CELSR1	cadherin EGF LAG seven-pass G-type receptor 1(CELSR1)	NM_014246	102.5	91.4	0.0497	0.86	NM_134394	3.46	15.03
ZNF607	zinc finger protein 607(ZNF607)	NM_032689	92.3	99.2	0.04971	1.094			
ZNF607	zinc finger protein 607(ZNF607)	NM_032689	107	98.8	0.04971	1.094			
CPE	carboxypeptidase E(CPE)	NM_001873	89.4	95.9	0.04971	1.137			
XRN1	5'-3' exoribonuclease 1(XRN1)	NM_001042604	120.6	103.6	0.04978	0.872			
KIAA0907	KIAA0907(KIAA0907)	NM_014949	98.4	89.4	0.0499	0.845			
		XM_931879	206.4	152.3	0.04994	0.525			
rab11fip5	RAB11 family interacting protein 5(RAB11FIP5)	NM_015470	506.4	534.8	0.04995	1.322			
PKNOX1	PBX/knotted 1 homeobox 1(PKNOX1)	NM_004571	91.9	86.3	0.04996	0.908			
PKNOX1	PBX/knotted 1 homeobox 1(PKNOX1)	NM_004571	136.7	127.3	0.04996	0.908			

OR2W3	olfactory receptor family 2 subfamily W member 3(OR2W3)	NM_001001957	108.8	92.8	0.04997	0.871
		NM_001004349	103.2	106.6	0.04999	1.142
RAB3A	RAB3A, member RAS oncogene family(RAB3A)	NM_002866	93.3	99.9	0.04999	1.127