Clone Id	Gene Name	Description	Refseq	GeneID	HDMVEC_6h	HDMVEC_6h	HDMVEC_12h	HDMVEC_12h	HDMVEC_12h	HDMVEC_12h	Fibro_6h	Fibro_6h	Fibro_12h	Fibro_12h	Fibro_12h	Fibro_12h	U87_6h	U87_6h	U87_12h	U87_12h	U87_12h	U87_12h
IMAGp998C10644	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA	NM_005845	10257	-0.81	-0.17	-0.46	-0.16	-0.08	-0.46	0.01	-0.22	-0.3	-0.6	-0.24	-0.02	0	0.32	0.52	0.22	1.3	0.38
IMAGp998E14213	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3 (ABCD3), mRNA	NM_002858	5825	-0.74	-0.38	-0.53	-0.51	-0.33	-1.48	0.11	0	-0.11	-0.25	0.3	-0.14	-0.32	-0.18	0.61	0.56	1.2	1.23
IMAGp998H08121	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1 (ABCE1), mRNA	NM_002940	6059	-0.66	-0.46	-0.86	-0.26	-0.49	-0.98	-0.28	0.4	-0.49	0.05	0.48	-0.2	0.14	-0.39	1.28	1.43	0	1.66
IMAGp998L12229	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), nuclear gene encoding mit	NM_007189	10061	-0.73	-0.09	-0.89	-0.18	-0.26	-1.15	-0.14	-0.19	-0.29	-0.29	-0.5	-0.41	0.01	-0.15	0.59	0.66	0.3	0.45
IMAGp998C06652	ACAT2	Acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase) (ACAT2), mRNA	NM_005891	39	-0.52	-0.67	-1.29	-0.97	-0.3	-0.97	0.09	0.31	-0.04	-0.25	0.25	0.11	-0.06	0.04	0.51	0.11	0.4	-0.53
IMAGp998D201785	ACR	Acrosin (ACR), mRNA	NM_001097		-0.39	-0.26	-0.31	-0.57	-0.5	0.04	0.34	-0.14	-0.24	-0.04	-0.22	0.63	-0.01	0.25	0.71	0.46	0	0.88
IMAGp998O002119	ACSL3	Acyl-CoA synthetase long-chain family member 3		2181	-0.89	-0.37	-0.46	-0.75	-1.03	-1.2	0.4	0.11	0.12	-0.47	-0.67	-0.03	0.38	0.2	0.92	1.2	0.8	-0.61
IMAGp998P01118	ACTR2	ARP2 actin-related protein 2 homolog (yeast) (ACTR2), mRNA	NM_005722		-0.99	-1.32	-0.97	-1.55	-1.68	-1.26	0.78	0.26	0.14	-0.19	-0.38	0.22	0.39	-0.12	2.59	2.01	2.5	1.89
IMAGp998G22650	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	NM_005721	10096	-0.29	-0.91	-0.24	-0.78	0.23	-1.48	0.27	0.06	-0.21	-0.75	0.56	-0.01	0.13	0.19	1.51	0.84	0.6	1.29
IMAGp998L183971	ACVR2	Activin A receptor, type IIA		92	-1.59	-0.75	-1.3	-0.46	0.27	-1.45	-0.26	0.33	-0.77	-0.25	0.75	0.03	0.02	-0.31	0.37	0.79	0.5	1.39
IMAGp998D18395	ADAM9	A disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA	NM_003816	8754	-0.49	-1.34	-0.27	-1.49	-1.32	-0.45	0.75	0	0.76	0.32	-0.65	0.3	0.14	0.35	1.92	1.29	1.2	1.13
IMAGp998N04617	ADK	Adenosine kinase (ADK), transcript variant ADK-long, mRNA	NM_006721	132	-0.73	-0.26	-1	-0.65	-0.65	-0.38	0.01	-0.03	-0.28	-0.34	-0.63	0.09	0.26	-0.47	0.68	0.75	0.4	0
IMAGp998L21872	ADORA2B	Adenosine A2b receptor (ADORA2B), mRNA	NM_000676	136	-0.67	0	-0.66	-0.46	-1.26	-0.5	-0.5	-0.54	-0.28	-0.55	0.07	0.3	0.05	-0.07	0.52	0.51	0.7	1.16
IMAGp998O132012	AF15Q14	Cancer susceptibility candidate 5		57082	-0.53	-0.36	-0.72	-1.05	-1.47	-1.46	0.63	-0.21	-0.19	-0.23	-0.74	0.11	0.23	-0.22	1.12	1.02	1.3	0.64
IMAGp998P051933	AGL	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycog	NM_000646	178	-0.67	-0.15	-0.38	-0.37	-0.33	-0.71	0.05	0.13	-0.15	-0.24	0.51	0.27	-0.2	0.24	0.59	0.42	0	0.39
IMAGp998C102004	AK3L1	Adenylate kinase 3 like 1 (AK3L1), mRNA	NM_016282	50808	-0.53	-0.62	-0.08	-0.44	-0.17	0.09	0.4	0.12	0.61	0.07	0.25	0.77	0.08	-0.01	1.43	1.01	0.9	1.41

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IMAGp998K041927   AK3L1 Adenylate kinase 3 like 1 (AK3L1), mRNA   NM_016282
      -0.64 -0.31 0.04  -0.67 -0.23 0.05  0.5   -0.06 0.96  0.12  -0.75 0.36
      0.01  0.12  1.3   0.77  1.5   1.15
IMAGp998H24133    ANLN  Anillin, actin binding protein (scraps homolog,
Drosophila) (ANLN), mRNA      NM_018685   54443 -0.72 -0.46 -1.3  -1.25 -1.62 -
1.66  0.36  0.02  -0.65 -0.05 -0.76 0.31  0.54  -0.31 2.57  2.24  1.8   2.07
IMAGp998N201999   ANP32B      Acidic (leucine-rich) nuclear phosphoprotein 32
family, member B              -1.8  -1.35 -2.32 -1.43 -1.37 -0.47 0.05  0.62  -
1.24  -0.75 -1.05 -0.36 0.32  -0.87 1.44  1.85  0.6   1.39
IMAGp998F221829   ANP32E      Acidic (leucine-rich) nuclear phosphoprotein 32
family, member E  NM_030920   81611 -0.63 0.08  -0.64 -0.59 -0.29 -1.23 0.3
      0.34  -0.03 0.01  0.68  0.21  0.47  -0.22 1.18  0.79  0.4   1.67
IMAGp998C10841    ANTXR1      Anthrax toxin receptor 1 (ANTXR1), transcript
variant 1, mRNA   NM_032208   84168 -0.42 -0.51 -0.76 -0.62 -0.31 -0.97 0.02
      0.09  -0.25 -0.13 0.37  0.45  -0.49 0.22  0.46  0.49  0.8   0.69
IMAGp998P03539    ANTXR1      Anthrax toxin receptor 1 (ANTXR1), transcript
variant 1, mRNA   NM_032208   84168 -0.48 -0.24 -0.26 -0.52 -0.73 -1.21 0.2
      0.06  -0.34 -0.11 -0.48 0.19  -0.42 -0.18 0.55  0.53  1.2   0.48
IMAGp998F03826    ANXA1 Annexin A1 (ANXA1), mRNA      NM_000700   301   -0.26 -
0.56  -0.31 -0.56 -0.31 -0.3  0.32  0.03  0.06  -0.29 0.48  0.43  0.3   -0.22
      1.19  1.04  0.6   0.58
IMAGp998I13537    APEX1 APEX nuclease (multifunctional DNA repair enzyme) 1
(APEX1), transcript variant 3, mRNA NM_080649   328   -0.66 -0.63 -0.72 -0.54 -
0.12  -0.06 0.04  0.08  -0.26 -0.32 -0.2  -0.23 0.09  -0.36 1.37  1.38  2
      1.31
IMAGp998J08160    APG5L APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA
      NM_004849   9474  -1.51 -0.2  -1.56 -0.11 -0.81 -0.61 -0.23 -0.02 -0.37 -
0.99  0.06  0.28  0.16  -0.23 1.01  1     0.4   0.66
IMAGp998G221118   API5  Apoptosis inhibitor 5 (API5), mRNA  NM_006595   8539  -
0.64  -0.33 -0.45 -0.79 -0.22 -0.2  0.33  -0.15 0.06  -0.39 -0.11 0.37  0.19
      0.09  1.17  0.84  0.7   1.69
IMAGp998E11601    APPBP1      Amyloid beta precursor protein binding protein 1,
59kDa (APPBP1), mRNA    NM_003905   8883  -0.87 -0.33 -0.79 -0.65 -0.14 -0.31
      0.07  0.2   -0.23 -0.27 -0.17 0.22  -0.15 -0.49 1     1.06  1     0.39
IMAGp998D141925   APPBP2      Amyloid beta precursor protein (cytoplasmic tail)
binding protein 2 (APPBP2), mRNA    NM_006380   10513 -0.33 -0.37 -0.24 -0.35
      0.33  -0.23 0.13  0.09  0.22  0.02  0.44  0.33  0.07  -0.12 0.69  0.58
      0.8   1.08
IMAGp998N21598    ARCN1 Archain 1 (ARCN1), mRNA NM_001655   372   -0.62 -0.61 -
0.7   -0.55 -0.9  -1.06 -0.28 -0.03 -0.39 -0.48 0.15  -0.31 -0.25 0.08  0.92
      0.94  0.8   1.53
IMAGp998O23564    ARFGAP3     ADP-ribosylation factor GTPase activating protein
3 (ARFGAP3), mRNA NM_014570   26286 -0.74 -0.75 -0.38 -0.59 -0.34 -0.98 0.01  -
0.05  0.12  0.22  1.26  0.41  -0.08 -0.02 0.11  0.08  0.1   0.8
IMAGp998J111165   ARFGEF2     ADP-ribosylation factor guanine nucleotide-
exchange factor 2 (brefeldin A-inhibited)       10564 -0.52 -0.75 -0.13 -0.68 -
0.38  -1.06 0.11  -0.16 0.33  -0.37 1.32  0.23  0.07  0.46  1.11  0.37  0.3
      1.29
IMAGp998H20886    ARGBP2      Sorbin and SH3 domain containing 2        8470  -
0.24  -0.88 -0.48 -0.93 -0.16 -0.07 0.3   -0.24 0.05  -0.13 0.05  0.15  -0.08
      0.31  1.01  0.6   0.2   0.33
IMAGp998M16644    ARID1A      AT rich interactive domain 1A (SWI- like)
(ARID1A), transcript variant 2, mRNA      NM_139135   8289  -0.37 -0.43 -0.07 -
0.71  -0.4  -0.1  0.19  -0.41 0.32  -0.13 -0.65 0.24  0.13  -0.05 0.86  0.42
      0.4   1.22
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IMAGp998P1492     ARL1  ADP-ribosylation factor-like 1 (ARL1), mRNA
      NM_001177   400   -0.83 -0.54 -0.88 -0.6  -0.56 -1.65 0.24  0.22  0.25  -
0.17  0.72  0.09  0.27  -0.14 0.71  0.51  0.5   0.9
IMAGp998E04437    ARL6IP2     ADP-ribosylation factor-like 6 interacting protein
2           64225 -0.53 -0.43 -0.67 -0.68 -0.71 -0.31 -0.4  -0.48 -0.66 -0.1  -
1.05  -0.05 0.18  -0.51 0.77  0.86  1.1   1.22
IMAGp998M201924   ARL8  ADP-ribosylation factor-like 8 (ARL8), mRNA
      NM_178815         -0.35 -0.4  -0.36 -0.3  -0.33 -0.55 0.2   0.16  0.27
      0.12  0.87  0.56  0.17  -0.02 1.15  0.85  0.2   1.1
IMAGp998A14375    ARMET Arginine-rich, mutated in early stage tumors (ARMET),
mRNA  NM_006010   7873  -0.66 -0.68 -0.99 -0.77 -0.78 -0.31 0.05  -0.19 -0.54 -
0.93  -0.84 -0.46 0.34  -0.44 1.48  1.25  0.4   0.25
IMAGp998N161907   ARPC5 Actin related protein 2/3 complex, subunit 5, 16kDa
(ARPC5), mRNA     NM_005717         0     -0.72 -0.6  -0.77 0     -0.78 0.45  -
0.31  -0.12 -0.87 0.32  0.14  0.16  0.07  1.48  0.79  0     0.68
IMAGp998O031961   ASK   Activator of S phase kinase (ASK), mRNA   NM_006716
      10926 -1.33 -0.72 -0.9  -1.45 -1.09 -0.01 -0.44 -0.47 -0.36 -0.67 -1.05
      0.29  0.12  -0.26 1.31  1.07  1.4   0.45
IMAGp998O021745   ASK   Activator of S phase kinase (ASK), mRNA   NM_006716
      10926 -1.31 -1.2  -1.54 -1.46 -0.87 -1.52 -0.44 -0.38 -0.79 -0.5  -0.54
      0.57  0.05  -0.4  1.01  1.14  0.6   1.5
IMAGp998A18227    ATP6AP2     ATPase, H+ transporting, lysosomal accessory
protein 2 (ATP6AP2), mRNA     NM_005765   10159 -1.15 0.08  -0.59 -0.16 -1.3  -
1.16  0     0.14  -0.12 0.03  0.16  0.41  -0.12 -0.46 0.96  1.39  1.1   1.46
IMAGp998D12182    ATP6V1A     ATPase, H+ transporting, lysosomal 70kDa, V1
subunit A (ATP6V1A), mRNA     NM_001690   523   -0.39 -0.3  -0.02 -0.62 -0.1  -
0.17  0.36  0.41  0.36  0.01  0.23  0.79  0.18  0.12  1.24  0.6   0.9   0.24
IMAGp998O10594    ATP6V1C1    ATPase, H+ transporting, lysosomal 42kDa, V1
subunit C, isoform 1          528   -0.17 -0.71 0.05  -0.99 -0.41 -0.54 0.88  -
0.43  0.47  -0.3  -0.35 -0.05 0.03  0.47  0.63  -0.01 0.8   0.58
IMAGp998D07421    ATP6V1H     ATPase, H+ transporting, lysosomal 50/57kD V1
subunit H (ATP6V1H), mRNA     NM_015941   51606 -0.66 -0.48 -0.71 -0.57 -0.62 0
      0.01  0.04  -0.07 -0.34 0.14  -0.22 0.08  -0.06 0.85  0.8   0     0.82
IMAGp998L04886    AZI2  5-azacytidine induced 2       64343 -0.67 -0.3  -1.08 -
0.27  -0.98 -0.52 -0.15 0.15  -0.23 -0.07 -0.94 -0.07 -0.2  -0.19 0.32  0.57  1
      0.1
IMAGp998G141155   BASP1 Brain abundant, membrane attached signal protein 1
(BASP1), mRNA     NM_006317         -0.55 -0.27 -0.27 -0.55 -0.6  -0.61 0.33  -
0.34  -0.38 -0.26 0.22  -0.29 0.08  0.05  1.14  0.7   0.3   0.86
IMAGp998F16646    BAZ1B Bromodomain adjacent to zinc finger domain, 1B (BAZ1B),
transcript variant 2, mRNA    NM_032408   9031  -0.73 -0.02 -0.69 -0.17 -0.52 -
0.84  -0.15 0.05  -0.26 -0.46 0.12  -0.22 0.22  -0.04 1.42  1.17  0.1   2.11
IMAGp998G03685    BCAS2 Breast carcinoma amplified sequence 2 (BCAS2), mRNA
      NM_005872   10286 -1.23 -0.32 -1.1  -0.65 -0.66 -0.84 0.04  0.27  -0.16
      0.15  0.71  0.92  0.26  -0.32 1     1.12  0.7   0.87
IMAGp998N24628    BCAT1 Branched chain aminotransferase 1, cytosolic (BCAT1),
mRNA  NM_005504         -0.73 -0.45 -0.68 -0.66 -0.29 -0.99 -0.09 -0.03 -0.31
      0.01  0.19  0.44  -0.09 0.05  0.09  0.24  0.1   1.01
IMAGp998A08613    BCCIP BRCA2 and CDKN1A interacting protein (BCCIP), transcript
variant C, mRNA   NM_078469   56647 -1.29 -0.08 -1.64 -0.63 -1.39 -1.06 0.26
      0.28  -0.45 0.03  -0.45 -0.1  0.19  -0.92 1.79  1.95  1.5   1.93
IMAGp998D24523    BRP44L      Brain protein 44-like (BRP44L), mRNA
      NM_016098         -0.45 0.02  -0.37 -1.18 -0.39 -1    0.26  0.24  0.2
      0.18  0.67  0.09  0.07  -0.19 0.16  0.37  0.5   0.65
IMAGp998K075264   BRWD3 Bromodomain and WD repeat domain containing 3
      254065      -0.57 -0.35 -0.94 -0.4  -0.72 0.08  0.12  0.12  0.34  -0.87 0
      -0.04 0.15  -0.1  0.97  0.93  0.9   0.44
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IMAGp998E161924   BUB1  BUB1 budding uninhibited by benzimidazoles 1 homolog
(yeast) (BUB1), mRNA    NM_004336   699   -0.56 -0.26 -1.59 -1.19 -1.31 -2.32 -
0.01  -0.02 -0.66 -0.59 0.02  0.4   0.27  -0.47 1.64  1.47  1.1   0.84
IMAGp998B01363    BUB3  BUB3 budding uninhibited by benzimidazoles 3 homolog
(yeast) (BUB3), mRNA    NM_004725   9184  -0.51 -0.17 -0.77 -0.37 -0.97 -1.32 -
0.31  0.03  -0.78 -0.31 -0.18 -0.45 -0.02 -0.18 0.9   1.02  1     0.9
IMAGp998H035765   C10orf3     Chromosome 10 open reading frame 3 (C10orf3), mRNA
      NM_018131   55165 -0.11 -0.25 -1.3  0.4   -1.65 -1.52 0.22  0.11  -0.47 -
0.31  -1.09 0     0.11  -0.04 2.05  1.66  1.4   2.42
IMAGp998C093379   C10orf3     Chromosome 10 open reading frame 3 (C10orf3), mRNA
      NM_018131   55165 -0.48 0.09  -1.88 0.54  -1.54 -1.02 0.4   -0.11 -0.53 -
0.48  0.6   -0.02 0.41  -0.17 2.51  1.92  1.1   0.56
IMAGp998O15353    C10orf61    Chromosome 10 open reading frame 61       26123 -
0.14  -0.35 -0.41 -0.15 -0.57 -0.22 -0.11 -0.36 -0.21 -0.2  -0.59 -0.24 0.2   -
0.03  0.27  0.35  0.8   0.94
IMAGp998N23415    C10orf69    Chromosome 10 open reading frame 69 (C10orf69),
mRNA  NM_006459   10613 -0.36 -0.19 -0.8  -0.64 -0.73 -1    0.13  0.03  -0.28 -
0.1   0.27  -0.05 -0.08 0.18  0.82  0.64  0.6   0.62
IMAGp998O081936   C10orf84    hypothetical protein FLJ13188 (FLJ13188), mRNA
      NM_022063   63877 -1.41 -0.17 -1.56 -0.29 -0.7  -1.35 -0.35 0.22  -0.28
      0.12  0.21  0.23  0.05  -0.47 0.27  0.84  0.4   0.55
IMAGp998N151205   C10orf9     Chromosome 10 open reading frame 9        219771
      -0.32 -0.66 -0.22 -0.67 -0.4  -0.49 -0.02 -0.23 -0.18 -0.43 -0.17 -0.32 -
0.23  0.36  0.73  0.41  0.4   1.54
IMAGp998N06152    C12orf22    Chromosome 12 open reading frame 22 (C12orf22),
mRNA  NM_030809   81566 -0.76 0.58  -0.98 -0.68 -1.18 -0.68 -0.28 -0.09 -0.35 -
1.01  0.49  0.62  0.03  -0.03 0.81  0.8   0.9   0.74
IMAGp998O10626    C13orf10    Chromosome 13 open reading frame 10 (C13orf10),
mRNA  NM_022118   64062 -0.43 -0.87 -0.17 -0.63 -0.33 0.26  0.1   -0.06 0.01
      0.38  0.26  0.28  -0.14 0.17  0.74  0.31  0.6   0.89
IMAGp998O09123    C14orf32    Chromosome 14 open reading frame 32 (C14orf32),
mRNA  NM_144578   93487 -0.71 -0.21 -0.6  -0.48 -0.48 -0.94 0.03  0.07  -0.1  -
0.26  0.18  0.34  -0.2  0     0.51  0.58  0     1.14
IMAGp998H02199    C15orf15    Chromosome 15 open reading frame 15 (C15orf15),
mRNA  NM_016304   51187 -1.47 -0.2  -1.32 -0.48 -1.03 -0.78 -0.11 0.32  -0.37
      0.13  -0.28 -0.33 0.03  -0.98 0.78  1.41  0.8   1.08
IMAGp998L01121    C15orf15    Chromosome 15 open reading frame 15 (C15orf15),
mRNA  NM_016304   51187 -0.73 -0.94 -0.33 -0.91 -0.09 -0.51 0.32  -0.14 -0.15 -
0.46  -0.03 0.26  0.23  -0.23 0.11  0.86  1.3   -0.24
IMAGp998F14648    C17orf25    CGI-150 protein (CGI-150), mRNA     NM_016080
      51031 -0.28 -0.74 -0.25 -0.67 -0.46 0.01  0.38  -0.29 0.05  -0.26 -0.59 -
0.09  0.13  0.19  1.33  0.57  -0.1  0.74
IMAGp998M23234    C1orf22     Chromosome 1 open reading frame 22 (C1orf22), mRNA
      NM_025191   80267 -0.36 -0.71 -0.29 -0.6  -0.23 -0.12 0.1   -0.18 -0.31 -
0.15  -0.43 0.21  -0.07 0.14  0.85  0.66  0.3   0.87
IMAGp998H19387    C1orf22     Chromosome 1 open reading frame 22 (C1orf22), mRNA
      NM_025191   80267 -0.35 -0.51 -0.33 -0.75 -0.64 -0.28 0.09  -0.11 -0.43
      0.38  -0.33 0.58  -0.15 0     0.88  0.71  0.1   0.43
IMAGp998E07608    C20orf45    Chromosome 20 open reading frame 45 (C20orf45),
mRNA  NM_016045         -0.62 -0.3  -0.29 -0.45 -0.71 -0.59 0.11  -0.06 -0.26 -
0.03  0.67  0.11  0     -0.09 1.07  0.78  1.2   2.35
IMAGp998L01349    C2orf18     Chromosome 2 open reading frame 18        54978 -
0.82  -0.72 -0.95 -0.56 -0.88 -0.8  -0.18 -0.08 -0.46 -0.09 0.04  -0.36 1.45  -
0.05  -0.24 -0.01 -0.2  -0.03
IMAGp998D13403    C2orf25     hypothetical protein CL25022 (CL25022), mRNA
      NM_015702   27249 -0.83 -0.93 -0.65 -0.9  -0.28 -0.28 -0.02 -0.06 -0.21
      0.07  -0.62 0.2   0.3   -0.35 1.2   1     0.9   0.42
```

```
IMAGp998I11692    C2orf30     XTP3-transactivated protein B (XTP3TPB), mRNA
      NM_015701   27248 -0.54 -0.41 -0.92 -0.99 -0.83 -0.7  0.3   0.3   0.02
      0.05  0.1   0.23  0.01  -0.3  0.96  0.8   1.7   0.48
IMAGp998K02731    C5orf6      Chromosome 5 open reading frame 6 (C5orf6), mRNA
      NM_016605   51307 -0.69 -0.22 -0.39 -0.41 -0.31 -0.22 -0.11 -0.21 -0.05 -
0.01  -0.36 -0.32 -0.09 0.14  0.35  0.15  0.3   -0.25
IMAGp998C15699    C9orf46     Chromosome 9 open reading frame 46 (C9orf46), mRNA
      NM_018465   55848 -0.85 -0.35 -0.57 -0.49 -0.17 -0.52 0.29  0.24  0.27  0
      -0.1  0.36  0.08  -0.33 0.79  0.64  0.5   0.54
IMAGp998O00995    CAB39 MO25 protein (MO25), mRNA     NM_016289         -0.76 -
0.29  -0.97 -0.17 0.33  -0.5  -0.16 0.05  -0.34 -0.14 -0.46 -0.05 0.33  -0.22
      1.16  1.27  1.9   1.23
IMAGp998P10643    CALM2 calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA
      NM_001743   805   -0.06 -0.74 0.08  -1.05 -0.9  -0.66 0.7   -0.21 -0.37 -
0.54  0.06  0     0.55  -0.11 2.25  1.52  1.1   2.12
IMAGp998E14736    CALU  calumenin (CALU), mRNA  NM_001219   813   0.55  -1.17
      0.23  -1.5  -0.43 -0.8  0.89  -0.34 0.58  -0.94 0.69  0.23  0.51  0.36
      2.08  0.97  0.8   1.87
IMAGp998J20727    CAPN7 calpain 7 (CAPN7), mRNA NM_014296   23473 -0.59 -0.46 -
0.68  -0.22 -0.22 -0.54 0.17  0.08  0     0.22  0.07  -0.07 -0.01 -0.19 0.79
      0.69  -0.3  0.77
IMAGp998J02842    CAPN8 Calpain 8 (nCL-2)       10754 -0.24 -0.35 -0.16 -0.56
      0.35  0.18  0.35  0.02  -0.02 0.21  -0.02 0.21  0.31  -0.17 1.19  0.74
      1.1   1.02
IMAGp998L152576   CAPZA1      capping protein (actin filament) muscle Z-line,
alpha 1 (CAPZA1), mRNA  NM_006135   829   -0.35 -0.51 -0.01 -0.52 -0.09 -0.39
      0.39  -0.09 -0.16 0.08  0.1   0.8   0.06  -0.06 1.2   0.47  0.3   1.1
IMAGp998M10971    CAPZB capping protein (actin filament) muscle Z-line, beta
(CAPZB), mRNA     NM_004930   832   -0.59 -0.1  -0.62 -0.11 -0.37 -0.4  -0.2
      0.14  -0.03 -0.09 -0.08 0.39  -0.09 -0.03 0.57  0.57  0.1   0.49
IMAGp998J061903   CART1 cartilage paired-class homeoprotein 1 (CART1), mRNA
      NM_006982         -0.53 -0.34 -0.51 -0.5  0.12  -0.08 0     -0.02 -0.46
      0.2   -0.1  0.21  -0.14 0.14  0.72  0.47  0.5   0.95
IMAGp998B15618    CASP7 caspase 7, apoptosis-related cysteine protease (CASP7),
transcript variant gamma, mRNA      NM_033339         -0.14 -0.78 -0.62 -0.5
      0.07  -0.44 0.54  0.28  0.26  0.04  0.23  0.52  0.35  -0.22 0.28  0.32
      0.5   0.83
IMAGp998D112036   CBWD2 dopamine responsive protein (LOC220869), mRNA
      NM_201453   55871 -0.65 -0.5  -0.71 -0.77 -0.09 -1.52 0.04  0.18  0.15  -
0.74  0.3   0.36  0.15  -0.1  0.84  0.08  0.2   0.28
IMAGp998H16656    CBX1  chromobox homolog 1 (HP1 beta homolog Drosophila )
(CBX1), mRNA      NM_006807   10951 -1.42 -0.32 -1.36 -0.91 -1    -1.56 0.24
      0.18  -0.5  -0.48 0.28  -0.21 0.06  -0.34 0.81  0.86  0.1   1.1
IMAGp998D08822    CCDC2 coiled-coil domain containing 2 (CCDC2), mRNA
      NM_025103         -0.16 -0.16 0.01  -0.64 -0.25 -0.11 0.81  -0.17 0.11  -
0.06  0     0.46  -0.08 0.42  1.09  0.46  0.2   0.88
IMAGp998I101004   CCNA2 cyclin A2 (CCNA2), mRNA NM_001237   890   -0.76 -0.41 -
1.58  -1.5  -0.78 -1.47 0.34  -0.5  -0.33 -0.71 -0.72 0.3   0.59  -0.7  1.21
      0.82  0.5   0.22
IMAGp998B191197   CCNB2 cyclin B2 (CCNB2), mRNA NM_004701   9133  -0.2  -0.33 -
1.39  -1.26 -0.83 -0.73 0.31  0.19  -0.86 -0.85 -0.59 -0.5  0.78  -0.57 2.23
      2.04  1.7   1.44
IMAGp998N071945   CCNC  cyclin C (CCNC), mRNA   NM_005190   892   -0.54 -0.52 -
0.46  -0.72 -0.19 -0.24 0.17  -0.04 0.1   -0.13 -0.03 -0.09 0.09  -0.01 0.77
      0.4   0     0
```

IMAGp998G091961	CCNH	cyclin H (CCNH), mRNA	NM_001239	902	-1.62	-0.13	-1.46	-0.31	-0.81	-1.19	-0.6	0.21	-0.4	-0.03	-0.12	0.05	0.05	-0.56	0.39	0.82	1	-0.2
IMAGp998F19578	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), mRNA	NM_001762	908	-0.61	-0.8	-0.61	-0.88	-0.67	-0.63	0	-0.17	-0.58	-0.35	-0.32	0	0	-0.07	0.75	0.58	0.1	0.44
IMAGp998H22222	CD2AP	CD2-associated protein (CD2AP), mRNA	NM_012120	23607	-0.79	-0.39	-0.59	-0.6	0	-0.76	-0.2	0.22	-0.22	0.04	0.57	0.27	-0.08	-0.1	0.72	0.59	0.4	0.49
IMAGp998F011167	CD58	CD58 antigen, (lymphocyte function-associated antigen 3) (CD58), mRNA	NM_001779	965	-0.15	-0.05	-0.16	-0.22	-0.39	-0.33	0.08	-0.08	-0.11	0.05	-0.26	0.04	-0.04	-0.02	0.63	0.24	0.6	0.38
IMAGp998C20974	CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae) (CDC16), mRNA	NM_003903	8881	-1.1	0.1	-1.03	-0.07	-0.2	-1.15	-0.3	0.39	-0.36	-0.04	-0.51	0.28	-0.02	-0.3	0.46	0.94	0.7	1.05
IMAGp998O131824	CDC2	cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 2, mRNA	NM_033379	983	-0.86	-0.71	-1.42	-1.58	-0.87	-0.79	-0.5	-0.91	0.05	-0.2	0.11	0.02	0.36	-0.25	1.32	1.21	2.7	0.24
IMAGp998K14639	CDC7	CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), mRNA	NM_003503	8317	-0.61	-0.31	-1.01	-0.64	-0.51	-0.77	-0.2	0.29	-0.01	0.06	0.12	0.58	-0.1	-0.27	0.18	0.42	0.4	0.58
IMAGp998D081794	CDCA1	cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA	NM_145697		-0.58	-0.24	-1.23	-1.27	-1.15	-2.12	0.22	-0.16	-0.49	-0.55	0.48	-0.1	0.29	-0.13	1.22	1.07	1.1	0.57
IMAGp998L151775	CDCA3	cell division cycle associated 3 (CDCA3), mRNA	NM_031299	83461	-0.11	-0.06	-1.41	-0.7	-1.29	-0.7	-0.06	-0.42	-0.78	-0.96	-1.04	-0.43	0.33	-0.51	1.04	0.92	1.4	0.49
IMAGp998G191932	CENPF	centromere protein F, 350/400ka (mitosin) (CENPF), mRNA	NM_016343		-0.53	0.16	-1.5	-0.57	-1.07	-0.68	-0.13	0.04	-0.47	-0.48	-0.07	-0.23	0.08	-0.39	1.4	1.54	0.8	1.54
IMAGp998D05121	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA	NM_017812	54927	-0.7	-0.45	-0.71	-1	-0.29	-0.42	-0.2	-0.16	-0.3	-0.62	-0.35	-0.53	0.29	-0.22	0.66	0.33	0.5	-0.58
IMAGp998O03327	CHD5	Chromodomain helicase DNA binding protein 5 (CHD5), mRNA	NM_015557	26038	-0.55	-0.41	-0.45	-0.5	-0.41	-0.27	0.07	-0.12	-0.28	-0.21	-0.42	0.1	-0.03	0.03	0.88	0.75	0.2	0.35
IMAGp998H08646	CHIC1	Cysteine-rich hydrophobic domain 1		53344	-0.01	-0.41	-0.57	-0.11	-0.18	0.01	0.48	0.02	0.14	-0.03	-0.15	-0.04	0.22	0.2	0.19	0.11	0.9	0.31
IMAGp998B09562	CHORDC1	Cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1)	NM_012124	26973	-1.19	-0.31	-0.22	-0.54	-0.07	-0.31	-0.46	-0.21	-0.32	0.07	-0.23	0.37	-0.08	-0.08	0.5	0.31	0.5	0.38
IMAGp998P0288	CIRH1A	Cirrhosis, autosomal recessive 1A (cirhin) (CIRH1A), mRNA	NM_032830	84916	-1.13	-0.48	-1.18	-0.59	-0.55	-0.96	-0.64	-0.39	-0.98	-0.72	-1.1	-0.09	-0.15	-0.1	0.5	0.58	0.6	-0.41
IMAGp998F08194	CKAP2	Cytoskeleton associated protein 2 (CKAP2), mRNA	NM_018204	26586	-0.46	-0.06	-0.78	-1.19	-0.89	-0.82	0.23	-0.23	-0.1	0.22	-0.39	-0.14	0.44	-0.29	1.38	0.73	1.5	1.06
IMAGp998M16679	CKAP4	Cytoskeleton-associated protein 4 (CKAP4), mRNA	NM_006825	10970	-0.3	0.02	-0.55	-0.72	-0.64	-0.56	0.35	0.05	-0.52	-0.59	0.27	-0.15	-0.09	-0.05	1.38	1.41	0.3	0.53
IMAGp998G143938	CKS1B	CDC28 protein kinase regulatory subunit 1B (CKS1B), mRNA	NM_001826	1163	0.18	0.06	-0.63	-0.83	-0.84	-0.69	0.42	0.07	-0.32	-0.16	0.3	-0.37	0.64	-0.54	2.03	1.6	0.8	1.43

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IMAGp998O04460    CKS1B CDC28 protein kinase regulatory subunit 1B (CKS1B), mRNA
      NM_001826   1163  0.34  -0.51 -0.41 -1.44 -0.45 -0.8  0.71  -0.44 0.52  -
0.85  -0.59 -0.12 0.92  0.09  1.97  0.56  0.9   1.08
IMAGp998N17408    CLASP1      Cytoplasmic linker associated protein 1
      23332 -0.15 -1.31 -0.7  -1.18 -0.69 -0.57 0.01  -0.09 -0.37 -0.43 -0.42 -
0.17  -0.15 -0.02 0.81  0.99  0.4   0.73
IMAGp998A111865   CMIP  C-Maf-inducing protein        80790 -0.61 -0.57 -0.29 -
0.5   -0.52 0.24  -0.21 -0.23 0.03  -0.24 -0.1  0.13  0.08  0.37  0.13  -0.06
      0.4   0.64
IMAGp998I24119    CNIH  cornichon homolog (Drosophila) (CNIH), mRNA
      NM_005776   10175 -0.51 -0.18 -0.34 -0.33 -0.01 -0.7  0.13  0.16  0.08
      0.38  0.43  1.1   0.02  0     0.72  0.6   0.3   1.39
IMAGp998O061892   CNIH  Cornichon homolog (Drosophila)            10175 0.05  -
0.11  0.06  -0.37 -0.52 -0.11 0.12  -0.17 -0.18 -0.1  0.36  0.07  0.14  0.16
      0.53  0.27  0.2   0.62
IMAGp998B221166   COL2A1      collagen, type V, alpha 2 (COL5A2), mRNA
      NM_000393         -0.45 -0.27 0     -0.31 -0.43 -0.46 0.49  0.18  0.57
      0.44  1.3   0.96  -0.22 0.2   0.74  0.5   0.5   0.95
IMAGp998D18616    COL8A1      Collagen, type VIII, alpha 1        1295  -0.09 -
0.87  -0.73 -1.3  -1.21 -1.38 -0.47 -0.65 -0.21 -0.06 0.46  0.48  -0.25 0.06
      0.48  0.58  0.7   1.22
IMAGp998E152011   COMMD8      COMM domain containing 8 (COMMD8), mRNA
      NM_017845   54951 -0.44 -0.77 -0.08 -0.86 -0.14 -0.53 0.59  -0.01 0.61
      0.1   0.81  0.2   0.33  0.45  1.24  0.22  0.8   0.79
IMAGp998P02588    COMMD8      COMM domain containing 8 (COMMD8), mRNA
      NM_017845   54951 -0.95 -0.32 -0.69 -0.54 -0.41 -1.21 0.02  0.3   -0.02
      0.22  0.79  -0.03 -0.05 -0.04 0.79  0.97  0.5   1.1
IMAGp998H03185    COMMD8      COMM domain containing 8 (COMMD8), mRNA
      NM_017845   54951 -0.91 -0.55 -0.71 -0.81 -0.29 -0.69 0.32  0.25  0.11
      0.16  0.1   0.31  0.13  -0.17 0.91  0.63  -0.1  1.06
IMAGp998P221198   COPS4 COP9 constitutive photomorphogenic homolog subunit 4
(Arabidopsis) (COPS4), mRNA   NM_016129   51138 -0.54 -0.44 -0.4  -0.66 -0.28 -
1.58  0.35  0.03  0.51  -0.01 1.26  0.43  0.33  -0.29 1.13  0.86  0.8   1.08
IMAGp998N081962   COPS5 COP9 constitutive photomorphogenic homolog subunit 5
(Arabidopsis) (COPS5), mRNA   NM_006837   10987 -0.16 -0.66 0.25  -0.62 -0.33 -
0.37  0.01  -0.15 0.39  0.11  0.49  0.03  0.17  0.27  0.78  0.24  0     0.5
IMAGp998K20869    CPB1  carboxypeptidase B1 (tissue) (CPB1), mRNA NM_001871
      -0.57 -0.21 -0.31 -0.72 -0.5  -1.3  0.2   0.03  0.17  0.02  0.9   0.5
      0.14  0.05  0.79  0.35  -0.2  1.24
IMAGp998F152230   CPZ   Carboxypeptidase Z            8532  0.2   -0.66 -0.34 -
0.55  -0.41 -0.93 0.68  0.23  1.09  0.62  1.14  0.82  -0.02 0.07  0.8   0.42
      1.5   1.21
IMAGp998F16559    CREM  cAMP responsive element modulator (CREM), transcript
variant 2, mRNA   NM_001881   1390  -0.43 -0.02 -0.46 -0.07 -0.12 -0.52 -0.19
      0.09  -0.1  0.1   0.3   0.09  0     -0.2  0.27  0.77  0.8   1.2
IMAGp998I03669    CRI2  CREBBP/EP300 inhibitory protein 2 (CRI2), mRNA
      NM_153232   163126      -0.68 -0.61 -0.57 -0.72 -0.54 -0.24 -0.1  -0.11
      0.3   0.16  0.23  0.47  0.12  -0.24 0.11  -0.01 0     -0.24
IMAGp998H05688    CRSP6 cofactor required for Sp1 transcriptional activation,
subunit 6, 77kDa (CRSP6), mRNA      NM_004268   9440  -0.96 -0.28 -0.54 -0.32 -
1.31  -0.75 0.13  -0.21 -0.52 -0.1  -0.34 0.27  0.03  -0.1  -0.05 0.4   -0.4
      0.87
IMAGp998L051781   CRYAB crystallin, alpha B (CRYAB), mRNA   NM_001885   1410  -
0.85  -0.88 -2.4  -1.72 -2.1  -2.79 -0.38 -0.01 -0.34 0.11  -0.73 0.11  -0.38 -
0.12  -0.63 0     -0.5  -0.1
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IMAGp998M074295   CSDA  cold shock domain protein A (CSDA), mRNA  NM_003651
      -1.28 -0.24 -1.44 -0.01 -0.51 -1.44 0.14  0.12  -0.22 -0.5  -0.11 0.02  -
0.36  0.03  1.12  1.23  2.2   0.1
IMAGp998I112690   CSDA  cold shock domain protein A (CSDA), mRNA  NM_003651
      -0.82 -0.75 -0.53 -0.92 -0.59 -0.97 0.23  -0.03 -0.39 0.29  1.32  0.47  -
0.05  0.8   -0.07 0     0.4   0.31
IMAGp998B18120    CSE1L CSE1 chromosome segregation 1-like (yeast) (CSE1L),
transcript variant 1, mRNA    NM_001316   1434  -0.46 -0.33 -0.89 -0.76 -0.52 -
0.3   0.19  -0.17 -0.13 -0.66 -0.68 -0.03 0.25  -0.16 1.15  0.69  0.2   0.2
IMAGp998C07117    CSE1L CSE1 chromosome segregation 1-like (yeast) (CSE1L),
transcript variant 1, mRNA    NM_001316   1434  -0.73 -0.35 -1.17 -0.72 -0.65 -
1.1   -0.05 0.21  -0.52 -0.03 -0.07 -0.04 0.16  -0.3  1.2   1.21  0.2   0.81
IMAGp998K242237   CSE1L CSE1 chromosome segregation 1-like (yeast) (CSE1L),
transcript variant 2, mRNA    NM_177436   1434  -0.21 -0.25 -0.23 -0.56 -0.26 -
1.47  0.33  0.22  0.15  -0.63 0.64  0.36  0.29  0.17  0.91  0.37  0     0.9
IMAGp998B04827    CSNK1A1     casein kinase 1, alpha 1 (CSNK1A1), mRNA
      NM_001892   1452  -0.72 -0.47 -0.57 -0.74 -0.44 -0.99 0.04  -0.29 -0.18 -
0.39  -0.05 -0.09 0.03  -0.11 0.97  0.63  0.2   0.02
IMAGp998E132690   CSNK1A1     casein kinase 1, alpha 1 (CSNK1A1), mRNA
      NM_001892         -1.12 -0.23 -0.66 -0.61 -0.3  -1.03 -0.03 -0.08 -0.17 -
0.06  0.39  0.24  -0.15 -0.01 0.59  0.61  0.3   1.32
IMAGp998J01842    CSNK2A2     Casein kinase 2, alpha prime polypeptide
      1459  -0.86 0.11  -0.92 -0.22 -0.35 -0.61 -0.06 0.02  -0.43 -0.26 -0.48 0
      -0.14 -0.21 0.41  0.6   0.8   0.15
IMAGp998P023938   CUBN  Cubilin (intrinsic factor-cobalamin receptor)
      8029  -0.6  -0.27 -0.41 -0.44 -0.43 -0.16 0.2   0.07  -0.3  -0.12 -0.51
      0.43  0.23  0     0.74  0.66  0.6   0.21
IMAGp998M071199   CUL2  cullin 2 (CUL2), mRNA   NM_003591   8453  -1.04 -0.45 -
0.91  -0.33 -0.56 -0.56 -0.3  0.02  0.1   -0.2  -0.43 0.05  -0.3  -0.2  0.91
      1.16  1.6   0.88
IMAGp998M091824   CUTC  CGI-32 protein (CGI-32), mRNA NM_015960   51076 -0.61
      0.06  -0.63 -0.32 -0.76 -0.98 -0.32 -0.13 -0.43 -0.01 0.45  0.17  0.02  -
0.27  0.51  0.57  0.6   1.05
IMAGp998H221208   DAP   Death-associated protein            1611  -0.43 -0.55 -
0.38  -0.63 -0.1  -0.42 -0.07 -0.33 -0.5  -0.81 0.07  -0.16 0     0.25  0.85
      0.56  0     0.4
IMAGp998G23609    DBC1  deleted in bladder cancer 1 (DBC1), mRNA  NM_014618
      -1.08 0.11  -1.02 -0.49 -0.48 -0.39 0.18  0.08  -0.47 0.07  -1.33 -0.25
      0.14  -0.51 1.57  1.58  1.4   1.32
IMAGp998P16471    DCTN6 dynactin 6 (DCTN6), mRNA      NM_006571   10671 -0.58 -
0.24  -0.25 -0.53 0.02  0.11  0.33  0.08  0     -0.02 -0.19 0.24  0.36  -0.44
      1.28  0.77  1.3   0.5
IMAGp998M161165   DDAH2 dimethylarginine dimethylaminohydrolase 2 (DDAH2), mRNA
      NM_013974   23564 -0.65 -0.29 -0.89 -0.55 -0.68 -0.96 -0.26 0.04  -0.49 -
0.03  0.41  0.33  -0.09 -0.16 0.72  0.77  -0.3  0.94
IMAGp998L1187     DDR2  Discoidin domain receptor family, member 2
      4921  -0.3  -0.35 -0.08 -0.34 -0.33 -0.09 -0.06 -0.05 0.01  -0.13 0.14
      0.24  0.1   -0.27 1.15  1.12  0.3   1.12
IMAGp998L111745   DDX18 DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), mRNA
      NM_006773   8886  -0.53 -0.31 -0.69 -0.63 -0.29 -1.73 -0.25 -0.48 -0.31 -
0.32  0.42  -0.07 0.11  -0.3  0.98  0.85  0.7   0.55
IMAGp998D06520    DDX24 DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 (DDX24), mRNA
      NM_020414   57062 -0.78 -0.53 -0.72 -0.65 -0.79 0.04  -0.18 -0.33 -0.5  -
0.27  -0.57 -0.39 0.1   -0.25 0.81  0.74  0.2   0.49
IMAGp998J221857   DDX42 DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (DDX42), mRNA
      NM_007372   11325 -0.59 -0.33 -0.29 -0.62 -0.38 -0.62 0.21  -0.38 0.34  -
0.09  -0.18 -0.11 -0.05 0.42  0.67  0.08  0     0.91
```

```
IMAGp998I151903   DDX46 DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (DDX46), mRNA
      NM_014829         -0.57 -0.55 -0.67 -0.57 0.17  -0.71 0.17  -0.13 0.18  0
      0.17  0.55  0.26  0.49  0.67  0.6   -0.5  0.65
IMAGp998B121791   DDX48 DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 (DDX48), mRNA
      NM_014740   9775  -0.72 -0.75 -0.96 -1.08 -0.45 -0.53 0.03  -0.49 -0.13 -
0.67  -0.1  -0.35 0.31  -0.13 1.03  0.48  0.8   0.23
IMAGp998H031906   DEK   DEK oncogene (DNA binding) (DEK), mRNA    NM_003472
      7913  -0.18 -1.14 -0.61 -1.05 -0.68 -0.52 0.58  0     0.02  -0.07 -0.5
      0.01  0.04  0.11  1.17  0.54  0.6   0.77
IMAGp998G031906   DEK   DEK oncogene (DNA binding) (DEK), mRNA    NM_003472
      -0.43 -0.89 -0.67 -1.05 -0.59 -1.34 0.4   0.13  0.03  -0.12 0.61  0.15
      0.04  0.14  1.11  0.68  0.5   0.9
IMAGp998K0780     DEPDC1      DEP domain containing 1       55635 -0.74 0.07  -
1.34  -1.04 -1.15 -0.78 -0.02 -0.29 -0.5  -0.55 -0.91 -0.14 0.43  -0.82 1.53
      1.41  2.3   1.59
IMAGp998A11231    DEPDC1B     HBxAg transactivated protein 1 (XTP1), mRNA
      NM_018369   55789 0.52  -0.61 -0.65 -0.64 -0.56 -1.28 -0.36 -0.05 -0.36 0
      -0.53 0.13  0     -0.35 1.49  0.71  1.3   1.15
IMAGp998E172035   DHX29 DEAH (Asp-Glu-Ala-His) box polypeptide 29 (DHX29), mRNA
      NM_019030   54505 -0.55 -0.96 -0.6  -0.73 -0.27 -1.27 0.09  -0.13 -0.03 -
0.33  0.79  0.14  0.17  0.03  1.2   0.85  0.8   1.31
IMAGp998C15664    DKFZP586F2423           XM_291242         -0.23 -0.38 -0.74 -
0.67  -0.55 -0.63 0.56  0.17  0.03  -0.34 -0.15 0.13  -0.25 0.17  0.36  0.96
      0.7   0.21
IMAGp998I181744   DLAT  dihydrolipoamide S-acetyltransferase (E2 component of
pyruvate dehydrogenase complex) (   NM_001931         -0.32 -0.53 -0.68 -1.11 -
0.75  -1.36 0.07  -0.04 0     -0.16 0.19  0.22  0.2   0.06  0.64  0.19  -0.2
      0.96
IMAGp998A08121    DLAT  dihydrolipoamide S-acetyltransferase (E2 component of
pyruvate dehydrogenase complex)           1737  -0.78 -0.44 -1.03 -0.73 -0.31 -
1.49  0.34  -0.46 0.47  -0.87 0.74  -0.29 0.76  0.7   0.79  -0.25 0.5   0.85
IMAGp998P14820    DLG7  discs, large homolog 7 (Drosophila) (DLG7), mRNA
      NM_014750   9787  -1.64 -0.14 -0.21 -0.87 -1.65 -2.56 -0.16 0.03  -0.33 -
0.65  0.13  -0.2  0.13  -0.62 2     2.36  1.7   3.65
IMAGp998O20783    DNAJB11     DnaJ (Hsp40) homolog, subfamily B, member 11
(DNAJB11), mRNA   NM_016306   51726 -0.36 -0.18 -0.56 -0.71 0.03  -0.32 -0.15
      0.09  -0.53 0.05  -0.29 0.07  -0.16 -0.02 0.6   0.63  0.1   0.27
IMAGp998L061945   DNAJB4      DnaJ (Hsp40) homolog, subfamily B, member 4
(DNAJB4), mRNA    NM_007034   11080 -1.07 -0.98 -0.47 -1.17 -0.3  -0.51 0.15
      0.05  0.32  -0.44 0.07  0.19  -0.08 0.07  0.35  0.21  0.8   1.59
IMAGp998N03975    DPM1  dolichyl-phosphate mannosyltransferase polypeptide 1,
catalytic subunit (DPM1), mRNA      NM_003859   8813  -0.59 -0.25 -0.5  -0.56 -
0.52  -0.3  0.34  -0.05 -0.18 -0.29 -0.56 -0.19 0.33  -0.29 0.63  1.05  1.5
      1.66
IMAGp998L101197   DPP8  Dipeptidylpeptidase 8         54878 -0.34 -0.26 -0.08 -
0.51  -0.27 -0.52 0.13  -0.13 -0.31 0.28  0.66  0.75  0.03  0.17  0.64  0.37
      0.6   1.54
IMAGp998P111924   DUT   dUTP pyrophosphatase (DUT), mRNA    NM_001948         -
0.39  0.19  -0.51 -0.35 -0.75 -0.88 0.32  0.25  0.51  0.48  1.23  0.3   0
      0.06  0.94  0.68  0.8   1.87
IMAGp998L061854   EBAG9 estrogen receptor binding site associated, antigen, 9
(EBAG9), transcript variant 2, mR   NM_198120         -0.68 -0.17 -1.16 -0.2  -
0.85  -1.31 0.1   0.27  -0.06 -0.22 -0.18 -0.13 -0.12 -0.55 0.35  1.17  0.8
      1.35
IMAGp998N171724   EEF2  Eukaryotic translation elongation factor 2 (EEF2), mRNA
      NM_001961   1938  -1.11 -0.92 -1.39 -0.5  -1.27 -1.88 -0.11 0.03  0.17  -
0.1   0.48  0.04  0.03  -0.1  1.77  1.42  1.1   1.79
```

IMAGp998K191725 EIF1AY Eukaryotic translation initiation factor 1A (EIF1A), mRNA NM_001412 1964 -1.1 0.04 -1 -0.4 0.01 -1.32 0.12 0.44 -0.36 -0.07 0.44 0.41 0.03 -0.35 1.19 1.4 0.7 1.62

IMAGp998O19880 EIF1AY Eukaryotic translation initiation factor 1A, Y-linked (EIF1AY), mRNA NM_004681 -0.43 -0.54 -0.6 -0.56 -0.03 -0.45 0.36 0.19 0.05 -0.06 0.27 0.47 0.42 0.29 0.68 0.29 2.7 0.5

IMAGp998E092615 EIF1AY Eukaryotic translation initiation factor 1A (EIF1A), mRNA NM_001412 -0.67 -0.57 -0.65 -0.84 -0.36 -0.95 0.36 0.03 -0.01 -0.21 0.04 0.87 0.14 0.09 1.22 0.47 0 0.66

IMAGp998N1995 EIF2B1 Eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa (EIF2B1), mRNA NM_001414 1967 -1.08 -0.74 -1.19 -0.82 -0.92 -0.91 -0.05 -0.17 -0.42 -0.54 -0.77 -0.24 0.03 -0.11 0.68 0.64 -0.2 0.22

IMAGp998C1585 EIF2B1 Eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa (EIF2B1), mRNA NM_001414 1967 -0.57 -0.45 -0.99 -0.69 -0.52 -1.14 -0.24 -0.09 -0.46 -0.37 0.69 -0.3 -0.07 -0.04 0.54 0.59 -0.2 0.56

IMAGp998I05460 EIF2S1 Eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1), mRNA NM_004094 1965 -0.71 -0.46 -0.76 -0.55 -0.75 -0.37 -0.05 -0.15 -0.36 -0.57 -1.14 -0.26 0.27 -0.3 0.75 0.89 0.1 0.53

IMAGp998G13174 EIF2S2 Eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), mRNA NM_003908 -2.1 -0.06 -2.04 -0.25 -0.3 -2.24 -0.19 0.15 -1.14 -0.85 0.03 0.05 0.36 -0.78 1.24 1.63 2.3 1.84

IMAGp998I06123 EIF3S10 Eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa (EIF3S10), mRN NM_003750 8661 -0.47 -1.03 -0.38 -1.16 -0.23 -0.48 0.18 -0.25 -0.3 -0.61 -0.61 -0.15 0.07 0.08 1.32 0.62 1 0.31

IMAGp998G232574 EIF3S6 Eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA NM_001568 3646 -0.54 -0.98 -0.42 -0.62 -0.29 -0.95 0.03 0.2 -0.08 0.31 1.38 0.32 0.18 -0.05 1.1 0.97 0.8 0.36

IMAGp998L11138 EIF3S6 Eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA NM_001568 3646 -1.71 -0.23 -1.42 -0.67 0.02 -2.33 0 0.2 -0.16 -2.17 0.9 0.69 0.09 -0.21 1.27 1.33 2.8 0.89

IMAGp998D122580 EIF3S9 Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa 8662 -0.18 -0.29 -0.35 -0.59 -0.13 -0.39 0.06 -0.04 -0.4 -0.21 0.65 0.02 0.18 -0.25 0.91 0.68 0.5 0.67

IMAGp998D195602 EIF4A1 Eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA NM_001416 -0.62 -0.35 -0.46 -0.2 0.19 -1.5 0.71 -0.18 0.35 -1.42 -0.37 0.24 0.89 0.92 1.56 0.52 1.8 0.23

IMAGp998N09644 EIF4E Eukaryotic translation initiation factor 4E (EIF4E), mRNA NM_001968 1977 -0.59 0.05 -0.34 -0.11 -0.17 -0.88 0.17 0.08 -0.13 0.2 0.7 0.47 0.19 -0.2 0.63 0.48 0.5 0.73

IMAGp998N09597 EIF4G2 Eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA NM_001418 1982 -0.17 -1.05 -0.11 -1.02 -0.51 -0.28 0.54 -0.24 -0.39 0.06 -0.49 -0.18 0.08 0.2 1.36 0.92 0.4 0.94

IMAGp998B052036 EIF4G3 Eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA NM_003760 8672 -0.51 -0.6 -0.82 -0.12 -0.94 -0.6 -0.17 0.04 -0.04 -0.01 0.09 0.29 -0.09 0.14 0.88 0.74 0.8 -0.37

IMAGp998F24110 EIF5 Eukaryotic translation initiation factor 5 NM_183004 1983 -1.03 -0.22 -0.9 -0.56 -0.51 -1.46 -0.29 -0.28 -0.33 -0.76 -0.02 -0.1 -0.1 -0.12 1.05 0.82 0.3 1.24

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IMAGp998J176053   EIF5  Eukaryotic translation initiation factor 5 (EIF5),
transcript variant 2, mRNA    NM_183004   1983  -1.76 -0.11 -1.69 -0.14 0.01  -
2.48  -0.43 -0.28 -0.73 -1.16 0.18  0.03  0.02  -0.19 1.04  1.08  1.5   0.18
IMAGp998F12617    EIF5B Eukaryotic translation initiation factor 5B (EIF5B),
mRNA  NM_015904   9669  -1.46 -0.45 -1.28 -0.71 -0.74 -0.59 -0.19 0     -0.28 -
0.37  -0.81 0.11  -0.04 -0.47 1.08  0.95  0.6   0.53
IMAGp998G09198    ELAVL1      ELAV (embryonic lethal, abnormal vision,
Drosophila)-like 1 (Hu antigen R) (ELAVL1), mR  NM_001419   1994  -0.45 -0.78 -
0.46  -1.25 -0.88 -0.73 0.68  -0.43 0.11  -0.54 -0.73 0.05  -0.05 0.27  0.9
      0.49  0.7   -0.07
IMAGp998A17115    ELOVL6      ELOVL family member 6, elongation of long chain
fatty acids (FEN1/Elo2, SUR4/Elo3-like,   NM_024090   79071 -1    0.32  -0.53 -
0.18  -0.4  -2.02 0.14  0.16  0.13  -0.06 0.26  -0.4  -0.29 0.14  0.79  0.83
      1.7   1.65
IMAGp998N094083   EML5  Echinoderm microtubule associated protein like 5 (EML5),
mRNA  NM_183387         -0.98 -0.59 -1.31 -0.13 -0.47 -1.13 -0.07 0.31  -0.86 -
0.19  0.46  -0.17 0     -0.55 0.65  0.88  1.2   1.15
IMAGp998D02121    ENAH  Enabled homolog (Drosophila)        55740 -0.26 -0.6  -
0.3   -0.8  -0.22 -0.28 -0.23 -0.34 -1.13 -0.09 -0.6  -0.05 -0.21 0.25  1.6
      1.22  0.8   1.76
IMAGp998F161945   ENAH  Enabled homolog (Drosophila) (ENAH), mRNA NM_018212
      55740 -0.73 0.06  -0.68 0.09  -0.23 0.18  1.01  -0.28 0.12  0.09  0.08  -
0.21  0.64  2.44  1.54  0.52  0.4   0.78
IMAGp998O01880    ENPP2 ectonucleotide pyrophosphatase/phosphodiesterase 2
(autotaxin) (ENPP2), mRNA     NM_006209         0.18  -0.57 -0.14 -1.16 -0.89 -
0.31  0.54  0.35  -0.06 -0.61 -0.45 -0.06 0.45  -0.17 1.27  0.86  0.3   0.95
IMAGp998P081906   ENTH  Enthoprotin       9685  -0.72 -0.16 -0.8  -0.2  -0.95 -1
      -0.21 0.27  -0.35 0.17  -0.11 0.19  0.27  -0.19 0.03  0.49  0.7   0.1
IMAGp998B101678   ENTPD5      ectonucleoside triphosphate diphosphohydrolase 5
(ENTPD5), mRNA    NM_001249         -0.95 -0.49 -1.11 -0.58 -0.46 -0.62 -0.14 -
0.15  0.07  -0.5  -0.25 -0.38 0.23  -0.26 0.49  0.2   0     -0.17
IMAGp998A09330    EXOSC7      KIAA0116 protein (KIAA0116), mRNA   NM_015004
      -1.04 -0.25 -1    -0.21 -0.61 -1.15 -0.06 -0.01 -0.08 -0.17 0.04  -0.07 -
0.16  -0.25 0.49  0.65  0.2   0.63
IMAGp998J21439    FAM18B      family with sequence similarity 18, member B
(FAM18B), mRNA    NM_016078   51030 -1.01 -0.15 -0.2  -1.65 -0.3  -1.28 0.28
      0.22  0.14  -0.34 0.79  0.07  0.13  -0.03 1.1   0.31  0     1.05
IMAGp998L1581     FAM3C family with sequence similarity 3, member C (FAM3C),
mRNA  NM_014888         -0.71 -0.39 -0.51 -0.8  -0.49 -0.51 0.2   -0.05 -0.59 -
0.51  -0.53 -0.08 0.01  -0.08 0.87  0.52  1.7   0.85
IMAGp998C151203   FBXO18      F-box only protein, helicase, 18 (FBXO18),
transcript variant 2, mRNA    NM_178150   84893 -0.85 -0.57 -0.89 -0.48 0.01
      0.19  -0.37 -0.26 -0.16 -0.23 0.02  -0.23 -0.18 -0.01 0.75  1.07  0.8
      0.65
IMAGp998L211112   FH    fumarate hydratase (FH), nuclear gene encoding
mitochondrial protein, mRNA   NM_000143   2271  -1    -0.25 -1.4  -0.57 -0.68 -
1.03  -0.3  0.32  -0.7  -0.05 0.38  0.19  0     -0.49 0.45  0.83  0.4   0.44
IMAGp998C12920    FKBP14      FK506 binding protein 14, 22 kDa (FKBP14), mRNA
      NM_017946         -0.27 -0.86 -0.69 -1.02 -1.09 -0.14 0     -0.11 -0.29 -
0.35  -0.54 -0.08 -0.15 -0.12 0.63  0.71  0.9   -0.08
IMAGp998O04567    FLJ13273    Hypothetical protein FLJ13273       79807 -0.23 -
0.33  -0.36 -0.73 -0.03 -0.58 0.12  -0.2  0.25  -0.29 -0.17 0.11  -0.03 -0.19
      0.33  0.15  0.8   1.06
IMAGp998B17411    FLJ21628    Zinc finger protein 2 homolog (mouse)
      80108 -1.13 -0.96 -1.25 -0.89 -1.64 -1.76 0.19  0.05  -0.02 -0.44 0.16
      0.03  0.04  -0.17 1.06  0.97  1.3   1.71
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IMAGp998M11730    FLJ21908    hypothetical protein FLJ21908       79657 -1.4  -
0.51  -1.12 -0.58 -0.32 -1.92 -0.08 0.08  0.11  0.21  1.13  0.6   0.05  -0.25
      0.62  0.8   0.3   1.34
IMAGp998J20124    FLJ37953    Hypothetical protein FLJ37953       129450      -
0.12  0.01  -0.43 -0.02 -0.74 -0.48 0.12  -0.15 0.33  0.14  0.3   -0.45 0.12
      0.18  0.46  0.19  1.7   0.9
IMAGp998D09822    FN1   Fibronectin 1 (FN1), transcript variant 1, mRNA
      NM_002026         0.04  -0.47 0.07  -0.71 -0.45 -0.49 0.7   -0.11 0.01
      0.03  0.26  0.51  -0.13 0.45  1.06  0.53  0.4   0.55
IMAGp998B18778    FN1   Fibronectin 1 (FN1), transcript variant 1, mRNA
      NM_002026   2335  -0.33 -0.27 -0.34 -0.68 -0.64 -0.98 0.61  0.73  0.07  0
      0.59  0.35  -0.28 0.32  0.66  0.77  0     1.47
IMAGp998J10666    FRDA  Friedreich ataxia (FRDA), nuclear gene encoding
mitochondrial protein, transcript varia   NM_000144   2395  -0.37 -0.54 -0.41 -
0.43  -0.4  -1.15 -0.11 -0.2  -0.56 -0.31 0.38  -0.14 0.17  -0.31 0.17  0.43
      0.2   0.56
IMAGp998C21621    FTH1  ferritin, heavy polypeptide 1 (FTH1), mRNA
      NM_002032         0.05  -0.49 -0.43 -0.48 -0.37 -0.42 0.2   0.02  0.01
      0.02  0.66  0.18  0.16  -0.06 0.86  0.65  -0.2   0.34
IMAGp998A061009   FXR1  fragile X mental retardation, autosomal homolog 1
(FXR1), mRNA      NM_005087   8087  -1.11 -0.56 -0.76 -0.21 -0.51 -0.23 0.14
      0.28  0.27  0.25  0.2   0.29  0     -0.29 0.73  0.76  0.9   0.35
IMAGp998L09972    FXYD5 FXYD domain containing ion transport regulator 5
(FXYD5), mRNA     NM_014164   53827 -0.48 -0.07 -0.7  0.09  -0.64 -0.47 -0.03
      0.27  -0.01 -0.14 0.57  -0.14 0.02  -0.07 0.39  0.39  0.3   0.83
IMAGp998P14697    GADD45A     growth arrest and DNA-damage-inducible, alpha
(GADD45A), mRNA   NM_001924   1647  -1.22 -0.73 -1    -1.8  -0.42 -1.8  -0.02
      0.2   -0.09 -0.17 0.53  0.24  0.13  0.05  0.53  0.26  -0.3  0.6
IMAGp998E23478    GAPD  glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
      NM_002046   2597  -0.33 -0.45 -0.02 -0.74 -0.46 -0.19 0.2   0.02  0.3   -
0.06  0.37  -0.01 0.2   0.29  1.04  0.6   0.1   0.87
IMAGp998G034013   GBAS  glioblastoma amplified sequence (GBAS), mRNA
      NM_001483   2631  -0.32 -0.38 -0.17 -0.3  -0.27 -0.13 0.33  0.4   0.36
      0.41  0.94  0.99  0.03  -0.03 0.18  0.28  0     0.7
IMAGp998J10115    GBE1  glucan (1,4-alpha-), branching enzyme 1 (glycogen
branching enzyme, Andersen disease, g     NM_000158   2632  -0.5  -0.92 -0.36 -
1.14  0     -0.24 0.46  -0.11 -0.29 -0.48 -0.48 -0.02 -0.24 0.38  0.96  0.36
      0.5   0.9
IMAGp998A201924   GBF1  golgi-specific brefeldin A resistance factor 1 (GBF1),
mRNA  NM_004193         -0.72 -0.95 -1.12 -0.93 -0.97 -0.65 0.11  -0.06 -0.25 -
0.48  -0.1  0.23  0.05  0.07  1.17  1.2   -0.1  0.36
IMAGp998N06536    GLDC  "glycine dehydrogenase (decarboxylating; glycine
decarboxylase, glycine cleavage system"   NM_000170   220758      -0.34 -0.55 -
0.11  -0.25 -0.92 -0.15 -0.14 -0.09 0.15  -0.11 0.24  0     0.08  0     0.13
      0.43  1     0.59
IMAGp998A112009   GMNN  geminin, DNA replication inhibitor (GMNN), mRNA
      NM_015895         -1.14 -0.57 -1.39 -0.75 -1.08 -1.41 0.01  -0.12 -0.47 -
0.75  0.1   0.39  0.16  -0.31 0.53  0.54  0.4   0.53
IMAGp998F05227    GNG10 guanine nucleotide binding protein (G protein), gamma 10
(GNG10), mRNA     NM_004125         -0.41 -0.49 0.17  -0.55 -0.08 0.43  0.54
      0.02  0.56  0.16  0.15  0.84  0.26  0.06  1.29  0.5   0.8   1.06
IMAGp998I191962   GNG10 guanine nucleotide binding protein (G protein), gamma 10
(GNG10), mRNA     NM_004125   2790  -0.32 -0.61 0.18  -0.57 -0.19 -0.49 0.57
      0.09  0.49  0.21  1.04  1.05  0.25  -0.02 1.43  0.89  0.8   1.71
IMAGp998F10393    GNG12 Guanine nucleotide binding protein (G protein), gamma 12
            55970 -0.16 -0.45 0.03  -0.44 -0.32 -0.16 0.44  0.22  0.12  0
      0.46  0.01  -0.04 0.07  1.44  1.05  0.6   0.91
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IMAGp998I01473	GOLGA4	golgi autoantigen, golgin subfamily a, 4 (GOLGA4),
mRNA	NM_002078		-0.32	-0.13	-0.31	-0.61	-0.25	0.01	0.06	-0.26	-0.01	-
0.12	-0.39	-0.07	0.12	0.02	0.4	0.64	0	0.17
IMAGp998D10228	GOLPH4	Golgi phosphoprotein 4		27333	-0.77	-0.26	-
0.35	-0.56	-0.34	-0.88	0.3	0.13	-0.33	-0.3	-0.08	-0.03	-0.3	0.12	0.55
	0.14	0.7	0.83
IMAGp998L215632	GPR143	G protein-coupled receptor 143 (GPR143), mRNA
	NM_000273	4935	-0.44	-0.06	-0.36	-0.28	-0.06	-0.69	0.24	0.15	0.14	-
0.19	-0.1	0.52	-0.03	0.07	0.36	0.44	0	0.73
IMAGp998A01737	GSDML	gasdermin-like (GSDML), mRNA	NM_018530		-0.36	-
0.23	-0.19	-0.71	-0.34	-0.28	0.08	-0.17	-0.18	0.19	-0.5	0.05	0.18	0.05
	1.33	0.71	0.6	1.14
IMAGp998J232973	GSK3B	glycogen synthase kinase 3 beta (GSK3B), mRNA
	NM_002093	2932	-1.41	-0.12	-1.48	-0.25	-0.63	-1.36	-0.39	0.24	-0.19
	0.05	0	-0.19	-0.42	-0.41	0.13	0.89	0.6	0.33
IMAGp998O19844	GSPT2	G1 to S phase transition 2 (GSPT2), mRNA	NM_018094
	23708	-1.22	-0.29	-1.1	-0.58	-1.01	-1.15	0.14	0.14	-0.32	0.11	0.51
	0.14	0.1	0.12	1.31	1.39	0.8	1.69
IMAGp998N06732	GTF2A2	general transcription factor IIA, 2 (12kD subunit)
(GTF2A2), mRNA	NM_004492	2958	-0.15	-0.64	0.06	-0.91	-0.05	-0.06	0.32	-
0.11	0.14	-0.45	0.17	0	0.35	0	1.31	0.73	0.2	0.78
IMAGp998B241781	GTF2H2	general transcription factor IIH, polypeptide 2,
44kDa (GTF2H2), mRNA	NM_001515		-0.51	-0.59	-0.04	-0.35	-0.4	-0.6
	0.22	-0.28	0.02	-0.36	-0.07	-0.31	0.22	-0.29	0.8	0.62	-0.2	0.73
IMAGp998G04445	GUCA1A	guanylate cyclase activator 1A (retina) (GUCA1A),
mRNA	NM_000409		-0.36	-1.08	-0.26	-1.17	-0.66	-0.96	0.33	-0.46	0.76	-
0.41	-0.16	0.45	-0.07	0.51	0.96	0.13	0.1	0.6
IMAGp998L231200	H3F3A	H3 histone, family 3B (H3.3B) (H3F3B), mRNA
	NM_005324		-0.1	-0.9	-0.2	-1.06	-0.83	-0.9	0.26	-0.39	-0.59	-
0.51	0.07	-0.63	0.3	0.09	1.33	0.72	0.3	0.49
IMAGp998M14201	H63	H63 breast cancer expressed gene (H63), transcript
variant 2, mRNA	NM_177974	113201		-0.41	-0.6	0.02	-0.85	0.28	-0.06	-
0.01	0.2	0.68	0.17	0.8	0.7	-0.03	0.24	1.46	0.79	1.4	0.58
IMAGp998I0375	HAT1	histone acetyltransferase 1 (HAT1), mRNA	NM_003642
	8520	-1.7	-0.33	-2.19	0.35	-1.26	-1.05	0.21	0.14	-0.28	-1.28	-0.52
	0.21	0.36	-0.46	0.98	1.04	0.6	0.68
IMAGp998G141793	HDAC2	histone deacetylase 2 (HDAC2), mRNA	NM_001527	3066	-
0.76	-0.5	-0.31	-0.75	-0.5	-0.37	0.23	-0.32	0.28	0.12	0.72	0.25	-0.17
	0.07	0.85	0.65	0.7	1.67
IMAGp998I19695	HEBP1	heme binding protein 1 (HEBP1), mRNA	NM_015987
	50865	-0.46	-0.51	-0.54	-0.57	-0.86	-0.65	0.22	0.13	0.08	0.06	0.46
	0.01	-0.25	-0.01	0.49	0.38	0.3	0.9
IMAGp998K121789	HECTD1	HECT domain containing 1 (HECTD1), mRNA
	NM_015382	25831	-0.54	-0.45	-0.26	-0.54	-0.21	-0.34	0.12	-0.15	-0.07	-
0.37	0.05	0.79	-0.08	-0.14	0.98	0.68	0.5	1.04
IMAGp998P01399	HELIC1	helicase, ATP binding 1 (HELIC1), mRNA
	NM_006828	10973	-1.15	-0.57	-0.68	-0.68	-0.66	-0.46	-0.42	-0.16	-0.21	-
0.01	0.01	0.21	-0.23	-0.08	0.51	0.52	2	-0.1
IMAGp998H02566	HERC4	DKFZP564G092 protein (DKFZP564G092), mRNA	NM_015601
	26091	-0.55	-0.63	-0.71	-0.36	-0.64	-0.69	0	0.24	-0.16	-0.1	0.07
	0.07	0.17	-0.38	1.42	1.83	1.3	0.11
IMAGp998F06310	HEY1	hairy/enhancer-of-split related with YRPW motif 1
(HEY1), mRNA	NM_012258	23462	-0.26	-0.44	-0.42	-0.76	-1.03	-0.79	0.16	-
0.32	0.05	-0.26	-1.24	-0.45	0.19	0.2	0.1	-0.29	0.4	0.41
IMAGp998M21210	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH),
transcript variant 1, mRNA	NM_014362	26275	-0.83	0.26	-0.59	-0.24	-0.35	-
1.07	-0.33	0.41	-0.04	0.07	0.92	0.42	-0.02	0.6	0.4	0.52	0.2	1.17
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IMAGp998P14736    HIF1A hypoxia-inducible factor 1, alpha subunit (basic helix-
loop-helix transcription factor)    NM_001530   3091  -0.74 -0.76 -0.6  -0.75 -
0.56  -1.08 0.38  -0.04 -0.4  -0.1  0.53  0.24  0.27  -0.14 2.31  1.75  1.5
      2.33
IMAGp998I13570    HMGA2 high mobility group AT-hook 2 (HMGA2), mRNA
      NM_003483   8091  -1.24 -0.67 -1.52 -0.66 -0.94 -1.39 -0.01 -0.37 0.2
      0.06  -0.72 -0.12 0.28  -0.17 0.35  0.12  1     -0.4
IMAGp998A211963   HMMR  hyaluronan-mediated motility receptor (RHAMM) (HMMR),
transcript variant 2, mRNA    NM_012485   3161  -0.02 0.3   -0.65 -0.92 -0.63 -
1.87  0.5   0.14  -0.04 -0.57 0.27  0.47  0.47  -0.43 2.16  1.55  1.6   2.19
IMAGp998P151789   HNRPD heterogeneous nuclear ribonucleoprotein D (AU-rich
element RNA binding protein 1, 37kDa      NM_002138         -0.28 -0.53 -0.81 -
0.88  -0.6  -0.27 0.23  0.1   -0.52 -0.66 -1.02 0.04  0.02  -0.06 1.21  0.97
      0.9   0.52
IMAGp998O16227    HNRPD Heterogeneous nuclear ribonucleoprotein D (AU-rich
element RNA binding protein 1, 37kDa)           3184  -0.31 -0.39 -0.52 -0.72 -
0.57  -0.76 0.22  -0.01 -0.29 -0.34 0.24  -0.02 0.06  0.09  0.81  0.68  1.2
      0.67
IMAGp998B20728    HNRPD Heterogeneous nuclear ribonucleoprotein D (AU-rich
element RNA binding protein 1, 37kDa)           3184  -0.82 -0.26 -0.47 -0.56 -
0.33  -1.23 0.13  -0.14 0.18  0.02  -0.25 0.43  0.1   0.15  0.52  0.26  -0.3  -
0.08
IMAGp998F21388    HNRPR heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA
      NM_005826   10236 -0.67 -0.52 -0.34 0.41  -0.72 -1.93 0.5   0.56  -0.34 -
0.27  0.15  0.08  0.31  -0.01 1.5   0.96  0.4   1.38
IMAGp998M141998   HNRPUL1     E1B-55kDa-associated protein 5 (E1B-AP5),
transcript variant 1, mRNA    NM_007040   11100 -0.22 -1.09 -0.83 -0.99 -0.58 -
0.33  0.02  -0.14 -0.22 -0.39 -0.69 0.03  -0.12 0     0.81  0.83  -0.2  -0.15
IMAGp998D242009   HRB   HIV-1 Rev binding protein                 -0.51 -0.8  -
0.4   -0.55 -0.8  -0.9  0.03  -0.82 0.11  -0.6  0.51  0.85  -0.09 0.51  1.04
      0.45  0.8   0.98
IMAGp998D15677    HRSP12      translational inhibitor protein p14.5 (UK114),
mRNA  NM_005836   10247 -0.8  -0.39 -0.73 -0.67 -0.07 -0.88 0.11  0.12  0.18
      0.28  0.68  0.68  0.28  -0.23 0.68  0.55  0.1   0.41
IMAGp998D05437    HS3ST1      heparan sulfate (glucosamine) 3-O-sulfotransferase
1 (HS3ST1), mRNA  NM_005114   9957  -0.24 -0.36 -0.78 -0.44 -0.75 -1.08 -0.18
      0.18  0.57  0.3   -0.31 -0.16 0.54  0.14  0.03  0.19  0.3   0.32
IMAGp998H102009   HSPA14      likely ortholog of mouse heat shock protein, 70
kDa 4 (HSP70-4), mRNA   NM_016299         -0.54 -0.7  -0.67 -0.76 -0.52 -0.92
      0.04  -0.17 -0.08 -0.44 -0.34 -0.11 0.24  -0.17 0.73  0.52  0.3   0.08
IMAGp998I22404    HSPA8 heat shock 70kDa protein 8 (HSPA8), transcript variant
1, mRNA     NM_006597   3312  -0.97 -0.8  -0.83 -0.55 -0.78 -1.26 -0.82 -0.61 -
1.44  -1.34 0     -0.74 0.53  -0.89 0.97  1.26  0.3   1.3
IMAGp998G2370     IARS  isoleucine-tRNA synthetase (IARS), transcript variant
short, mRNA NM_002161   3376  -1.57 -0.05 -2    0.2   -0.57 -2.22 -0.02 -0.1  -
0.35  -1.7  0.18  0.3   0.4   -0.33 1.11  0.99  1.1   0.89
IMAGp998J061962   IDI1  isopentenyl-diphosphate delta isomerase (IDI1), mRNA
      NM_004508   3422  -0.45 -0.1  -0.63 -0.44 -0.6  -0.35 0.18  0.32  0.04
      0.23  0.78  0.33  0.21  -0.3  0.1   0.26  -0.1  -0.23
IMAGp998O05114    IFRD1 interferon-related developmental regulator 1 (IFRD1),
mRNA  NM_001550   3475  -1.1  -0.24 -1    -1.04 -0.72 -0.8  -0.16 -0.47 -0.43 -
0.44  -0.33 -0.67 0.04  -0.34 1.18  0.96  1.8   -0.04
IMAGp998M075808   IGHG1 Immunoglobulin heavy constant gamma 1 (G1m marker)
            -2.4  -0.73 -2.4  -0.11 -0.27 -1.46 0.36  0.78  -1.41 -0.59 -1.44 -
0.64  0.73  -0.93 1.77  2.22  2     0.86
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IMAGp998K031012   IKIP  IKK interacting protein       121457      -0.99 -0.13 -
0.9   -0.36 -0.42 -0.99 0.03  0.29  -0.48 0.14  0.58  0.59  -0.14 -0.17 0.37
      0.68  0.5   1.22
IMAGp998M08735    IL1B  interleukin 1, beta (IL1B), mRNA    NM_000576   3553  -
0.51  -0.49 -0.67 -0.23 -0.17 -1.67 -0.21 0.12  0.12  -0.24 -0.26 0.04  -0.05
      0.27  0.53  -0.02 0     0.6
IMAGp998A11656    ILF2  interleukin enhancer binding factor 2, 45kDa (ILF2),
mRNA  NM_004515   3608  -0.65 -0.77 -0.96 -0.93 -0.64 -0.42 0.3   -0.12 -0.08 -
0.47  -0.28 -0.06 0.33  -0.23 0.98  1.44  0.5   1.2
IMAGp998N13233    IMPA1 inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA
      NM_005536   3612  -0.46 0.09  -0.12 -0.66 -0.74 -0.49 0.24  -0.11 -0.35 -
0.24  0.32  0.21  0.14  -0.01 0.83  0.15  0.2   1.21
IMAGp998H03838    INSIG1      insulin induced gene 1 (INSIG1), transcript
variant 3, mRNA   NM_198337   3638  -0.49 0.01  -0.75 -0.51 -0.5  -0.52 0.56
      0.47  0.1   0.14  0.7   0.72  -0.65 0.37  0.57  0.32  0.2   0.21
IMAGp998K232006   IPO11 importin 11 (IPO11), mRNA     NM_016338         -0.45 -
0.4   -0.43 -0.36 0.08  -0.86 0.07  0.16  -0.14 0     0.35  0.03  0.48  -0.36
      1.21  1.19  0.6   0.7
IMAGp998K01789    IPO7  "IMPORTIN 7; RAN-BINDING PROTEIN 7.
[Source:RefSeq;Acc:NM_006391]"            10527 -0.55 -0.31 -0.22 -0.3  -0.16 -
0.33  0.06  -0.25 -0.04 -0.14 -0.18 0.14  0.06  -0.08 0.88  0.47  0.8   0.43
IMAGp998K21390    IQWD1 IQ motif and WD repeats 1                 -0.15 0.1   -
0.09  0.07  -0.37 -0.76 0.09  -0.03 0.01  0     0.14  -0.22 0.16  0.14  0.23
      0.28  0.7   0.56
IMAGp998P212457   ITGB3BP     integrin beta 3 binding protein (beta3-endonexin)
(ITGB3BP), mRNA   NM_014288   23421 -0.53 -0.32 -0.8  -0.76 -0.29 -1.39 0.19
      0.11  0.26  -0.06 0.84  0.79  0.36  -0.11 0.84  0.53  0.5   0.37
IMAGp998H17200    ITPR2 Family with sequence similarity 20, member C
      -0.32 -0.27 -0.62 -0.55 -0.89 -0.93 -0.03 0.17  -0.38 -0.2  -0.07 0.2   -
0.38  -0.08 0.07  0.4   0.2   0.42
IMAGp998P05518    KARS  lysyl-tRNA synthetase (KARS), mRNA  NM_005548   3735  -
1.03  -0.37 -1.11 -0.58 -0.6  0.04  -0.18 0.17  -0.54 -0.2  -0.25 -0.3  -0.09 -
0.17  1.12  1.24  0.5   0.7
IMAGp998G181888   KCNMB4      potassium large conductance calcium-activated
channel, subfamily M, beta member 4 (KCNM NM_014505   27345 -1.07 -0.14 -0.96 -
0.5   -0.92 -1.39 -0.23 -0.67 -0.28 -0.74 -0.48 0.19  0.03  -0.36 0.72  0.51  -
0.2   0.57
IMAGp998F08435    KCTD15      Potassium channel tetramerisation domain
containing 15           79047 -0.25 -0.57 -0.16 -0.71 -0.31 -0.7  -0.24 -0.62 -
0.48  -0.93 -0.11 -0.23 0     0.23  0.74  0.32  -0.1  0.65
IMAGp998G15525    KDELC1      KDEL (Lys-Asp-Glu-Leu) containing 1 (KDELC1), mRNA
      NM_024089   79070 -0.52 -2.22 -0.75 -0.44 -0.18 -0.78 -0.02 -0.08 -0.07 -
0.25  -0.65 0.28  0.24  -0.26 0.77  0.67  0     0.52
IMAGp998O21375    KIAA0372    KIAA0372 (KIAA0372), mRNA     NM_014639   9652  -
0.93  -0.46 -0.99 -0.64 -0.08 -0.6  0.1   0.06  0.27  -0.29 -1.1  0.14  0.38  -
0.18  1.32  1.49  -0.2  0.5
IMAGp998E16540    KIAA0586    KIAA0586 (KIAA0586), mRNA     NM_014749   9786  -
0.58  -0.26 -1.26 -0.58 -1.17 -0.88 -0.03 0.46  -0.53 -0.16 -0.26 -0.11 -0.14 -
0.51  0.41  1     0.9   0.27
IMAGp998G11613    KIAA0853    KIAA0853          23091 -0.08 -0.72 -0.14 -0.4  -
0.1   0.11  -0.04 -0.08 -0.08 -0.17 -0.02 0.11  0.15  0.03  0.95  0.94  0.6
      1.73
IMAGp998M11121    KIAA0992    palladin    NM_016081   23022 -0.4  -0.23 -0.44 -
0.33  -0.16 -2.53 1.6   -0.52 0.41  -0.3  1.53  -0.57 0.32  -0.01 2.05  1.69
      1.8   2.41
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IMAGp998D171932   KIAA1212    KIAA1212          55704 -0.86 0.17  -0.79 -0.38 -
0.88  -0.84 -0.14 -0.04 -0.36 0.04  -0.6  -0.25 0.09  -0.63 1.19  1.27  1.9
      1.29
IMAGp998P18311    KIAA1279    KIAA1279 (KIAA1279), mRNA     NM_015634   26128 -
0.39  -0.39 -0.18 -0.51 -0.24 -0.5  0.33  0.03  0.11  -0.07 0.26  0.63  0.03
      0.11  0.95  0.51  0.5   1.32
IMAGp998M02131    KIAA1892    KIAA1892 (KIAA1892), mRNA     NM_015397   25853
      0.1   -0.26 -0.42 -0.1  -0.79 -0.65 0.19  0.04  -0.02 -0.34 -0.19 -0.17 -
0.02  -0.2  0.61  0.68  1.7   1.06
IMAGp998J15154    KIF2  kinesin heavy chain member 2 (KIF2), mRNA NM_004520
      3796  -0.66 0.2   -0.81 -0.42 -0.95 -0.17 0.15  -0.05 0     -0.98 0.23
      0.22  0.25  -0.15 0.69  0.45  1.4   1.01
IMAGp998L16376    KIF23 Kinesin family member 23            9493  -0.42 -0.39 -
0.84  -0.35 -0.18 -1.16 -0.06 0.32  0.09  -0.21 -0.01 -0.27 0.1   -0.26 0.73
      1.23  1.7   2.69
IMAGp998F051869   KIF4A kinesin family member 4A (KIF4A), mRNA    NM_012310
      24137 0.07  -0.33 -0.92 -0.7  -0.44 -0.99 0.08  -0.13 -0.57 0.5   -1.14 -
0.14  0.23  -0.31 0.61  0.63  1.2   1.09
IMAGp998O002205   KIF5B Kinesin family member 5B            3799  -0.52 -0.76 -
0.5   -1.06 -0.95 -0.93 0.09  -0.23 -0.57 0.26  -0.19 0.68  0.11  0.13  1.87
      1.52  1.2   2.05
IMAGp998N05221    KRT7  keratin 7 (KRT7), mRNA  NM_005556         -1.47 -0.85 -
1.89  -0.63 -1.48 -0.19 0.56  0.44  0.04  -0.34 -0.89 -0.04 0.14  0.01  1.62
      1.48  1.4   0.21
IMAGp998P091197   KTN1  kinectin 1 (kinesin receptor) (KTN1), mRNA
      NM_182926   3895  -0.59 -1.27 -0.35 -0.94 -0.1  -0.08 0.37  0.07  0.05  -
0.26  0.08  0.54  0.07  -0.01 1.37  0.88  0.9   0.82
IMAGp998I011898   LAMB1 laminin, beta 1 (LAMB1), mRNA NM_002291   3912  -1.56 -
1.28  -1.63 -0.92 -0.56 -0.69 0.03  0.66  0.68  0.13  -0.29 -0.04 -0.05 -0.59
      1.1   1.55  1.8   0.71
IMAGp998K211159   LAP3  leucine aminopeptidase 3 (LAP3), mRNA     NM_015907
      51056 -0.7  -0.12 -0.74 -0.32 -0.33 -1.17 -0.08 0.54  0     0.05  1.16
      0.61  0.25  -0.23 0.77  0.66  0.4   1.66
IMAGp998C231927   LDHAL6      lactate dehydrogenase A -like (LDHL), mRNA
      NM_033195         -1.04 -0.31 -1.22 -0.44 -0.48 -0.12 0.25  -0.34 -0.65 -
0.27  -0.27 -0.17 0.17  -0.5  1.25  1.13  0.9   0.9
IMAGp998D03220    LIFR  Leukemia inhibitory factor receptor       3977  -0.63 -
0.07  -0.72 -0.45 -0.38 -0.63 -0.07 0.04  -0.32 -0.16 -0.97 0.07  0.02  -0.08
      0.71  0.41  0.2   1.05
IMAGp998N14836    LMAN1 Lectin, mannose-binding, 1          3998  -0.59 -0.44 -
0.36  -1.05 -0.87 -0.9  0.51  -0.15 0.48  -0.13 0.09  0.01  0.05  0.22  1.37
      0.43  0.6   1.27
IMAGp998I151787   LOC112714   similar to alpha tubulin (LOC112714), mRNA
      XM_053177   113457      -1.17 -0.13 -1.61 -0.78 -1.69 -0.52 0.08  0.56  -
0.82  0.33  -1.33 -0.32 0.03  -0.71 1.26  1.3   0.3   0.95
IMAGp998O09892    LOC163782   Ankyrin repeat domain 38            163782      -
0.66  -0.35 -0.94 -0.38 -0.53 -0.76 0.12  0.22  -0.26 0.05  0.71  0.27  -0.14 -
0.29  0.12  0.46  0.3   0.49
IMAGp998C10188    LOC286148   Hypothetical protein LOC203107                  -
0.5   -0.29 -0.03 -0.45 0.19  -1.02 0.21  0.1   0.04  0.16  0.85  -0.2  -0.03
      0.1   0.74  0.33  0.9   1.18
IMAGp998I241928   LOC51252    Hypothetical protein LOC51252       51252 -1.05 -
0.04  -0.43 -0.38 0.35  0     0.03  -0.22 0.24  -0.08 0.85  -0.33 1.48  0.12
      1.12  0.71  0.6   2.46
IMAGp998L093815   LRPPRC      Leucine-rich PPR-motif containing         10128 -
1.39  -0.13 -1.21 -0.48 -1.43 -1.02 -0.04 0.07  -0.73 -0.38 -0.73 0.1   -0.26 -
0.51  0.93  1.34  1.5   1.28
```

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IMAGp998N13117    LTA4H leukotriene A4 hydrolase (LTA4H), mRNA    NM_000895
      -0.73 -0.3  -0.37 -0.04 0.21  0.26  0.3   0.2   0.54  0.22  0.57  0.31
      0.23  -0.12 1.09  0.95  1.7   0.63
IMAGp998I15695    LTBP1 latent transforming growth factor beta binding protein 1
(LTBP1), mRNA     NM_000627   4052  -0.55 -0.86 -0.39 -0.99 -0.5  -0.49 0.52
      0.05  0.24  -0.33 0.13  0.31  -0.23 0.26  1     0.51  1     0.14
IMAGp998B12591    LUC7A Cisplatin resistance-associated overexpressed protein
(LUC7A), mRNA     NM_016424         -0.61 -0.61 -0.14 -0.6  -0.16 0.13  0.23  -
0.02  0.23  0.05  -0.01 0.28  0.25  -0.19 1.34  0.99  1.2   0.63
IMAGp998J061888   LYCAT Lysocardiolipin acyltransferase           253558      -
0.54  -0.03 -0.63 -0.31 -0.36 -0.22 -0.18 -0.21 -0.03 -0.24 -0.3  0.08  -0.08 -
0.06  0.66  0.4   0.1   1.07
IMAGp998I222038   LZIC  Leucine zipper and CTNNBIP1 domain containing
      84328 -0.41 -0.36 -0.41 -0.23 -0.32 -0.88 0.12  0     -0.04 -0.23 0.62
      0.66  0.01  0.13  0.58  0.01  0.2   0.86
IMAGp998J21134    MAD2L1      MAD2 mitotic arrest deficient-like 1 (yeast)
(MAD2L1), mRNA    NM_002358   4085  -0.49 -0.6  -1.05 -1.61 -1.36 -1.78 0.42
      0.07  -0.13 0.04  0.82  0.47  0.65  -0.56 1.79  1.38  1.2   2.45
IMAGp998H161932   MAGED1      melanoma antigen, family D, 1 (MAGED1), mRNA
      NM_006986         -0.63 -0.58 -1.19 -1    -0.54 0.17  -0.05 -0.12 -0.04 -
0.29  -0.62 0.01  -0.09 0.01  0.61  0.49  -0.2  -0.15
IMAGp998H141937   MAN1A2      Mannosidase, alpha, class 1A, member 2
      10905 -0.77 -0.1  -0.65 -0.71 -0.9  -1.38 -0.06 -0.28 -0.41 -0.31 0.75
      0.11  -0.14 0.19  0.93  0.72  0.2   1.27
IMAGp998P20567    MAP3K7IP2   mitogen-activated protein kinase kinase kinase 7
interacting protein 2 (MAP3K7IP2), tra    NM_145342   23118 -0.75 -0.16 -0.5  -
0.57  -0.11 0.01  -0.06 -0.19 -0.38 -0.13 -0.22 0.32  -0.02 0.02  0.75  0.44
      0.4   0.23
IMAGp998G09383    MAPK14      mitogen-activated protein kinase 14 (MAPK14),
transcript variant 1, mRNA    NM_001315   1432  -0.51 -0.12 -0.53 -0.4  -0.46 -
0.63  -0.09 -0.08 -0.33 -0.32 0.26  -0.03 0.04  -0.44 0.53  0.66  0     0.52
IMAGp998P02643    MARK1 MAP/microtubule affinity-regulating kinase 1 (MARK1),
mRNA  NM_018650         -0.09 -0.69 0.02  -1.01 -0.81 -0.18 0.6   -0.19 -0.38 -
1.08  -1    0.08  0.52  -0.23 1.55  1.45  1.5   1.28
IMAGp998I151748   MBD2  methyl-CpG binding domain protein 2 (MBD2), transcript
variant 1, mRNA   NM_003927   8932  -0.69 -0.62 -0.58 -0.87 -0.55 -0.45 0.33
      0.04  0.02  -0.08 0.16  0.01  0.08  0.14  0.57  0.27  0.2   0.18
IMAGp998N11792    MCFD2 multiple coagulation factor deficiency 2 (MCFD2), mRNA
      NM_139279   90411 -0.39 -0.89 -0.45 -1.24 -0.88 -1.11 0.28  -0.23 -0.18 -
0.3   0.24  0.54  0.09  0.18  1     0.47  0.1   0.94
IMAGp998H122977   MCP   membrane cofactor protein (CD46, trophoblast-lymphocyte
cross-reactive antigen) (MCP),      NM_172361         -0.25 -0.63 0.2   -0.88 -
0.2   -0.27 0.62  -0.16 0.84  -0.21 0.17  0.5   0.29  0.36  1.28  0.3   1.9
      0.96
IMAGp998O08642    METAP2      methionyl aminopeptidase 2 (METAP2), mRNA
      NM_006838   10988 -0.87 -0.83 -0.71 -0.91 -1.07 -1.43 0.1   0     -0.09
      0.16  0.5   0.63  0.38  -0.34 1.38  1.31  1.2   0.87
IMAGp998A222401   MGC11242    Hypothetical protein MGC11242       79170 -0.01 -
0.84  0.03  -1    -0.67 -0.42 0.72  -0.34 0.29  -0.49 -0.32 0.71  0.22  0.25
      1.44  0.68  0.6   0.04
IMAGp998N165945   MGC20579    Family with sequence similarity 70, member B
      348013      -1.21 -0.82 -0.73 0.04  -0.57 -2.39 0.75  -1.36 1.02  -0.69 -
0.66  -0.1  0.93  1.46  1.36  -0.45 1.2   0.54
IMAGp998O23668    MID1  Midline 1 (Opitz/BBB syndrome)            4281  -0.15 -
0.8   -0.98 -0.54 -0.26 -0.66 -0.54 -0.43 0.14  -0.13 0.13  0.32  0.08  0.09
      1.05  0.85  0.5   0.63
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IMAGp998F12245    MKLN1 Muskelin 1, intracellular mediator containing kelch
motifs            4289  -1.43 -0.49 -0.37 -0.14 -0.59 -0.96 -0.18 -0.16 0.26
      0.12  0.57  0.15  -0.06 0.06  0.93  0.57  0.2   0.97
IMAGp998K13881    MNAT1 menage a trois 1 (CAK assembly factor) (MNAT1), mRNA
      NM_002431   4331  -0.81 -0.67 -0.63 -0.51 -0.7  -0.6  -0.16 -0.06 -0.47 -
0.21  -0.03 0.31  0.12  -0.28 0.74  0.96  0     0.74
IMAGp998J16123    MOBK1B      MOB1, Mps One Binder kinase activator-like 1B
(yeast)           55233 -0.45 -0.64 -0.35 -1.15 -0.4  -0.5  0.5   -0.35 0.15  -
0.74  -0.61 -0.04 0.13  0.38  1.44  0.67  0.5   1.41
IMAGp998C20296    MOCS2 molybdenum cofactor synthesis 2 (MOCS2), transcript
variant 2, mRNA   NM_183418   4338  -1.36 -0.45 -1.49 -0.6  -0.85 -0.63 0.03
      0.25  -0.35 0     -0.51 0.02  0.08  -0.53 0.36  0.82  1.3   0.69
IMAGp998A122331   MORF4L1     mortality factor 4 like 1 (MORF4L1), mRNA
      NM_006791         -0.1  -0.69 -0.24 -0.63 -0.35 -0.57 0.51  0.13  0.34  -
0.04  1.17  0.53  0.41  -0.23 1.51  1.05  0.5   0.96
IMAGp998P131831   MPHOSPH6    M-phase phosphoprotein 6 (MPHOSPH6), mRNA
      NM_005792   10200 -1.27 0.08  -0.73 -0.11 -0.27 -1.07 0.28  0.13  0
      0.07  -0.48 0.07  0.33  -0.41 0.69  0.64  0.9   1.77
IMAGp998B16471    MPP6  membrane protein, palmitoylated 6 (MAGUK p55 subfamily
member 6) (MPP6), mRNA  NM_016447   51678 -1.58 0.01  -1.33 -0.61 -0.82 -1.05 -
0.3   -0.23 -0.11 -0.38 -1.09 -0.5  -0.34 -0.48 0.06  0.46  0.9   0.04
IMAGp998F10422    MRPL3 Mitochondrial ribosomal protein L3 (MRPL3), nuclear gene
encoding Mitochondrial protein      NM_007208   11222 -0.79 -0.49 -0.71 -0.87 -
0.62  -1.31 0.13  -0.16 -0.27 -0.62 0.51  0.17  0.19  -0.11 1.33  0.96  0.4
      0.61
IMAGp998B11727    MRPL50      Mitochondrial ribosomal protein L50 (MRPL50),
nuclear gene encoding Mitochondrial prote NM_019051   54534 -0.91 -0.96 -0.77 -
1.23  -0.64 -0.66 0.07  -0.28 0.1   -0.21 -0.21 0.05  0.26  -0.16 0.91  0.6
      1.7   0.92
IMAGp998G16732    MRPL50      Mitochondrial ribosomal protein L50 (MRPL50),
nuclear gene encoding Mitochondrial prote NM_019051   54534 -1.1  -0.84 -0.83 -
1.13  -0.21 -0.51 -0.07 -0.26 -0.1  -0.18 0.12  0.4   0.15  -0.21 1.02  0.67
      1.9   1
IMAGp998K131999   MRPS10      Mitochondrial ribosomal protein S10 (MRPS10),
nuclear gene encoding Mitochondrial prote NM_018141   55173 -0.56 -0.23 -0.38 -
0.37  -0.12 -1.06 0     -0.19 0.01  -0.23 0.87  0.17  0.32  -0.12 0.76  0.72
      0.1   0.85
IMAGp998C24650    MRPS23      Mitochondrial ribosomal protein S23 (MRPS23),
nuclear gene encoding Mitochondrial prote NM_016070   51649 -0.44 -0.47 -0.4  -
0.39  -0.31 -0.75 0.04  -0.29 -0.14 -0.67 0.28  0.05  0.59  -0.09 1.31  0.75
      0.4   0.83
IMAGp998C09646    MRPS35      Mitochondrial ribosomal protein S35 (MRPS35),
nuclear gene encoding Mitochondrial prote NM_021821         -0.47 -0.33 -0.43 -
0.11  -0.64 -0.7  -0.47 -0.22 -0.39 -0.12 0.53  0.21  0.17  -0.25 1.19  1.08  0
      1.02
IMAGp998N09516    MSI2  Musashi homolog 2 (Drosophila)            124540      -
0.55  -0.26 -0.62 -0.41 -0.79 -0.99 0.16  0.12  0.09  0.18  0.89  0.04  -0.24 -
0.35  0.25  0.26  0.4   0.9
IMAGp998G191115   MTCH2 Mitochondrial carrier homolog 2 (C. elegans) (MTCH2),
nuclear gene encoding mitochondri   NM_014342   23788 -0.57 -0.3  -0.29 -0.43 -
0.16  -1.04 0.16  -0.11 -0.17 -0.48 0.84  0.29  -0.01 -0.15 0.61  0.44  0.4
      0.65
IMAGp998P18114    MTRR  5-methyltetrahydrofolate-homocysteine methyltransferase
reductase (MTRR), transcript va     NM_002454   4552  -0.07 -0.58 -0.08 -0.61 -
0.28  -0.46 0.04  -0.17 -0.29 -0.73 -0.19 -0.2  -0.08 0.11  0.3   0.5   0.3
      0.89
```

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IMAGp998N012010   MYBL1 v-myb myeloblastosis viral oncogene homolog (avian)-like
1 (MYBL1), mRNA   XM_034274         -0.23 -0.86 0.01  -1.29 -0.59 -0.28 0.53  -
0.02  0.61  -1.1  -0.71 0.19  0.23  0.71  1.2   -0.06 0.8   0.93
IMAGp998D171775   MYC   v-myc myelocytomatosis viral oncogene homolog (avian)
(MYC), mRNA NM_002467   4609  -1    0.24  -0.53 -0.1  -0.37 -0.45 -0.02 -0.12 -
0.21  0.08  -0.01 -0.01 -0.06 -0.04 0.59  0.51  0.8   1.03
IMAGp998C09561    MYCBP c-myc binding protein (MYCBP), mRNA NM_012333         -
0.27  -0.08 -0.42 -0.1  -0.19 -0.81 -0.01 0.12  -0.17 0.28  0.59  0.25  0.26  -
0.34  0.57  0.49  0.5   1.12
IMAGp998H01379    MYO1B myosin IB (MYO1B), mRNA XM_290989   4430  -0.86 -0.19 -
1.34  -0.54 -0.85 -0.53 -0.28 -0.32 -0.37 -0.26 -0.19 -0.13 -0.21 -0.23 0.59
      0.66  0.9   0.1
IMAGp998E031722   NAP1L napsin B pseudogene (NAP1L), misc RNA     XR_000169
      256236      -0.09 -0.32 -0.41 -0.27 -1.09 0.16  0.12  -0.21 -0.22 0.13
      0.01  0.16  0.24  0.26  0.08  0.16  0.9   1.07
IMAGp998G202010   NCF4  neutrophil cytosolic factor 4, 40kDa (NCF4), transcript
variant 1, mRNA   NM_000631         -1.9  -1.75 -2.61 -1.7  -1.83 -2.82 1.19
      0.36  0.08  -0.67 -0.61 -0.18 0.47  -0.48 2.16  2.28  1.7   2.44
IMAGp998F09192    NCKAP1      NCK-associated protein 1 (NCKAP1), mRNA
      NM_013436   10787 -0.2  -0.71 -0.16 -0.7  -0.21 -0.31 0.13  -0.06 -0.32
      0.13  0.21  0.61  -0.21 0.34  1.2   0.77  0.5   1.38
IMAGp998C09872    NDEL1 nudE nuclear distribution gene E homolog like 1 (A.
nidulans) (NDEL1), mRNA NM_030808   81565 -0.53 -0.19 -0.69 -0.18 -0.31 -0.31 -
0.18  -0.14 -0.24 -0.29 -0.63 -0.48 -0.16 0.02  0.45  0.29  1.1   0.53
IMAGp998F07443    NDUFA10     NADH dehydrogenase (ubiquinone) 1 alpha
subcomplex, 10, 42kDa         4705  -1.25 -0.38 -0.8  -0.2  -0.6  -0.72 -0.09
      0.22  0.17  0.09  0.54  0.36  -0.23 -0.15 0.43  0.39  0.8   0.39
IMAGp998C16517    NEDD4 neural precursor cell expressed, developmentally down-
regulated 4 (NEDD4), mRNA     NM_198400         -0.69 -0.66 -0.38 -0.65 -0.35 -
0.58  -0.04 -0.01 -0.37 0.13  -0.39 -0.48 -0.09 -0.23 2.45  0.54  1.5   0.71
IMAGp998K23921    NEDD5 neural precursor cell expressed, developmentally down-
regulated 5 (NEDD5), mRNA     NM_004404   4735  -0.03 -0.63 -0.02 -0.66 -0.28 -
0.62  0.35  -0.03 -0.24 -0.38 0.5   0.3   0.13  -0.06 0.9   0.67  0     0.44
IMAGp998H10785    NEDD5 neural precursor cell expressed, developmentally down-
regulated 5 (NEDD5), mRNA     NM_004404   4735  -0.03 -0.62 -0.05 -0.57 -0.4  -
0.63  0.13  0.26  -0.42 -0.18 0.01  0.08  0.01  -0.15 0.82  0.87  0     0.31
IMAGp998H161888   NF2   neurofibromin 2 (bilateral acoustic neuroma) (NF2),
transcript variant 2, mRNA    NM_016418   4771  -0.73 -0.17 -0.92 -0.16 -0.44 -
0.83  -0.15 0.13  -0.36 -0.06 0.61  -0.02 0.13  -0.44 0.47  0.76  0.3   0.55
IMAGp998A20687    NFYB  nuclear transcription factor Y, beta (NFYB), mRNA
      NM_006166   4801  -0.54 -0.24 -0.37 -0.29 -0.64 -0.19 0.51  0.2   0.02
      0.4   0.1   0.05  0.09  -0.42 0.94  0.95  0.5   0.72
IMAGp998I13529    NGRN  mesenchymal stem cell protein DSC92 (NEUGRIN), mRNA
      NM_016645   51335 -0.39 -0.24 -0.54 -0.7  -0.61 -0.09 0.23  0.01  0.08  -
0.22  -0.3  0.2   0.22  -0.23 0.75  0.52  0.2   -0.08
IMAGp998D121005   NIPA2 non-imprinted in Prader-Willi/Angelman syndrome 2
(NIPA2), mRNA     NM_030922   23191 -1.13 0.4   -1.28 -0.12 -0.37 -1.84 -0.2  -
0.17  -0.69 -0.51 -0.61 0.17  0.14  -0.18 0.67  0.78  1.2   0.61
IMAGp998A131725   NMI   N-myc (and STAT) interactor (NMI), mRNA   NM_004688
      9111  -0.72 -0.6  -0.75 -0.51 0.02  -0.19 0.16  0.38  0.19  0.13  0.74
      0.44  0.31  -0.51 0.52  0.66  0.7   0.91
IMAGp998H025601   NOLA1 nucleolar protein family A, member 1 (H/ACA small
nucleolar RNPs) (NOLA1), transcript v     NM_032993   54433 -0.87 -1.41 -1.01
      0.05  -1.35 -0.97 0.36  -0.2  -0.25 -0.48 -1.15 -0.27 0.23  0.06  0.83
      0.83  -0.4  0.46
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IMAGp998O21642    NRCAM neuronal cell adhesion molecule (NRCAM), mRNA
      NM_005010         -0.85 -0.4  -1.05 -0.74 -0.98 -1.64 -0.44 -0.2  -0.63 -
0.29  0.55  0.39  -0.09 0.03  0.18  0.36  0.7   1.11
IMAGp998L211205   NRP1  neuropilin 1 (NRP1), mRNA     NM_003873         -0.89 -
0.45  -0.66 -0.85 -0.13 -0.78 0.56  0.37  -0.35 -0.77 -0.34 -0.2  -0.19 0.28
      1.38  0.99  1.9   1.11
IMAGp998J02870    NS3TP1      HCV NS3-transactivated protein 1 (NS3TP1), mRNA
      NM_019048   54529 -1.42 -0.54 -1.12 -0.65 -0.37 -0.75 -0.38 -0.38 -0.35 -
0.12  -0.2  -0.49 -0.12 -0.39 0.52  0.55  1.4   -0.29
IMAGp998G07613    NSF   N-ethylmaleimide-sensitive factor (NSF), mRNA
      NM_006178         -1.03 -0.72 -0.36 -0.93 -0.21 -0.78 0.18  -0.09 -0.23 -
0.49  -0.3  -0.22 0.15  -0.04 1.17  0.01  1     -0.16
IMAGp998E11660    NSMAF neutral sphingomyelinase (N-SMase) activation associated
factor (NSMAF), mRNA    NM_003580         -0.25 -0.46 -0.38 -0.49 -0.14 -0.45
      0.17  -0.29 -0.12 -0.38 -0.54 0.27  0.01  -0.06 0.38  0.72  0     0.48
IMAGp998I151945   NTHL1 nth endonuclease III-like 1 (E. coli) (NTHL1), mRNA
      NM_002528         -0.35 -0.84 -0.03 -0.73 -0.22 -1.23 0.16  -0.3  0.08  -
0.55  0.79  -0.05 0.13  0.16  1.19  0.51  0.8   0.69
IMAGp998N191936   NUDT9 nudix (nucleoside diphosphate linked moiety X)-type
motif 9 (NUDT9), transcript variant NM_198039   53343 -0.87 -0.21 -0.92 -0.33 -
0.43  -0.84 -0.34 0.09  -0.16 -0.19 0.22  0.22  -0.06 -0.06 0.37  0.61  0.5
      0.37
IMAGp998F021787   NUDT9 nudix (nucleoside diphosphate linked moiety X)-type
motif 9 (NUDT9), transcript variant NM_198039   53343 -0.73 -0.12 -0.7  -0.32 -
0.39  -0.76 -0.2  0.13  -0.07 0.25  0.32  0.29  -0.18 0.04  0.18  0.27  0
      0.29
IMAGp998D17244    NUP107      nuclear pore complex protein (NUP107), mRNA
      NM_020401   57122 -0.04 -1.08 -0.86 -0.9  -0.73 -0.89 0.09  0.02  0.14
      0.15  0.2   -0.08 0.19  -0.03 1.2   0.83  1.2   0.97
IMAGp998E01631    NUP153      Nucleoporin 153kDa (NUP153), mRNA   NM_005124
      9972  -0.54 -0.99 -0.27 -1.02 -0.58 -0.43 -0.14 -0.51 -0.18 -0.67 -0.59
      0.15  -0.23 0.39  0.5   -0.09 0.7   0.79
IMAGp998N04179    NUP155      Nucleoporin 155kDa (NUP155), transcript variant 1,
mRNA  NM_153485         -0.35 -0.72 -1.11 -0.81 -0.93 -0.84 -0.22 -0.17 -0.17 -
0.04  0.23  -0.04 0.18  -0.43 0.24  0.38  0.5   0.88
IMAGp998M221166   NUP205      Nucleoporin 205kDa      NM_015135   23165 -0.35 -
0.78  -0.17 -1.01 -0.01 -2.08 0.73  -0.44 0.61  -0.63 0.74  0.01  0.35  0.78
      1.16  0.06  0.5   0.62
IMAGp998F15369    NUP37 Nucleoporin Nup37 (Nup37), mRNA     NM_024057   79023 -
0.68  -0.19 -0.48 -0.57 -0.27 -0.67 0.14  -0.08 0.03  -0.27 -0.37 0.32  0.41  -
0.28  1.31  1.09  0.9   1.33
IMAGp998F021780   NUP54 Nucleoporin 54kDa (NUP54), mRNA     NM_017426   53371 -
0.57  -0.28 -0.64 -0.52 -0.73 0.06  0.07  -0.21 -0.21 -0.31 -0.09 0.27  0.04
      0.25  0.66  0.44  0.5   2.32
IMAGp998D14670    NUSAP1      nucleolar and spindle associated protein 1
(NUSAP1), mRNA    NM_016359   51203 -0.01 -0.48 -1.07 -1.22 -1.38 -0.63 0.03  -
0.27  -0.43 0.07  -0.33 0.5   0.36  -0.33 1.69  1.51  0.6   1.69
IMAGp998M211869   OAT   Ornithine aminotransferase (gyrate atrophy) (OAT),
nuclear gene encoding mitochondrial NM_000274   4942  -0.64 -0.6  -0.26 -1.09 -
0.26  -0.67 0.68  0.29  0.39  -0.2  0.1   0.57  0.32  -0.08 0.98  0.35  1.5
      0.6
IMAGp998D12672    ODC1  Ornithine decarboxylase 1 (ODC1), mRNA    NM_002539
      4953  -0.42 -0.43 -0.72 -0.94 -0.35 -1.1  0.29  0.01  -0.76 -1.04 -0.03 -
0.18  0.59  -0.48 1.52  1.33  0.1   0.61
IMAGp998H05131    OGFRL1      Opioid growth factor receptor-like 1 (OGFRL1),
mRNA  NM_024576   79627 -0.94 -0.71 -1.12 -0.62 -0.24 -0.15 -0.26 -0.02 -0.38 -
0.26  -0.2  -0.03 -0.08 -0.39 0.46  0.53  0     0.41
```

```
IMAGp998N02421    OSBPL3      oxysterol binding protein-like 3 (OSBPL3),
transcript variant 6, mRNA    NM_145324   26031 -0.78 -0.61 -0.61 -0.36 -0.09
      0.03  -0.06 -0.15 -0.01 0.08  -0.38 -0.09 -0.01 -0.18 0.01  0.21  0.1
      0.21
IMAGp998G02646    OSTF1 Osteoclast stimulating factor 1           26578 -0.19 -
0.45  -0.68 -0.56 -0.77 -0.28 0.12  0.33  -0.19 -0.16 -0.12 -0.2  -0.15 -0.18 -
0.01  0.4   1.5   1.08
IMAGp998N181795   PABPC1      poly(A) binding protein, cytoplasmic 1 (PABPC1),
mRNA  NM_002568   5042  -0.31 -1.01 -0.24 -1.02 -0.37 -1.25 0.4   -0.04 0.37  -
0.01  0.63  0.96  -0.1  0.46  1.12  0.61  0.5   1.26
IMAGp998E15620    PAICS phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxami   NM_006452         -1.11 -0.79 -
1.65  -1.12 -0.83 -0.83 -0.26 0.2   -0.62 -0.15 -1.45 -0.88 0.03  -0.5  0.93
      1.1   0.9   -0.06
IMAGp998C021205   PAIP1 poly(A) binding protein interacting protein 1 (PAIP1),
transcript variant 3, mRNA    NM_183323   10605 -0.97 -0.66 -0.86 -0.8  -0.28 -
0.61  -0.05 0.04  -0.22 -0.31 0.21  0.32  -0.06 -0.37 0.97  0.89  1.5   0.08
IMAGp998B071199   PAIP1 poly(A) binding protein interacting protein 1 (PAIP1),
transcript variant 3, mRNA    NM_183323         -0.85 -0.99 -0.65 -0.86 -0.54 -
0.64  0.04  -0.08 -0.1  -0.37 -0.11 0.07  0.14  -0.28 0.27  0.91  1.6   0.34
IMAGp998M04841    PCNA  proliferating cell nuclear antigen (PCNA), transcript
variant 2, mRNA   NM_182649   5111  -0.55 -1    -0.73 -1.18 -0.61 -0.6  0.78
      0.14  0.77  0.09  0.55  0.53  0.16  0.08  0.94  0.33  0.6   0.85
IMAGp998D0486     PCNA  proliferating cell nuclear antigen (PCNA), transcript
variant 2, mRNA   NM_182649   5111  -0.66 -1.13 -0.91 -1.43 -0.15 -0.74 0.78
      0.36  0.76  0.42  1.24  0.22  0.09  -0.04 0.86  0.49  0.9   0.66
IMAGp998E05199    PDCD10      programmed cell death 10 (PDCD10), transcript
variant 3, mRNA   NM_145860   11235 -0.67 -0.36 -0.09 -0.59 -0.37 0.12  0.28  -
0.15  0.07  -0.34 -0.18 0.27  0.27  -0.19 0.97  0.48  0.2   0.83
IMAGp998C112979   PDCD8 programmed cell death 8 (apoptosis-inducing factor)
(PDCD8), nuclear gene encoding mito NM_145813   9131  -0.74 -0.08 -0.99 -0.22 -
0.76  -0.15 -0.29 0.29  -0.39 -0.27 -0.07 0.02  0.09  -0.39 0.47  0.88  0.5
      0.34
IMAGp998G161157   PDCL3 phosducin-like 3 (PDCL3), mRNA      NM_024065   79031 -
0.56  -0.34 -0.88 -0.38 -0.38 -0.43 0     0.05  -0.31 0.03  0.21  -0.19 0.12  -
0.51  1.23  1.4   1.6   2.08
IMAGp998G053500   PDCL3 phosducin-like 3 (PDCL3), mRNA      NM_024065   79031 -
1.24  0.41  -1.31 0.02  -0.81 -0.34 0.05  0.05  -0.57 0.05  -0.23 0.12  0.04
      3.22  1.02  1.25  1.5   0.33
IMAGp998J021165   PDE7B phosphodiesterase 7B (PDE7B), mRNA  NM_018945   27115 -
0.21  -0.46 -0.54 -0.77 -0.24 -1.19 0.33  0.07  -0.1  -0.42 0.23  0.03  0.43  -
0.18  1.7   1.25  0.6   1.12
IMAGp998L10643    PDHX  pyruvate dehydrogenase complex, component X (PDHX), mRNA
      NM_003477   8050  -1.1  -0.14 -0.87 -0.62 -0.85 -0.74 -0.09 -0.14 -0.07
      0.02  0.02  0.19  -0.05 0     0.67  0.5   1.1   0.37
IMAGp998O11603    PDLIM1      PDZ and LIM domain 1 (elfin) (PDLIM1), mRNA
      NM_020992   9124  -0.16 -0.6  -0.14 -0.44 -0.17 0.21  -0.02 0.07  0.06
      0.12  0.21  0.21  0.04  0.04  0.83  0.53  0     0.67
IMAGp998F211933   PFKM  phosphofructokinase, muscle (PFKM), mRNA  NM_000289
      -0.58 -0.73 -0.09 -0.82 -0.72 -0.94 0.32  -0.1  0.43  -0.69 0.93  0.68
      0.25  0.43  1.2   0.3   1     1.26
IMAGp998L01525    PGM2  phosphoglucomutase 2 (PGM2), mRNA   NM_018290   55276 -
0.69  -1.18 -0.95 -0.89 -3.57 -0.64 0.06  0.31  -0.16 -0.05 -0.39 0.09  -0.06 -
0.44  0.52  0.72  0.7   0.47
IMAGp998M241118   PGM3  phosphoglucomutase 3 (PGM3), mRNA   NM_015599   5238  -
0.81  -0.18 -0.95 -0.42 -0.76 -1.45 0.15  0.18  0.1   0.42  1.39  0.56  0.04  -
0.24  0.24  0.38  0.9   1.55
```

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IMAGp998C213904   PHTF1 putative homeodomain transcription factor 1 (PHTF1),
mRNA  NM_006608         -0.39 -0.01 -0.19 -0.34 -0.09 -0.48 0.41  -0.06 0.23  -
0.06  0.66  0.25  0.4   0.09  0.69  0.57  0.8   1.08
IMAGp998P19602    PIK3CA      phosphoinositide-3-kinase, catalytic, alpha
polypeptide (PIK3CA), mRNA    NM_006218   5290  -0.49 -0.19 -0.28 -0.15 -0.2  -
0.42  0.25  0.34  0.06  -0.01 -0.17 0.63  -0.28 0.03  0.66  0.5   1.3   0.99
IMAGp998A192002   PIP3AP      phosphatidylinositol-3-phosphate associated
protein (PIP3AP), mRNA  NM_019061   54545 -0.41 -0.84 -0.18 -0.92 0.11  -0.28
      0.2   -0.17 -0.29 0.12  -0.41 -0.24 0.13  0.04  1.25  0.77  0.3   1.37
IMAGp998E22473    PIR   Pirin (PIR), mRNA NM_003662   8544  -0.87 -0.16 -1.15 -
0.32  -0.62 -0.89 -0.15 0.46  0.07  0.02  0.52  0.14  0.05  -0.66 0.09  0.63
      0.6   1.03
IMAGp998F12383    PLK2  Polo-like kinase 2 (Drosophila) (PLK2), mRNA
      NM_006622         -0.54 -0.41 -0.34 -0.58 -0.42 -0.59 -0.38 -0.43 -0.31
      0.05  0.16  0.25  -0.2  0.26  0.54  0.35  -0.3  0.36
IMAGp998B22257    PLK4  Polo-like kinase 4 (Drosophila) (PLK4), mRNA
      NM_014264   10733 -1.12 0     -0.8  -0.91 -0.39 -1.2  0.12  -0.2  -0.13 -
0.3   0.09  0.16  0.09  -0.18 0.58  0.37  0.5   0.59
IMAGp998F19569    PLOD2 Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine
hydroxylase) 2 (PLOD2), transc      NM_000935   5352  -0.49 0.23  -0.77 -0.24 -
0.53  -1.31 -0.37 -0.07 -0.37 0.1   0.06  0.13  -0.44 -0.04 0.69  1.06  1
      1.04
IMAGp998K09590    PMSCL1      Polymyositis/scleroderma autoantigen 1, 75kDa
(PMSCL1), mRNA    NM_005033   5393  -1.52 -0.49 -1.42 -0.99 -0.06 -0.73 -0.5
      0.04  -0.5  0     -0.2  -0.29 -0.43 -0.21 0.47  0.71  0.2   0.14
IMAGp998C02631    PNPT1 Polyribonucleotide nucleotidyltransferase 1 (PNPT1),
mRNA  NM_033109   87178 -0.81 -0.21 -0.98 -0.35 -0.41 -0.37 -0.35 -0.07 -0.31
      0.1   -0.55 -0.24 0     -0.55 1.09  1.52  0.5   1.06
IMAGp998G071937   POLE2 Polymerase (DNA directed), epsilon 2 (p59 subunit)
(POLE2), mRNA     NM_002692         -0.54 -0.43 -0.69 -0.44 -0.43 -1.68 0.21  -
0.02  0.29  0.22  0.28  0     -0.15 -0.04 0.17  0.26  0.3   0.31
IMAGp998P242008   POLR1B      Polymerase (RNA) I polypeptide B, 128kDa (POLR1B),
mRNA  NM_019014   84172 -0.61 -0.5  -0.38 -0.38 -0.16 -1.72 0.34  -0.36 0.23  -
0.26  0.35  -0.51 0.33  -0.14 1.02  0.84  1.2   0.35
IMAGp998G20400    POLR2K      Polymerase (RNA) II (DNA directed) polypeptide K,
7.0kDa (POLR2K), mRNA   NM_005034         -0.35 -0.3  -0.15 -0.34 -0.45 -0.62
      0.3   0.13  -0.05 0.07  1.2   0.18  0.28  -0.2  1.14  0.76  0.6   0.66
IMAGp998N17150    PP    Pyrophosphatase (inorganic) (PP), mRNA    NM_021129
      5464  -1.68 -0.31 -1.85 -0.19 -0.29 -0.83 0     0.1   -0.56 -1.68 -0.37 -
0.04  0.17  -0.34 1.02  1.12  1     0.79
IMAGp998B12325    PPARBP      PPAR binding protein          5469  -0.67 -0.22 -1
      -0.22 -0.49 -0.64 -0.15 0.05  -0.12 0.04  -0.66 0.18  -0.29 -0.29 0.43
      0.29  1.2   0.6
IMAGp998M07660    PPAT  phosphoribosyl pyrophosphate amidotransferase (PPAT),
mRNA  NM_002703   5471  -1.18 -0.58 -0.81 -0.76 -0.42 -0.97 -0.45 -0.46 -0.42 -
0.01  -0.72 0.54  -0.12 -0.02 0.04  0.33  -0.3  1.68
IMAGp998F23578    PPP1CB      Protein phosphatase 1, catalytic subunit, beta
isoform (PPP1CB), mRNA  NM_002709         -0.28 -0.41 -0.15 -0.35 -0.25 -0.73
      0.24  0.16  -0.2  0.01  0.17  0.35  -0.35 0.18  0.73  0.51  0.6   1.01
IMAGp998H01617    PPP1CC      Protein phosphatase 1, catalytic subunit, gamma
isoform (PPP1CC), mRNA  NM_002710   5501  -0.58 -0.51 -0.05 -0.81 -0.42 -0.92
      0.19  -0.42 -0.17 -0.57 -0.28 0.4   0.18  0.03  1.49  0.93  0.9   0.8
IMAGp998N171933   PRC1  Protein regulator of cytokinesis 1 (PRC1), transcript
variant 3, mRNA   NM_199414   9055  0     -0.34 -1    -1.17 -0.94 -0.83 0.27  -
0.29  -0.46 -1.03 -0.64 -0.47 0.4   -0.25 1.83  1.35  0.5   1.36
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IMAGp998G243521   PRDX6 peroxiredoxin 6 (PRDX6), mRNA NM_004905   9588  -0.59 -
0.51  -0.61 -0.81 -0.65 0     0.6   0.06  0.6   0.02  0.07  0.43  0.18  0.05
      0.95  0.58  -0.2  0.67
IMAGp998E171156   PRKACB      Protein kinase, cAMP-dependent, catalytic, beta
(PRKACB), transcript variant 1, mRNA      NM_182948   5567  -1.11 -0.54 -0.74 -
0.89  -0.94 -1.36 -0.16 -0.11 -0.21 0.13  0.58  0.59  -0.22 -0.03 0.59  0.44
      0.4   0.65
IMAGp998A03646    PRKCN Protein kinase C, nu (PRKCN), mRNA  NM_005813   23683 -
0.79  -0.29 -0.27 -0.35 -0.44 -0.18 0.11  -0.18 0.49  -0.18 -0.09 -0.22 0.05
      0.33  0.92  0.36  1     2.03
IMAGp998H101937   PRKDC Protein kinase, DNA-activated, catalytic polypeptide
(PRKDC), mRNA     NM_006904   5591  -0.31 -0.38 -0.59 -0.66 -0.52 -0.02 0.24  0
      -0.25 -0.28 0.61  0.43  0.22  -0.13 1.46  1.08  0.5   1.13
IMAGp998B10117    PRKRA Protein kinase, interferon-inducible double stranded RNA
dependent activator (PRKRA), m      NM_003690   8575  -0.65 -0.33 -0.38 -0.34 -
0.23  -1    0.04  -0.27 -0.11 -0.03 0.34  0.4   0.11  -0.02 0.77  0.3   0
      1.1
IMAGp998B14677    PRPF18      PRP18 pre-mRNA processing factor 18 homolog
(yeast) (PRPF18), mRNA  NM_003675   8559  -1.12 0.01  -0.97 -0.3  -0.7  -0.43 -
0.04  0     -0.32 0.04  -0.44 0.34  0.23  -0.76 1.12  1.09  0.2   1.16
IMAGp998M011964   PSAT1 Phosphoserine aminotransferase 1 (PSAT1), transcript
variant 1, mRNA   NM_058179   29968 -0.48 -0.62 -1.5  -2.02 -2.06 -1.7  0.06  -
0.62  -0.05 -0.56 0.09  0     0.03  0.2   0.72  0.11  -0.1  0.26
IMAGp998J20593    PSD3  ADP-ribosylation factor guanine nucleotide factor 6
(EFA6R), mRNA     NM_015310   23362 0.2   -0.26 0.11  -0.11 -0.11 -0.29 0.02  -
0.04  0.24  -0.23 -0.04 0.04  -0.15 0.33  1.33  0.96  1.1   1.29
IMAGp998L101118   PSMA3 proteasome (prosome, macropain) subunit, alpha type, 3
(PSMA3), transcript variant 1, m    NM_002788   5684  -0.91 -0.41 -1.03 -0.55 -
0.84  -1.21 -0.24 0.34  -0.61 0.13  0.19  0.04  0.12  -0.56 0.74  1.13  0.2
      0.69
IMAGp998H16402    PSMA5 proteasome (prosome, macropain) subunit, alpha type, 5
(PSMA5), mRNA     NM_002790   5686  -0.17 -0.52 -0.21 -0.5  -0.18 -0.76 0.21  -
0.06  -0.06 -0.46 0.65  -0.06 0.41  -0.29 1.27  0.89  0.6   1.15
IMAGp998F042585   PSMA5 proteasome (prosome, macropain) subunit, alpha type, 5
(PSMA5), mRNA     NM_002790   5686  -0.52 -0.42 -0.54 -0.27 -0.07 0.12  0.14  -
0.01  -0.2  -0.1  -0.21 -0.43 0.38  -0.36 1.26  0.88  1.2   0.59
IMAGp998N22698    PSMA6 proteasome (prosome, macropain) subunit, alpha type, 6
(PSMA6), mRNA     NM_002791   5687  -0.33 -0.59 -0.57 -0.48 -0.53 -0.17 0.08
      0.21  -0.43 -0.12 0.16  -0.02 0.29  -0.33 0.58  0.57  0.1   0.36
IMAGp998E231726   PSMC1 proteasome (prosome, macropain) 26S subunit, ATPase, 1
(PSMC1), mRNA     NM_002802   5700  -0.3  -0.86 -0.31 -0.74 -0.43 -0.59 0.33
      0.24  0.11  0.01  0.49  -0.13 0.44  -0.02 1.23  0.87  0.4   0.57
IMAGp998H07420    PSMC2 proteasome (prosome, macropain) 26S subunit, ATPase, 2
(PSMC2), mRNA     NM_002803   5701  -0.74 -0.55 -0.96 -0.56 -0.48 -0.81 -0.12
      0.2   -0.24 -0.18 -0.48 0.16  0.28  -0.59 0.49  1.2   0.1   -0.05
IMAGp998K02101    PSMC2 proteasome (prosome, macropain) 26S subunit, ATPase, 2
(PSMC2), mRNA     NM_002803   5701  -0.75 -0.4  -1.04 -0.41 -1.25 -0.32 -0.06
      0.26  -0.92 -0.16 -0.35 0.2   0.15  -0.57 0.93  1.16  0.9   0.72
IMAGp998P2197     PSMD1 proteasome (prosome, macropain) 26S subunit, non-ATPase,
1 (PSMD1), mRNA   NM_002807         -1.7  -0.59 -1.72 -0.84 -0.81 -1.54 0.05
      0.13  -0.32 0.07  -0.49 -0.37 0.39  -0.65 1.58  1.82  1.9   0.98
IMAGp998C201163   PTK9  PTK9 protein tyrosine kinase 9 (PTK9), transcript
variant 2, mRNA   NM_198974   5756  -0.26 -0.6  -0.24 -0.31 -0.16 -0.45 0.21
      0.2   -0.09 0.28  -0.21 0.32  -0.04 0.09  0.53  0.47  0.9   1.35
IMAGp998N01880    PTPDC1      Protein tyrosine phosphatase domain containing 1
            138639      -0.12 -0.52 -0.83 -1.15 -0.72 -0.49 0.57  0.53  -0.1  -
0.42  -0.64 0.17  0.52  -0.56 1.52  1.12  1.2   0.61
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IMAGp998F211165   PTS   6-pyruvoyltetrahydropterin synthase (PTS), mRNA
      NM_000317   5805  -0.46 -0.48 -0.41 -0.63 -0.28 -0.81 0.05  -0.28 -0.57 -
0.92  -0.26 -0.19 0.24  -0.14 0.85  0.69  0     0.47
IMAGp998O06523    PURB  Purine-rich element binding protein B           5814  -
0.21  -0.12 -0.23 -0.2  -0.19 -0.48 0.15  -0.02 -0.11 -0.25 0.32  -0.28 0.12
      0.1   0.81  0.44  0     0.43
IMAGp998D23974    PXMP3 peroxisomal membrane protein 3, 35kDa (Zellweger
syndrome) (PXMP3), mRNA NM_000318   5828  -0.16 -0.19 -0.53 -0.24 -0.22 -0.43
      0.24  0.05  0.09  0.41  0.18  0.26  0.33  -0.63 0.7   1.09  1.6   0.73
IMAGp998E1983     Q9Y645      "DNA HELICASE HOMOLOG (FRAGMENT).
[Source:SPTREMBL;Acc:Q9Y645]" XM_290643         -0.35 0.2   -0.9  -0.44 -0.55 -
1.37  -0.49 -0.02 -0.25 -0.57 -0.21 -0.42 0.44  -0.61 1     0.89  0.9   1.36
IMAGp998O131155   RAB10 RAB10, member RAS oncogene family (RAB10), mRNA
      NM_016131   10890 -0.59 -0.66 -0.43 -0.48 0.03  -0.12 -0.15 -0.39 -0.14 -
0.39  -0.09 -0.11 0.1   -0.06 0.71  0.45  1.3   0.04
IMAGp998K04612    RAB11A      RAB11A, member RAS oncogene family        8766  -
0.11  -0.5  -0.07 -0.8  -0.34 0.05  0.47  -0.08 0.07  -0.23 -0.27 0.05  0.21
      0.23  0.91  0.36  0.7   0.47
IMAGp998K074785   RAB2  RAB2, member RAS oncogene family (RAB2), mRNA
      NM_002865   5862  -0.86 0.2   -1.42 -0.16 -1.1  -1.15 -0.33 -0.12 -0.48 -
0.82  -0.19 -0.19 -0.05 -0.24 0.71  0.24  0.4   -0.06
IMAGp998N072035   RAB23 RAB23, member RAS oncogene family         51715 -0.68 -
0.42  -0.45 -0.56 0.12  -1.1  -0.13 -0.09 -0.02 -0.25 0.33  -0.22 -0.17 -0.01
      0.21  0.35  0.9   1.02
IMAGp998P03136    RAB3B RAB3B, member RAS oncogene family         5865  -0.24 -
0.78  -0.45 -1.03 -0.43 -0.54 0.38  -0.43 -0.36 -0.57 -0.23 -0.63 0.09  0.22
      0.79  0.26  -0.5  1.16
IMAGp998F191927   RABL5 RAB, member of RAS oncogene family-like 5 (RABL5), mRNA
      NM_022777         -0.79 -0.4  -1.23 -0.36 -0.83 -0.08 -0.09 0.31  -0.22
      0.24  -0.26 -0.32 -0.35 -0.02 0.21  0.45  0     0.13
IMAGp998P161782   RACGAP1     Rac GTPase activating protein 1 (RACGAP1), mRNA
      NM_013277   29127 -0.59 0.01  -1.44 -1    -0.95 -1.27 0.13  -0.03 -0.39 -
0.61  -0.58 0.07  0.41  -0.51 1.29  0.74  2.2   -0.41
IMAGp998J071856   RAD21 RAD21 homolog (S. pombe) (RAD21), mRNA    NM_006265
      5885  -0.39 -0.52 -0.33 -1.27 0.04  -0.25 0.57  -0.14 -0.01 0.18  -0.58
      0.61  0.09  0.28  1.52  0.85  0.8   1.51
IMAGp998J034316   RAD21 RAD21 homolog (S. pombe) (RAD21), mRNA    NM_006265
      5885  -0.46 -0.17 -1.01 0.32  -1.02 -1.15 0.57  -0.36 0     -1.09 -0.29
      0.04  0.22  0.34  1.62  0.84  0.2   1.28
IMAGp998L07472    RAF1  v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1),
mRNA  NM_002880   23609 -0.5  -0.25 -0.6  -0.4  -0.51 -0.56 -0.23 -0.12 -0.26 -
0.24  0.32  -0.16 -0.09 -0.03 0.48  0.52  -0.3  0.58
IMAGp998K031009   RANBP1      RAN binding protein 1 (RANBP1), mRNA
      NM_002882   5902  -0.68 -0.07 -1.04 -0.69 -0.4  -0.36 0.09  0.01  -0.31 -
0.32  -0.33 0.01  0.12  -0.53 0.09  0.77  1.2   0.52
IMAGp998I041165   RANBP2      RAN binding protein 2 (RANBP2), mRNA
      NM_006267   5903  -0.93 -0.54 -0.69 -0.44 -0.51 -0.52 -0.19 -0.06 -0.29
      0.14  0.11  0.75  -0.05 -0.21 0.68  0.9   0.3   0.83
IMAGp998O03840    RANBP9      RAN binding protein 9 (RANBP9), mRNA
      NM_005493   10048 -0.39 -0.08 -0.13 -0.42 -0.21 -0.28 -0.09 -0.27 0
      0.09  0.61  0.31  -0.12 0.01  0.55  0.37  0.3   0.86
IMAGp998P0577     RAP1A RAP1A, member of RAS oncogene family (RAP1A), mRNA
      NM_002884   5906  -0.93 -0.27 -1.24 -0.09 -0.78 -1.06 0.31  -0.21 0.31  -
1.5   0.43  -0.62 0.09  0.16  1.24  0.76  0.5   0.38
IMAGp998C09110    RAP1GDS1    RAP1, GTP-GDP dissociation stimulator 1
(RAP1GDS1), mRNA  NM_021159         -0.74 -0.43 -0.86 -0.73 -0.7  -0.63 0.12  -
0.08  -0.34 -0.35 -0.66 -0.15 0.07  -0.42 0.84  0.73  0.8   0.45
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IMAGp998B14385    RBBP7 retinoblastoma binding protein 7 (RBBP7), mRNA
      NM_002893         -0.43 -0.57 -0.7  -0.96 -0.58 -0.75 0.29  0     -0.26 -
0.51  0.55  0.31  0.15  -0.08 0.95  0.59  0     0.57
IMAGp998K131889   REPS1 RALBP1 associated Eps domain containing 1 (REPS1), mRNA
      NM_031922         -0.6  -0.57 -0.3  -0.98 -0.34 -0.15 -0.06 -0.42 0.06  -
0.87  -0.64 0.08  -0.03 -0.03 1.04  0.69  2.2   0.92
IMAGp998G171933   RFC3  Replication factor C (activator 1) 3, 38kDa
      NM_002915   5983  -0.48 -0.61 -0.64 -1.1  -0.47 -1.84 0.31  -0.39 0.14  -
0.42  0.56  0     0.2   0.08  0.9   0.31  -0.2  0.05
IMAGp998M01695    RFC4  Replication factor C (activator 1) 4, 37kDa (RFC4),
transcript variant 2, mRNA    NM_181573         -0.84 -0.32 -1.18 -0.63 -1.22 -
0.79  0.29  0.51  0.02  0.74  -0.07 0.22  -0.06 -0.3  0.26  0.3   0.6   -0.07
IMAGp998F191792   RFX1  Regulatory factor X, 1 (influences HLA class II
expression) (RFX1), mRNA      NM_002918         -0.78 -0.41 -0.65 -0.37 -1.1  -
0.22  -0.37 0.14  0.03  -0.24 0.37  -0.03 -0.26 0.1   0.01  0.31  0.6   0.58
IMAGp998K20882    RFXAP Regulatory factor X-associated protein (RFXAP), mRNA
      NM_000538   5994  -0.71 -0.23 -0.4  -0.51 -0.39 -0.65 0.18  0.36  0.65  -
0.14  -0.02 0.04  2.25  -0.06 0.28  0.21  0.4   1.97
IMAGp998M22367    RHOA  Ras homolog gene family, member A (ARHA), mRNA
      NM_001664   387   0     -0.6  0.1   -0.67 -0.07 -0.65 0.51  -0.02 -0.05 -
0.1   0.93  0.14  0.07  0.08  1.66  1.15  0.8   1.26
IMAGp998F17438    RNASE3L     Ribonuclease III, nuclear           29102 0.25  -
0.41  -0.77 -0.37 -0.08 -0.26 0.13  0.1   0.23  -0.27 -0.08 -0.14 0.56  0.53
      0.18  0.61  0     0.01
IMAGp998H211827   RNF134      Ring finger protein 134 (RNF134), mRNA
      NM_032154   84108 -0.45 -0.49 -0.43 -0.58 -0.75 -0.49 -0.08 -0.12 -0.04
      0.02  -0.41 0.15  -0.25 0.21  0.1   0.18  0.5   0.62
IMAGp998D141924   RNF138      Ring finger protein 138 (RNF138), transcript
variant 1, mRNA   NM_016271   51444 -0.96 -0.5  -0.18 -0.68 -0.73 -1.17 0
      0.04  -0.44 0.17  0.24  0.08  -0.24 0.18  0.47  0.44  0.4   1.23
IMAGp998C013858   RNF2  Ring finger protein 2         6045  -0.38 -0.82 -0.24 -
0.86  -0.74 -1.01 0.56  0.07  0.1   -0.07 1.04  -0.03 0.3   -0.16 1.25  0.79
      0.5   0.85
IMAGp998L012009   RPN2  Ribophorin II (RPN2), mRNA    NM_002951         -1.13 -
0.08  -1.27 -0.32 -1    -0.31 0.42  0.08  -0.22 -0.46 -0.46 -0.19 0.04  -0.45
      0.62  1.32  0.2   0.68
IMAGp998I07358    RPP30 Ribonuclease P (30kD) (RPP30), mRNA NM_006413   10556 -
0.67  -0.47 -0.99 -0.41 -0.81 -0.5  -0.18 -0.21 -0.33 -0.25 -0.26 0.16  0.33  -
0.36  0.77  0.81  0.2   0.04
IMAGp998G03694    RPS3A Ribosomal protein S3A (RPS3A), mRNA NM_182777         -
0.27  -0.84 -0.61 -0.68 -0.33 0.3   0.29  0.36  -0.23 0.08  -0.19 0.08  0.32  -
0.47  0.89  0.85  0.6   0.35
IMAGp998P07203    RRAS2 Related RAS viral (r-ras) oncogene homolog 2 (RRAS2),
mRNA  NM_012250   22800 -0.48 -0.84 -0.22 -0.75 -0.63 -0.31 0.07  -0.18 -0.61 -
0.36  -0.41 0.4   0.01  0.03  0.79  0.57  0.7   1.38
IMAGp998J01977    RRM2  Ribonucleotide reductase M2 polypeptide (RRM2), mRNA
      NM_001034   6241  -0.68 -0.31 -1.46 -1.17 -0.85 -0.92 -0.06 0.01  -0.35 -
0.01  0.34  -0.26 0.1   -0.18 0.82  0.73  0.3   0.19
IMAGp998E19311    RRM2B Ribonucleotide reductase M2 B (TP53 inducible) (RRM2B),
mRNA  NM_015713   50484 -0.71 -0.74 -0.07 -0.62 -0.38 -1.11 0.37  -0.05 0.36
      0.08  0.68  -0.18 0.22  -0.04 1.46  0.83  0.7   1.25
IMAGp998M15620    RTCD1 RNA terminal phosphate cyclase domain 1 (RTCD1), mRNA
      NM_003729   8634  -0.59 -0.49 -0.51 -0.42 -0.22 -0.22 0.23  0.16  -0.1  -
0.03  -0.16 0.51  0.16  -0.25 0.96  0.77  0.7   0.49
IMAGp998E05168    RTN4  Reticulon 4 (RTN4), mRNA      NM_007008   57142 -1.25
      0.03  -1.54 -0.02 -1.12 -0.31 0.33  0.45  -1.25 0.43  -1.21 0.43  0.21  -
0.41  2.59  2.62  1.6   2.01
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IMAGp998P14882    RTN4  Reticulon 4 (RTN4), mRNA      NM_020532         -0.3  -1
      -0.44 -1.07 -0.83 -0.61 0.53  0.27  -1.3  -0.68 -0.86 0.52  0.45  -0.33
      2.97  2.66  2     2.54
IMAGp998P182573   RTN4  Reticulon 4 (RTN4), mRNA      NM_007008   57142 -0.62 -
0.71  -0.71 -0.97 -0.81 -0.07 0.44  0.27  -1.11 -1.03 -1.54 -0.34 0.36  -0.46
      2.43  2.3   1.6   1.81
IMAGp998E085767   RTN4  Reticulon 4 (RTN4), mRNA      NM_007008   57142 -0.35 -
0.05  -0.72 0     -1.11 0.08  0.63  -0.23 0.23  0.4   -0.89 -0.21 0.39  0.41
      1.71  0.88  0.8   1.6
IMAGp998P073628   RUNX2 Runt-related transcription factor 2 (RUNX2), mRNA
      NM_004348         -0.35 -0.21 -0.47 -0.5  -0.51 -0.5  0.09  0.09  -0.27
      0.13  0.36  0.5   0.19  -0.2  1.02  0.77  0.4   0.59
IMAGp998D161907   RWDD1 RWD domain containing 1 NM_015952   51389 -0.9  -0.31 -
0.74  -0.27 0.04  -1.57 -0.07 0.37  -0.17 -0.1  1     0.07  0.19  -0.34 0.97
      0.97  0.8   0.19
IMAGp998C212936   SCAMP1      secretory carrier membrane protein 1 (SCAMP1),
transcript variant 1, mRNA    NM_004866         -0.53 -0.48 -0.19 -0.53 -0.07 -
0.6   0.01  -0.33 -0.23 -0.21 0.61  0.25  0.12  0.11  0.98  0.23  0     0.57
IMAGp998O24380    SDHD  succinate dehydrogenase complex, subunit D, integral
membrane protein (SDHD), nuclear g  NM_003002   6392  -0.9  -0.62 -0.67 -0.66 -
0.64  -0.58 0.29  0.26  0.14  -0.06 0.96  0.11  -0.01 -0.07 0.97  0.73  1.5   1
IMAGp998D221852   SEC23A      Sec23 homolog A (S. cerevisiae) (SEC23A), mRNA
      NM_006364   10484 -0.77 -0.85 -0.53 -0.73 -0.78 -0.91 0.25  0.1   0.02
      0.37  0.65  0.57  -0.09 -0.06 0.61  0.23  0.1   0.06
IMAGp998C18167    SEC24B      SEC24 related gene family, member B (S.
cerevisiae) (SEC24B), mRNA    NM_006323   10427 -0.45 -0.27 -0.68 -0.04 -0.58 -
0.33  0.12  -0.28 -0.06 -0.34 0.18  -0.51 0.02  0.12  0.77  0.67  2.5   1.63
IMAGp998F05646    SEC24D      SEC24 related gene family, member D (S.
cerevisiae) (SEC24D), mRNA    NM_014822   9871  -0.74 -1.19 -0.49 -1.22 -0.01 -
0.58  0.18  -0.7  0.25  -0.12 0.12  0.2   -0.16 0.57  1.23  0.43  0.8   1.63
IMAGp998O19186    SEC24D      SEC24 related gene family, member D (S.
cerevisiae) (SEC24D), mRNA    NM_014822   9871  -0.6  -0.43 -0.47 -0.92 -0.52 -
0.6   0.03  -0.18 0.02  -0.03 0.12  0.08  -0.26 0.15  0.66  0.54  1     1.53
IMAGp998K02358    SENP6 SUMO-1-specific protease (SUSP1), mRNA    NM_015571
      26054 -1.28 -0.7  -0.95 -0.8  -0.57 -0.33 -0.04 0.02  -0.4  -0.17 -0.21
      1.02  -0.21 -0.3  0.24  0.31  1     1.4
IMAGp998L08642    SESN3 Sestrin 3         143686      -0.11 -0.48 -0.2  -0.58 -
0.77  0.4   0.33  0.01  -0.24 0.03  -0.44 0.21  0.17  -0.15 0.77  0.69  0.8
      0.9
IMAGp998H05595    SET   SET translocation (myeloid leukemia-associated) (SET),
mRNA  NM_003011         -0.31 -0.63 -0.51 -0.74 -0.56 -0.68 0.3   0.06  -0.25 -
0.22  0.97  0.16  0.3   -0.15 1.27  0.97  0     0.42
IMAGp998H235501   SF3B3 Splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA
      NM_012426         -0.77 0.43  -1.06 -0.56 0.09  -1.39 -0.21 0.05  -0.67 -
0.62  0.15  0.28  0.29  -0.05 1.15  0.89  1.4   0.76
IMAGp998K05583    SFRS10      Splicing factor, arginine/serine-rich 10
(transformer 2 homolog, Drosophila) (SFRS10),   NM_004593   6434  -0.32 -0.83 -
0.54  -1.14 -0.73 -0.6  0.44  -0.09 -0.33 -0.15 -0.6  -0.03 0.16  -0.03 0.55  -
0.03  0.5   -0.36
IMAGp998K131167   SFRS11      Splicing factor, arginine/serine-rich 11 (SFRS11),
mRNA  NM_004768   9295  -0.71 -0.57 -0.39 -0.67 -0.38 -0.24 -0.03 -0.28 -0.23
      0.02  -0.07 0.41  0.01  0.01  1.58  1.29  1.4   1.16
IMAGp998O121170   SFRS11      Splicing factor, arginine/serine-rich 11 (SFRS11),
mRNA  NM_004768   9295  -0.81 -0.45 -0.51 -0.44 -0.03 -1.34 -0.08 -0.02 -0.29 -
0.07  0.1   0.82  -0.14 -0.22 1.3   1.11  1     1.59
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IMAGp998D2317     SFRS3 Splicing factor, arginine/serine-rich 3 (SFRS3), mRNA
      NM_003017         -1.34 0.2   -1.43 0.14  -0.63 -1.86 -0.09 -0.5  -0.37 -
0.99  -0.22 0.26  0.24  0     1.32  0.85  2.3   1.62
IMAGp998H07193    SFRS4 Splicing factor, arginine/serine-rich 4 (SFRS4), mRNA
      NM_005626   6429  -1    -0.25 -1.02 -0.65 -0.73 -1.02 -0.14 -0.02 -0.37 -
0.66  -0.4  -0.38 -0.29 -0.13 0.91  1.04  1     1.05
IMAGp998M031746   SIP1  Survival of motor neuron protein interacting protein 1
(SIP1), mRNA      NM_003616         -0.9  0.01  -0.82 -0.46 -1.08 -0.61 -0.06
      0.02  -0.15 -0.02 -0.16 0.23  0.2   -0.78 0.8   0.67  1.1   1.53
IMAGp998C012010   SIP1  Survival of motor neuron protein interacting protein 1
(SIP1), mRNA      NM_003616   8487  -0.84 -0.12 -1.1  -0.49 -1.04 -0.65 0     -
0.12  0.67  0.17  0.08  0.14  0.2   -0.96 0.73  0.67  0.9   1.17
IMAGp998K09679    SKIIP SKI-interacting protein (SNW1), mRNA      NM_012245
      22938 -0.81 -0.18 -0.45 -0.58 -0.52 -0.59 -0.1  -0.13 -0.27 -0.06 0.65
      0.23  0.29  -0.24 1.28  1.2   0.5   1.15
IMAGp998O08191    SLC16A1     Solute carrier family 16 (monocarboxylic acid
transporters), member 1 (SLC16A1), mRNA   NM_003051   6566  -0.6  -0.22 -0.71 -
0.37  -0.41 -0.86 -0.32 -0.24 -0.87 -0.39 0.03  0.36  -0.27 0.2   0.31  0.28
      0.3   0.9
IMAGp998G17247    SLC30A5     Solute carrier family 30 (zinc transporter),
member 5 (SLC30A5), mRNA      NM_022902         -0.75 -0.14 -0.86 -0.4  -0.39 -
0.64  -0.15 0.4   -0.35 -0.29 -0.14 0.06  -0.35 -0.1  0.23  0.31  0.4   -0.13
IMAGp998K1393     SLC35B1     Solute carrier family 35, member B1 (SLC35B1),
mRNA  NM_005827   10237 -0.3  -0.19 -0.66 -0.21 -0.55 -0.79 -0.07 0.05  -0.3  -
0.2   0.78  -0.45 0.06  -0.04 0.65  0.58  0.4   0.41
IMAGp998I052037   SLC35B1     Solute carrier family 35, member B1 (SLC35B1),
mRNA  NM_005827   10237 -0.34 -0.21 -0.77 -0.12 -0.52 -0.45 -0.03 -0.02 -0.14 -
0.37  -0.24 -0.34 0.12  -0.1  0.96  0.75  1.2   0.13
IMAGp998K21671    SLC35B3     Solute carrier family 35, member B3 (SLC35B3),
mRNA  NM_015948   51000 -0.34 -0.15 -0.37 -0.07 -0.71 -0.73 -0.14 0.24  -0.17
      0.16  0.33  0.22  0.1   -0.18 0.33  0.49  0     0.77
IMAGp998P091722   SLC35F5     Solute carrier family 35, member F5 (SLC35F5),
mRNA  NM_025181         -0.3  -0.42 0.05  -0.33 0.09  -0.36 0.36  0.27  0.44  -
0.14  0.9   0.18  0.12  0.17  1.01  0.62  0.7   1.09
IMAGp998P12221    SLC39A8     Solute carrier family 39 (zinc transporter),
member 8 (SLC39A8), mRNA      NM_022154   64116 -0.8  -0.03 -1.21 -0.57 -0.98 -
1.27  -0.08 0.15  -0.16 -0.09 -0.27 0.13  -0.25 -0.14 -0.03 0.44  1.2   0.39
IMAGp998N173850   SLC4A1AP    Solute carrier family 4 (anion exchanger), member
1, adaptor protein (SLC4A1AP), mRNA NM_018158   22950 -0.94 -0.03 -2.09 -0.67 -
0.91  -1.29 -0.06 0.33  -0.44 0.12  -0.95 0.18  -0.08 -0.53 0.43  0.75  1.6
      1.44
IMAGp998P0693     SLC9A6      Solute carrier family 9 (sodium/hydrogen
exchanger), isoform 6 (SLC9A6), mRNA      NM_006359         -0.38 -0.26 -0.25 -
0.54  0.06  0.12  -0.32 -0.03 -0.05 -0.04 0.14  0.25  0.03  0.14  0.35  0.19
      0.2   0.57
IMAGp998H19228    SMAD5 SMAD, mothers against DPP homolog 5 (Drosophila)
      4090  -0.35 -0.03 0.06  -0.45 -0.27 0.04  0.14  -0.25 -0.08 0.17  -0.27
      0.41  0.07  0.16  0.79  0.29  0.6   0.66
IMAGp998E10314    SMARCA4     SWI/SNF related, matrix associated, actin
dependent regulator of chromatin, subfamily a   NM_003072   6597  -0.79 -0.17 -
0.97  -0.32 -0.95 -1.24 -0.3  -0.02 -0.49 -0.29 0.14  -0.17 -0.01 -0.12 -0.02
      0.23  0     0.15
IMAGp998C04270    SMBP  SM-11044 binding protein            56889 -1.26 0.01  -
1.1   -0.2  -1.03 -0.26 -0.03 0.17  -0.68 -0.49 -0.33 0.37  -0.12 -0.21 0.89
      0.83  0.4   0.33
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IMAGp998P0884	SMC1L1	SMC1 structural maintenance of chromosomes 1-like 1 (yeast) (SMC1L1), mRNA	NM_006306	8243	-0.45	-0.39	-0.6	-1.04	-0.65	-0.57	0.04	-0.35	-0.25	-0.94	-0.52	0.13	-0.15	0.13	0.25	-0.04	0.4	1.01
IMAGp998B111962	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast) (SMC4L1), mRNA	NM_005496	10051	-0.85	-0.56	-1.24	-1.19	-1.38	-1.41	0.01	-0.24	-0.53	-0.48	-0.24	0.2	0.01	-0.24	1.67	1.62	1.4	1.96
IMAGp998L111794	SMS	spermine synthase (SMS), mRNA	NM_004595		0.01	-0.48	0.1	-0.68	-0.35	-0.66	0.55	0	-0.19	-0.04	-0.13	0.27	0.06	0.16	1.33	0.61	0	0.96
IMAGp998D192035	SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA	NM_003082	6617	-0.63	-0.18	-0.43	-0.37	-1.02	-1.04	0.28	0.04	0.04	-0.05	0.46	0.04	0.3	0.14	2.01	1.32	1.2	1.73
IMAGp998D08646	SNX3	sorting nexin 3 (SNX3), transcript variant 1, mRNA	NM_003795	8724	-0.13	-1	-0.15	-0.78	-0.48	-0.77	0.44	0.08	0.29	-0.26	0.79	0.22	0.17	0.14	1.58	1.04	0.9	1.13
IMAGp998L061167	SNX4	sorting nexin 4 (SNX4), mRNA	NM_003794	8723	-0.09	-0.76	0.15	-0.74	-0.29	-0.21	0.42	-0.42	0.21	-0.23	-0.35	0.14	0.19	0.08	1.08	0.35	1.1	1.49
IMAGp998J19535	SOCS5	suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, mRNA	NM_144949	9655	0.15	-0.1	-0.23	-0.26	-0.57	-0.51	0.07	-0.07	-0.31	0.01	-0.25	0.23	-0.03	-0.03	0.95	0.64	0.9	1.54
IMAGp998A051793	SRP19	Signal recognition particle 19kDa (SRP19), mRNA	NM_003135	6728	-1.1	-0.52	-0.82	-0.64	-0.37	-0.64	-0.27	-0.33	-0.31	-0.22	-0.36	-0.01	-0.02	-0.4	0.08	0.64	1.1	-0.48
IMAGp998I185323	SRP54	Signal recognition particle 54kDa (SRP54), mRNA	NM_003136	6729	-0.16	-0.55	-0.82	0.07	-0.15	-0.15	1.58	-0.2	-0.09	-0.23	0.12	0.73	0.38	-0.06	1.37	1.34	1.3	0.85
IMAGp998B23841	SRP68	Signal recognition particle 68kDa (SRP68), mRNA	NM_014230	6730	-0.86	-0.19	-0.83	-0.51	-0.68	-0.77	-0.42	-0.3	-0.46	-0.37	0.07	-0.3	0.02	-0.1	0.55	0.41	-0.1	-0.34
IMAGp998G22206	SSFA2	sperm specific antigen 2 (SSFA2), mRNA	NM_006751	6744	-0.71	-0.47	-0.08	-0.72	-0.16	-1.01	0.18	-0.29	0.03	-0.42	0.4	0.33	-0.07	0.21	1.2	0.6	0	1
IMAGp998I12734	SSR1	Signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA	NM_003144	6745	-1.33	-0.56	-1.46	-1.03	-1.68	-1.42	0.02	0.04	-0.26	0.02	-0.26	-0.13	0.28	-0.36	0.83	0.93	0.3	0.67
IMAGp998J21420	SSR1	Signal sequence receptor, alpha (translocon-associated protein alpha)		6745	-0.76	-0.58	-0.79	-0.72	-0.99	-0.74	-0.17	-0.08	-0.45	-0.24	0.16	-0.1	0.15	-0.43	0.84	0.78	0	0.61
IMAGp998I22869	SSR1	Signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA	NM_003144	6745	-0.22	-0.27	-0.35	-0.87	-0.72	-0.37	0.16	0.08	0.21	-0.31	0.12	0.78	0.05	-0.07	0.74	0.22	1	0.83
IMAGp998G241904	SSR1	Signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA	NM_003144	6745	-0.62	-0.48	-0.67	-0.74	-0.23	-0.98	0.08	-0.04	-0.08	0.27	0.77	0.73	0.01	-0.2	0.98	0.86	0.4	1.68
IMAGp998F21595	STAM	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA	NM_003473	8027	-0.47	-0.07	-0.36	-0.61	-0.82	-0.22	-0.06	-0.29	-0.07	0.33	-0.11	0.26	-0.05	0.22	0.55	0	0.3	0.84
IMAGp998A14177	STXBP3	syntaxin binding protein 3 (STXBP3), mRNA	NM_007269	6814	0.03	-0.13	-0.88	-0.08	-0.71	-0.94	0.16	0.19	0.33	-1.24	0.14	0.22	-0.14	0.15	1.42	0.97	0.6	1.48
IMAGp998I23116	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae) (SUPT16H), mRNA	NM_007192	11198	-0.56	-0.17	-0.62	-0.59	-0.46	-1	0.27	-0.01	-0.36	-0.42	0.45	-0.12	0	-0.49	0.73	0.33	0	0.72
IMAGp998L041161	SYNJ2	synaptojanin 2 (SYNJ2), mRNA	NM_003898	8871	-0.34	-0.41	-0.82	-0.07	-0.08	-0.6	-0.15	0.26	0.15	-0.32	0.28	-0.32	-0.03	-0.37	1.33	1.3	2.2	0.93

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IMAGp998K05821    SYNJ2BP     synaptojanin 2 binding protein (SYNJ2BP), mRNA
      NM_018373          -1.21 -0.74 -1.17 -0.67 -1.2  -1.21 0.02  0.02  -0.14
      0.47  0.62  0.18  -0.22 0.25  1.41  1.4   0.5   1.19
IMAGp998L0885     TAF7  TAF7 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 55kDa (TAF7),    NM_005642   6879  -1.47 -0.35 -1.28 -0.48 -
0.84  -0.93 -0.11 0.3   -0.4  -0.1  0.3   -0.26 -0.15 0.63  1.22  1.62  0.4
      1.51
IMAGp998H23880    TAF9  TAF9 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 32kDa (TAF9),    NM_016283   5884  -0.85 -0.31 -0.58 -0.34 -
0.3   -1.3  -0.52 -0.27 -0.75 -0.54 -0.38 -0.24 0.08  -0.26 0.7   0.86  0
      0.95
IMAGp998E09175    TARS  threonyl-tRNA synthetase (TARS), mRNA     NM_152295
      6897  -2.97 -1.01 -2.81 0.79  -1.53 -1.85 -0.34 -0.32 -0.82 -1.05 0.08
      0.04  -0.05 -0.41 1.3   1.57  2.4   0.81
IMAGp998M2018     TCERG1      transcription elongation regulator 1 (CA150)
(TCERG1), mRNA    NM_006706   10915 -0.63 -0.53 -0.44 -0.72 -0.02 -0.76 0.02  -
0.37  -0.41 -0.61 -0.34 -0.19 -0.18 0.15  1     0.79  -0.2  1.1
IMAGp998L061202   TCP1  t-complex 1 (TCP1), mRNA      NM_030752   6950  -0.33 -
0.66  -0.94 -0.87 -0.5  -0.64 0.07  0.07  -0.2  0.12  0.3   0.15  -0.13 0.22
      0.4   0.09  -0.2  -0.08
IMAGp998D23618    TEX10 Testis expressed sequence 10        54881 -0.27 -0.14 -
0.5   -0.39 -0.5  -0.86 0.13  0.15  0.43  -0.16 -0.13 0.23  -0.35 0.1   -0.1
      0.12  0.3   0.3
IMAGp998B171780   TFAP2C      transcription factor AP-2 gamma (activating
enhancer binding protein 2 gamma) (TFAP2C),     NM_003222   7022  -0.86 -0.29 -
1.28  -0.67 -0.98 -0.65 -0.01 -0.07 -0.51 -0.09 -0.71 0.67  -0.37 -0.37 0.17
      0.44  0     0.84
IMAGp998C12394    TFDP1 transcription factor Dp-1 (TFDP1), mRNA   NM_007111
      7027  -0.37 0.07  -0.35 -0.75 -0.71 -0.93 0.25  -0.17 -0.28 -0.12 0.03
      0.07  -0.2  0.17  1.01  0.48  0.3   1.23
IMAGp998K20778    THOC3 THO complex 3 (THOC3), mRNA   NM_032361   84321 -0.42
      0.13  -0.55 -0.4  -0.61 -0.43 0.05  0.06  -0.39 -0.12 0.07  -0.15 0.04  -
0.45  0.82  0.86  0.3   0.34
IMAGp998I08190    TIMM23      translocase of inner mitochondrial membrane 23
homolog (yeast) (TIMM23), mRNA      NM_006327   10431 -1.14 -0.52 -0.95 -0.87 -
1.11  -0.82 -0.11 -0.13 -0.58 -0.12 0.18  -0.3  0.16  -0.23 0.8   0.64  0
      0.58
IMAGp998L102037   TLE4  transducin-like enhancer of split 4 (E(sp1) homolog,
Drosophila) (TLE4), mRNA      NM_007005   11050 -0.6  -0.77 -0.82 -0.6  -0.42 -
0.54  -0.14 -0.17 -0.28 -0.59 -0.46 0.13  -0.02 -0.07 0.42  0.42  -0.6  0.82
IMAGp998K17667    TLOC1 translocation protein 1 (TLOC1), mRNA     NM_003262
      7095  -0.18 -0.36 0.03  -0.24 -0.19 -0.82 0.05  -0.19 -0.14 0.09  0.64
      0.24  0.16  0.12  0.91  0.48  0.3   0.9
IMAGp998J061897   TMEM19      hypothetical protein FLJ10936 (FLJ10936), mRNA
      NM_018279   55266 -0.34 -0.03 -0.34 -0.44 -0.43 -0.34 0.64  0.01  0.22  -
0.1   0.23  0.02  0.21  -0.07 0.71  0.42  0.4   0.82
IMAGp998A142002   TMEM23      mob protein (MOB), mRNA NM_147156   259230      -
0.27  -0.38 -0.1  -0.44 -0.27 -1.23 -0.04 -0.24 0.22  -0.53 0.62  0.06  -0.08
      0.55  0.62  -0.04 0.5   1.43
IMAGp998P041205   TMOD3 tropomodulin 3 (ubiquitous) (TMOD3), mRNA NM_014547
      29766 -0.86 -0.39 -0.65 -0.39 -0.77 -0.47 0.12  -0.12 0.12  -0.07 -1.13 -
0.3   0.01  -0.44 0.35  0.67  0.3   0.43
IMAGp998J151933   TNC   Tenascin C (hexabrachion)           3371  -0.77 -0.73 -
0.8   -0.89 -0.85 -0.66 0.43  0.54  0.37  0.21  0.31  0.22  0     -0.23 0.79
      0.9   2     1.16
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IMAGp998G031945   TNNT2 troponin T2, cardiac (TNNT2), mRNA  NM_000364         -
0.21  -0.95 -0.08 -1.09 -0.56 -0.73 0.61  -0.29 0.56  -0.08 -0.15 0.57  0.33
      0.06  1.31  0.58  0     0.21
IMAGp998I01384    TOPBP1      topoisomerase (DNA) II binding protein (TOPBP1),
mRNA  NM_007027   11073 -0.4  -0.65 -0.72 -0.7  -1.01 -0.92 -0.15 0.02  -0.16 -
0.38  0.08  0.13  0.01  -0.03 0.54  0.42  -0.1  1.01
IMAGp998J21697    TOR1B torsin family 1, member B (torsin B) (TOR1B), mRNA
      NM_014506   27348 -0.38 -0.16 -0.5  -0.14 -0.77 -0.85 -0.07 0.3   -0.27
      0.12  0.18  0.43  -0.23 -0.09 0.4   0.75  0.1   0.75
IMAGp998A13699    TPM3  tropomyosin 3 (TPM3), mRNA    NM_153649   7170  0.06  -
0.82  -0.23 -0.92 -0.47 -0.52 0.46  -0.04 -0.29 -0.67 0.33  -0.34 0.22  -0.04
      1.95  1.62  0.7   1.36
IMAGp998M1095     TPM3  tropomyosin 3 (TPM3), mRNA    NM_153649         -0.95 -
0.5   -1.15 -0.77 -0.53 -0.21 0.5   0.29  -0.3  -0.18 -0.99 0     0.17  -0.56
      2.32  2.4   1.8   1.86
IMAGp998F22731    TRA1  tumor rejection antigen (gp96) 1 (TRA1), mRNA
      NM_003299   7184  -0.48 -1.34 -0.42 -1.38 -0.24 -1.37 0.64  0.03  0.39  -
0.71  0.61  0.05  0.19  0.2   1.33  0.81  0.1   1.08
IMAGp998J231203   TRAM1 translocation associated membrane protein 1 (TRAM1),
mRNA  NM_014294   23471 -0.48 -0.57 -0.39 -0.86 -0.03 -0.3  0.28  0.03  0.27
      0.52  0.42  0.47  -0.05 0.03  1.61  1.24  1.3   1.19
IMAGp998A13650    TTRAP TRAF and TNF receptor associated protein (TTRAP), mRNA
      NM_016614   51567 -0.87 -0.35 -0.66 -0.31 0.24  -0.27 -0.21 0.03  -0.01 -
0.08  0.14  -0.02 0.03  -0.06 0.69  0.44  1.7   0.76
IMAGp998G09524    TUBA1 tubulin alpha 6 (TUBA6), mRNA NM_032704   10376 -0.24 -
0.53  -0.87 -1    -1.19 -0.47 0.34  0.2   -0.24 -0.29 -0.09 -0.21 0.27  -0.17
      1.26  1.18  0.3   0.86
IMAGp998D08167    TUBA1 tubulin, alpha 1 (testis specific) (TUBA1), mRNA
      NM_006000   8576  -1.43 -0.09 -2.17 0.02  -1.92 -0.85 0.19  0.16  -0.73 -
1.39  -0.38 -0.05 0.25  -0.18 1.19  0.96  0     0.43
IMAGp998D10123    TUBAL3      hypothetical protein FLJ21665 (FLJ21665), mRNA
      NM_024803   79861 -1.02 -0.18 -1.39 -0.56 -1.33 -0.73 -0.05 0.5   -0.61
      0.24  -0.3  -0.16 0.19  -0.58 0.69  1.42  0.5   1.16
IMAGp998L17389    TXNDC9      ATP binding protein associated with cell
differentiation (APACD), mRNA NM_005783   10190 -0.42 -0.79 -0.08 -0.89 -0.29
      0.13  0.18  -0.17 -0.3  -0.24 -0.65 -0.06 0.24  -0.25 1.43  1.09  1
      1.12
IMAGp998P161786   TYMS  thymidylate synthetase (TYMS), mRNA NM_001071   7298  -
1.33  -0.92 -2.09 -1.69 -1.96 -1.38 0.3   0.53  -0.65 -0.05 -0.81 0.37  0.5   -
0.73  1.25  1.38  1.6   0.72
IMAGp998F191931   UBE1DC1     ubiquitin-activating enzyme E1-domain containing 1
(UBE1DC1), transcript variant 2, mRN      NM_198329         -0.74 -0.3  -1.01 -
0.47  -0.99 -0.5  -0.25 0.06  0.01  0.2   -0.29 0.17  -0.16 -0.04 0.26  0.24  0
      0.48
IMAGp998L132037   UBE2G1      ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog,
C. elegans) (UBE2G1), transcript vari     NM_003342         -0.52 -0.94 -0.43 -
0.85  -0.52 -1.03 0.24  -0.5  -0.15 -0.98 0.45  -0.05 0.07  0.21  1.63  0.94
      0.6   1.18
IMAGp998M23888    UBE2J1      ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog,
yeast) (UBE2J1), mRNA   NM_016021   51465 -0.54 -0.06 -0.23 -0.22 -0.52 -0.37
      0.14  0.06  -0.08 0.15  0.56  0.24  -0.12 -0.11 0.45  0.67  0.9   1.6
IMAGp998A171819   UBE2Q ubiquitin-conjugating enzyme E2Q (putative) (UBE2Q),
mRNA  NM_017582   55585 -0.72 -0.34 -0.59 -0.61 -0.59 -0.01 0.02  -0.4  -0.02 -
0.06  -0.37 0.02  0.14  0.04  0.79  0.53  0     -0.18
IMAGp998L211794   UBE2V2      ubiquitin-conjugating enzyme E2 variant 2
(UBE2V2), mRNA    NM_003350   7336  -0.83 -1.03 -0.8  -1.05 -1.2  -1.03 0.03  -
0.24  -0.37 -0.15 -0.06 0.49  0.26  -0.04 0.86  0.61  0.1   0.96
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IMAGp998M15400    UBP1  upstream binding protein 1 (LBP-1a) (UBP1), mRNA
      NM_014517   7342  -0.28 -0.46 -0.12 -0.57 -0.53 -0.09 0.19  -0.13 -0.4  -
0.14  -0.04 0.04  -0.05 0.07  1     0.49  0.6   0.41
IMAGp998O14642    UBQLN2      ubiquilin 2 (UBQLN2), mRNA    NM_013444   29978 -
0.8   -0.57 -0.94 -0.95 -0.29 -0.53 0.04  0.27  -0.05 -0.15 -0.15 0.51  -0.19
      0.01  0.29  0.37  1     0.84
IMAGp998L22560    UCHL3 ubiquitin carboxyl-terminal esterase L3 (ubiquitin
thiolesterase) (UCHL3), mRNA  NM_006002   7347  -0.16 -0.96 0.04  -1.3  -0.68 -
0.66  0.29  -0.24 0.46  -0.68 0     0.03  0.33  0.35  0.89  0.18  0.3   0.54
IMAGp998O054015   UCHL3 ubiquitin carboxyl-terminal esterase L3 (ubiquitin
thiolesterase) (UCHL3), mRNA  NM_006002         -0.49 -0.31 -0.72 -0.65 -1.24 -
0.29  -0.09 0.05  -0.25 -0.41 -0.95 0.35  0.13  -0.22 0.61  0.42  0.8   0.92
IMAGp998M15836    UCHL5 Ubiquitin carboxyl-terminal hydrolase L5        51377 -
0.03  -0.61 -0.99 -0.54 -0.44 -0.89 -0.29 -0.05 -0.37 -0.16 -0.43 -0.12 -0.06 -
0.27  -0.16 0.23  0.2   0.77
IMAGp998D112573   UCHL5 ubiquitin carboxyl-terminal hydrolase L5 (UCHL5), mRNA
      NM_015984   51377 -0.82 -0.12 -1.57 -0.52 -1.55 -1.61 -0.5  0.6   -0.6
      0.21  -0.27 0.81  -0.07 -0.58 0.28  0.82  1.8   1.43
IMAGp998H091163   UGP2  UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
      NM_006759   7360  -0.37 -0.62 -0.2  -0.56 -0.37 -0.66 -0.05 -0.46 -0.44
      0.25  0.4   0.53  0.02  0.22  0.42  0.04  0     0.41
IMAGp998N221793   UPF3A UPF3 regulator of nonsense transcripts homolog A (yeast)
(UPF3A), transcript variant 2,      NM_080687   65110 -0.8  -0.55 -0.65 -0.59 -
0.43  -1.07 0.05  -0.18 0.04  0.01  -0.05 0.44  0.11  -0.2  0.89  0.53  0
      1.28
IMAGp998D131865   UQCRFS1     ubiquinol-cytochrome c reductase, Rieske iron-
sulfur polypeptide 1 (UQCRFS1), mRNA      NM_006003   7386  -0.84 -0.14 -0.37 -
0.65  -0.74 -0.53 0.03  0.16  0.17  -0.26 0.12  0.06  0.4   -0.12 0.79  0.51
      0.6   1.06
IMAGp998E144009   USP1  ubiquitin specific protease 1 (USP1), mRNA
      NM_003368   7398  -0.64 0.32  -0.64 -0.22 -0.83 -1.22 0.36  0.29  -0.04
      0.06  -0.42 0.08  -0.31 -0.2  0.72  1.08  1.8   2.41
IMAGp998L14516    USP10 ubiquitin specific protease 10 (USP10), mRNA
      NM_005153   9100  -0.51 -0.69 -0.46 -0.93 -0.35 -0.37 -0.15 -0.52 -0.22
      0.06  -0.27 0.11  -0.25 0.21  0.43  0.09  0.7   0.42
IMAGp998E09195    USP15 ubiquitin specific protease 15 (USP15), mRNA
      NM_006313   9958  -0.56 -0.56 -0.89 -0.38 -1.01 -1.11 -0.7  -0.1  -0.46
      0.17  0.19  0.69  -0.09 -0.25 0.52  0.85  0.4   0.72
IMAGp998N20870    VBP1  von Hippel-Lindau binding protein 1 (VBP1), mRNA
      NM_003372   7411  -0.55 -0.35 -0.7  -0.68 -0.52 -0.71 0.09  0.14  -0.19 -
0.05  0.55  0.98  0.08  -0.13 0.91  0.69  0.3   0.78
IMAGp998B22668    VIM   vimentin          7431  -0.1  -1.1  -0.22 -0.92 0.57  -
1.64  0.55  0.28  0.13  -0.18 0.89  0.21  -0.17 0.15  1.66  1.48  0.5   1.66
IMAGp998L171162   VPS13C      vacuolar protein sorting 13C (yeast) (VPS13C),
mRNA  NM_017684         -0.1  -1.14 -0.16 -0.6  -0.13 -0.69 -0.06 -0.26 -0.07
      0.1   -0.66 -0.01 0.09  0.27  0.57  0.12  1     1.55
IMAGp998C041744   WARS  tryptophanyl-tRNA synthetase (WARS), mRNA NM_004184
      7453  -0.7  -0.01 -0.96 -0.59 -0.51 -0.37 -0.23 0.03  -0.69 -0.39 -0.02 -
0.13  -0.15 -0.16 0.51  0.61  0.1   0.15
IMAGp998F231792   WASPIP      Wiskott-Aldrich syndrome protein interacting
protein           7456  -0.64 -0.75 -0.68 -0.89 0.06  -1.51 0.21  -0.28 -0.37 -
0.96  0.3   -0.34 0.3   -0.07 1.43  0.85  0     0.07
IMAGp998O03588    WDR26 WD repeat domain 26 (WDR26), mRNA   NM_025160   80232 -
0.44  -0.54 -0.57 -0.65 -0.4  -0.3  0.04  -0.05 0.07  0.12  -0.07 0.45  -0.14 -
0.08  0.84  0.63  0.1   0.32
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IMAGp998P111198   WWP1  WW domain-containing protein 1 (WWP1), mRNA
      NM_007013   11059 -0.81 -0.44 -1.03 -0.53 0.24  -0.72 0.16  -0.35 0.08  -
0.13  -0.46 -0.03 -0.05 0.16  0.84  0.47  0.7   0.89
IMAGp998L21565    XPO1  exportin 1 (CRM1 homolog, yeast) (XPO1), mRNA
      NM_003400   7514  -0.2  -0.61 -0.2  -0.94 -0.68 -0.62 0.02  -0.23 -0.06
      0.27  -0.07 0.49  0.02  0.16  1.38  0.99  0.5   1.16
IMAGp998P241782   XPOT  exportin, tRNA (nuclear export receptor for tRNAs)
(XPOT), mRNA      NM_007235   11260 -0.85 -0.81 -0.67 -0.84 -1.07 -0.77 -0.11 -
0.53  -0.23 0.03  0.11  0.78  -0.11 0.14  1.42  0.96  1.1   1.81
IMAGp998M151781   XPOT  exportin, tRNA (nuclear export receptor for tRNAs)
(XPOT), mRNA      NM_007235   11260 -1.02 -0.44 -0.71 -0.45 -0.93 -1.37 -0.35 -
0.41  -0.33 -0.43 -0.91 0.32  -0.17 0.03  1.21  1.01  0.8   1.39
IMAGp998G16153    XPOT  exportin, tRNA (nuclear export receptor for tRNAs)
(XPOT), mRNA      NM_007235         -1.23 -0.33 -1.44 0.36  -1.25 -0.47 -0.14 -
0.73  -0.45 -1.17 -1.04 0.01  -0.07 0.04  1.67  1.15  0.7   1.95
IMAGp998O12929    XRCC3 X-ray repair complementing defective repair in Chinese
hamster cells 3         7517  -1.09 -1.06 -0.83 -0.8  -0.49 -0.9  0.19  -0.03 -
0.21  -0.3  0.45  -0.03 0.39  -0.23 1.2   1.16  0.8   1
IMAGp998N221781   XRN2  5'-3' exoribonuclease 2 (XRN2), mRNA      NM_012255
      22803 -0.04 -0.77 -0.05 -0.48 -0.07 -0.15 0.42  -0.19 0.39  -0.01 0.04
      0.2   0.19  0.17  0.85  0.33  0.3   1.04
IMAGp998C0793     YWHAQ tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, theta polypepti NM_006826   10971 -0.2  -0.91 -0.22 -0.87 -
0.42  -0.28 0.55  0.32  0.03  0.05  0.65  0.44  0.44  -0.34 1.51  1.21  0.4
      1.39
IMAGp998L112014   YY1   YY1 transcription factor (YY1), mRNA      NM_003403
      7528  -0.41 -0.12 -0.19 -0.25 -0.38 -1.06 0.07  0.02  0.11  0.19  0.22
      0.21  0.08  0.18  0.88  0.8   0.7   1.5
IMAGp998H1687     ZCCHC9      zinc finger, CCHC domain containing 9 (ZCCHC9),
mRNA  NM_032280   84240 -0.33 -0.42 -0.26 -0.34 -0.33 -0.65 0.29  0.2   0.08  -
0.24  1.12  -0.02 0.36  0.01  0.78  0.62  0.8   1.47
IMAGp998O221784   ZFML  NP220 nuclear protein (NP220), mRNA NM_014497   27332 -
0.52  -0.53 -0.18 -0.29 -0.59 0.24  0.05  0.06  0.45  0.26  0.7   0.29  -0.16
      0.1   0.37  0.47  0.8   0.53
IMAGp998J15598    ZFP106      Zinc finger protein 106 homolog (mouse) (ZFP106),
mRNA  NM_022473   64397 -0.98 -0.65 -0.89 -0.64 0.14  -0.11 -0.31 -0.15 -0.3  -
0.3   -0.07 -0.32 -0.22 -0.15 0.93  1.06  1.1   0.42
IMAGp998E09596    ZFP91 Zinc finger protein 91 homolog (mouse) (ZFP91),
transcript variant 1, mRNA    NM_053023         -0.55 -0.66 -0.51 -0.84 -0.33 -
0.98  -0.24 -0.43 -0.36 -0.5  0.13  0.28  0.17  0.16  1.14  0.65  -0.2  0.78
IMAGp998O17195    ZFR   Zinc finger RNA binding protein (ZFR), mRNA
      NM_016107   51663 -0.6  -0.72 -0.26 -0.67 -0.13 0.1   0.14  0.01  -0.25
      0.06  -0.39 -0.03 0     0.03  1.12  0.52  0.6   0.57
IMAGp998O0496     ZNF135      Zinc finger protein 135 (clone pHZ-17) (ZNF135),
mRNA  NM_003436         -0.7  0.31  -1.14 -0.76 -1.18 -0.44 0.04  -0.09 -0.32 -
0.29  -0.81 -0.07 0.31  -0.4  1.3   1.18  1.6   0.74
IMAGp998H114114   ZNF207      Zinc finger protein 207       7756  -0.61 0.08  -
0.59  0.06  -0.31 -0.57 0.11  0.17  -0.29 0     -0.62 -0.04 0.06  -0.16 0.59
      0.88  0.6   0.36
IMAGp998D21377    ZNF313      Zinc finger protein 313 (ZNF313), mRNA
      NM_018683   55905 -1.1  0.08  -0.85 -0.19 0.03  -0.87 -0.28 -0.41 -0.24 -
0.08  0.22  0.21  0.07  -0.06 1.08  0.87  0.3   1.46
IMAGp998M034019   ZNF539      Zinc finger protein 254             -0.51 -0.11 -
0.69  -0.5  -1.11 -0.84 0     0.09  -0.13 -0.23 -0.21 0.24  0.01  -0.35 0.38
      0.2   0.8   0.63
```

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IMAGp998O054417   ZNF597      hypothetical protein FLJ33071 (FLJ33071), mRNA
      NM_152457   146434      -0.43 -0.22 -0.5  0.16  -1.77 -0.98 0.05  -0.06
      0.12  -0.13 -0.17 -0.1  0     0.3   0.27  0.03  0.8   1.11
IMAGp998M211781   ZWINT ZW10 interactor (ZWINT), transcript variant 1, mRNA
      NM_007057   11130 -0.16 -0.55 -0.55 -1.27 -0.78 -1.41 0.27  -0.81 0.22  -
0.87  0.21  0.46  0.54  0.1   1.55  0.55  0     0.75
IMAGp998N121943   ZZZ3  Zinc finger, ZZ domain containing 3 (ZZZ3), mRNA
      NM_015534   26009 -0.53 -0.42 -0.12 -0.52 -0.42 -0.87 0.23  -0.23 0.27  -
0.24  0.2   -0.09 -0.04 0.28  0.83  0.48  0.1   1.12
IMAGp998O06662    ADCK4 AarF domain containing kinase 4           79934 0.24
      0.4   0.05  0.54  0.72  0.52  -0.15 0.15  -0.17 0.06  -0.21 -0.17 -0.16 -
0.16  -0.06 0.07  0.3   -0.18
IMAGp998J19624    AIP1  Atrophin-1 interacting protein 1 (AIP1), mRNA
      NM_012301   9863  0.21  0.5   0.22  0.53  0.3   0.15  -0.09 0.17  0.11
      0.09  -0.13 -0.28 -0.15 -0.08 -0.09 -0.13 -0.2  -0.6
IMAGp998F11373    AKT2  V-akt murine thymoma viral oncogene homolog 2
      208   0.43  0.31  0.13  0.24  0.35  0.51  -0.03 -0.15 0.09  0.05  -0.17
      0.19  -0.02 0.02  -0.76 0.02  -0.6  -0.24
IMAGp998I181064   ANK1  Ankyrin 1, erythrocytic       286   0.09  0.57  0.26
      0.63  0.4   0.7   0.03  -0.04 -0.02 0.44  -0.16 -0.2  -0.14 -0.04 -0.05 -
0.13  0.1   0.1
IMAGp998B11522    ANKRD10     Ankyrin repeat domain 10            55608 0.05
      0.81  -0.01 0.46  0.5   0.67  -0.1  0.01  0.09  0.15  -0.53 -0.25 -0.1  -
0.11  -0.11 -0.1  -0.6  -0.43
IMAGp998E06522    ARHGAP12    Rho GTPase activating protein 12          94134
      0.24  0.61  0.05  0.64  0.73  0.33  -0.15 -0.12 0.16  0.15  -0.47 -0.44 -
0.09  -0.05 -0.18 -0.22 -0.7  -0.37
IMAGp998N07208    BIRC4 baculoviral IAP repeat-containing 4 (BIRC4), mRNA
      NM_001167         0.24  0.34  0.28  0.69  0.56  0.41  -0.11 -0.07 0.07  0
      -0.31 0.14  -0.07 -0.03 -0.45 -0.3  -0.3  0.34
IMAGp998F231015   BLVRB Biliverdin reductase B (flavin reductase (NADPH))
      645   0.37  0.32  0.12  0.46  0.43  0.57  -0.1  0.1   -0.11 0.12  -0.3  -
0.3   -0.05 -0.09 -0.05 0.1   0.1   0.35
IMAGp998F02647    C13orf9     Vacuolar protein sorting 36 (yeast)       51028
      0.64  -0.07 0.18  0.55  0.29  0.77  -0.11 -0.02 -0.01 0.34  0.21  -0.03 -
0.1   -0.05 -0.1  -0.18 -0.6  -0.17
IMAGp998L15369    C14orf101   Chromosome 14 open reading frame 101
      54916 0.51  0.22  0.34  0.29  0.13  0.74  0.12  -0.23 0.18  -0.06 -0.01
      0.09  0.03  0.08  -0.8  -0.22 -1.1  -0.68
IMAGp998G06246    C18orf8     Chromosome 18 open reading frame 8        29919
      0.4   0.84  0.43  1.43  1.31  0.91  -0.41 0.07  -0.23 -0.08 -0.35 -0.01 -
0.67  0.29  -0.24 0.14  0.4   -0.06
IMAGp998C07794    C1QTNF2     C1q and tumor necrosis factor related protein 2
(C1QTNF2), mRNA   NM_031908         -0.04 0.65  0.04  0.58  0.37  0.44  -0.13
      0.06  -0.1  -0.07 0.05  0.07  -0.1  -0.08 -0.12 -0.05 0     -0.1
IMAGp998E04118    C20orf64    chromosome 20 open reading frame 64 (C20orf64),
mRNA  NM_033550         0.11  1.04  0.4   0.88  0.44  0.8   0.06  -0.01 -0.06
      0.12  0.27  -0.78 -0.04 -0.31 0.05  -0.56 0.2   -0.5
IMAGp998A09358    C21orf13    Chromosome 21 open reading frame 13       150082
      0.14  0.47  0.41  0.54  0.36  0.51  -0.13 -0.06 0.08  0.12  -0.26 -0.01 -
0.23  -0.04 -0.07 -0.05 0.3   0.27
IMAGp998A18114    C6orf148    Chromosome 6 open reading frame 147
      0.16  0.51  0.14  0.72  0.52  0.47  -0.22 0.14  -0.08 0.36  -0.05 -0.28 -
0.16  -0.1  -0.31 -0.15 -0.1  0.13
IMAGp998K17378    C9orf3      Chromosome 9 open reading frame 3         84909
      0.01  0.63  -0.07 0.74  0.94  0.53  -0.27 0.3   -0.21 0.02  0.22  -0.19 -
0.82  -0.21 -0.28 -0.05 -0.4  -0.88
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IMAGp998D05381    C9orf52     Chromosome 9 open reading frame 52        158219
      0.46  0.17  0.33  0.3   0.36  0.87  0.03  -0.18 0.06  0.06  -0.69 -0.07
      0.04  0.07  -0.02 -0.1  -0.6  -0.27
IMAGp998M06198    CCL5  chemokine (C-C motif) ligand 5 (CCL5), mRNA
      NM_002985         0.12  0.74  0.14  0.64  0.63  0.92  -0.23 0.03  -0.01
      0.4   -0.29 -0.09 -0.19 -0.07 -0.14 -0.1  -0.5  -0.15
IMAGp998E10534    CCR6  chemokine (C-C motif) receptor 6 (CCR6), transcript
variant 2, mRNA   NM_031409   1235  0.26  0.39  0.12  0.63  0.63  0.52  -0.3
      0.06  -0.08 0.31  -0.11 -0.21 -0.15 -0.05 -0.31 -0.11 -0.6  -1.28
IMAGp998A032401   CHRNA5      Cholinergic receptor, nicotinic, alpha polypeptide
5           1138  0.23  0.69  0.09  0.4   0.67  0.12  -0.05 0     0.05  0.17  -
0.28  -0.04 -0.06 -0.2  -0.15 -0.12 0     0.14
IMAGp998I181818   CHST12      carbohydrate (chondroitin 4) sulfotransferase 12
(CHST12), mRNA    NM_018641   55501 0     0.19  0.1   0.48  0.08  0.19  -0.16 -
0.09  -0.13 0.08  0.3   -0.26 -0.12 -0.2  -0.39 -0.11 -0.3  -0.44
IMAGp998J181863   CLASP2      Cytoplasmic linker associated protein 2
      23122 0.03  0.93  0.18  0.75  0.66  0.38  -0.19 0.03  -0.04 0.27  0.14  -
0.16  -0.16 -0.13 -0.27 -0.22 -0.7  -1.28
IMAGp998L05129    DELGEF      Deafness locus associated putative guanine
nucleotide exchange factor          26297 0.38  0.15  0.4   0.49  0.68  0.17
      0.04  -0.28 0.23  -0.26 0.16  -0.36 0.14  -0.04 -0.47 -0.41 -1.3  -0.93
IMAGp998F04889    DKFZP566D1346     Ankyrin repeat domain 13C           81573
      0.16  0.43  0.01  0.43  0.44  0.69  -0.05 -0.07 0.11  0.05  -0.17 0.09
      0.01  -0.08 -0.08 -0.09 -0.9  -0.76
IMAGp998G15621    DKFZp762K222      Storkhead box 2         56977 0.11  0.4
      0.08  0.51  0.58  0.73  -0.22 -0.09 -0.02 0.22  0.08  -0.19 -0.13 -0.16 -
0.17  -0.29 -0.6  -0.33
IMAGp998N21660    DUSP10      dual specificity phosphatase 10 (DUSP10),
transcript variant 1, mRNA    NM_007207         0.34  0.14  0.28  0.32  0.58
      1.16  -0.05 -0.12 0.05  -0.02 -0.17 -0.27 -0.01 0.04  0.04  -0.08 -0.1  -
0.3
IMAGp998J08399    EPB41 Erythrocyte membrane protein band 4.1 (elliptocytosis 1,
RH-linked)        2035  0.05  0.52  0.1   0.57  -0.14 1.14  -0.08 -0.06 -0.07
      0.33  -0.41 0     -0.57 -0.25 -0.31 -0.14 -1.1  -0.91
IMAGp998K05979    EPB41L4B    Erythrocyte membrane protein band 4.1 like 4B
      54566 0.14  0.51  -0.03 0.46  0.37  0.36  -0.21 0     0.07  0.05  -0.08 -
0.21  -0.06 -0.03 -0.54 0.01  -0.4  -0.09
IMAGp998O02587    FEZ2  fasciculation and elongation protein zeta 2 (zygin II)
(FEZ2), mRNA      NM_005102         0.42  0.38  0.34  0.65  1     1.23  -0.05 -
0.03  0     0.7   -0.09 0.16  -0.12 -0.09 -0.22 -0.24 -0.1  -0.88
IMAGp998H09834    FLJ10996    Hypothetical protein FLJ10996       54520 0.27
      0.29  0.17  0.46  0.49  0.61  -0.19 0.08  -0.07 0.24  -0.1  0.02  -0.11 -
0.03  -0.08 -0.04 -0.6  -0.5
IMAGp998A24829    FLJ14011    Zinc finger protein 667       63934 0.53  0.25
      0.54  0.73  0.47  0.56  0.08  0.18  -0.08 0.37  0.22  0.17  0.01  0.03  -
0.26  -0.41 0.4   -0.1
IMAGp998I20742    FLJ32130    Hypothetical protein FLJ32130       146540
      0.44  0.23  0.16  0.51  0.35  0.62  -0.1  0.03  -0.1  0.31  0.34  -0.09 -
0.08  0.04  -0.12 -0.01 -0.3  -0.03
IMAGp998I1581     FOXO3A      forkhead box O3A (FOXO3A), transcript variant 1,
mRNA  NM_001455   2309  0.18  1.03  0.96  1.09  1.26  1.4   -0.43 -0.06 -0.99 -
0.41  -0.56 -0.86 -0.58 -0.34 0.56  0.78  0.2   0.07
IMAGp998B16657    FUBP3 Far upstream element (FUSE) binding protein 3
      8939  0.3   0.38  0.18  0.31  0.13  0.72  0.02  -0.09 0.13  -0.07 0.12
      0.08  0.01  0     -0.4  -0.04 -0.8  -0.22
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IMAGp998H03331    GDI1  GDP dissociation inhibitor 1 (GDI1), mRNA NM_001493
      2664  0.15  0.43  0.02  0.68  0.57  1.38  -0.3  -0.01 -0.05 0.16  -0.38 -
0.31  -0.22 -0.04 -0.4  -0.27 -0.2  -0.48
IMAGp998G154526   GFRA1 GDNF family receptor alpha 1        2674  0.62  0.74
      0.25  0.64  0.85  0.85  -0.07 -0.22 0.09  0     -0.29 -0.16 -0.42 0.02  -
0.24  0.46  0.3   0.2
IMAGp998B15117    GYPA  Glycophorin A (includes MN blood group)         2993
      0.11  0.33  0.29  0.64  0.93  0.49  0.02  -0.05 0.02  0.31  0.31  -0.08
      0.01  0     -0.4  -0.27 -0.2  -1.02
IMAGp998A17604    HOMER1      Homer homolog 1 (Drosophila)        9456  -0.18
      0.77  1.32  0.79  0.68  0.14  -0.16 0.07  -0.39 0.23  0.02  -0.08 -0.21 -
0.56  -0.33 0.02  -0.5  -0.64
IMAGp998I15523    HSD17B7     hydroxysteroid (17-beta) dehydrogenase 7
(HSD17B7), mRNA   NM_016371         0.37  0.32  0.24  0.64  0.49  0.5   -0.14
      0.05  0.09  0.04  -0.13 0.43  -0.09 -0.01 -0.03 -0.13 0.1   -0.07
IMAGp998L2183     IDE   Insulin-degrading enzyme            3416  0.6   0.38
      0.74  0.34  0.86  0.77  0.24  0.3   0.04  0     0.18  0.46  0.08  0.18  -
0.35  -0.46 -1.2  -0.08
IMAGp998M151786   IER2  immediate early response 2 (IER2), mRNA   NM_004907
      0.25  0.5   -0.1  0.06  0.38  0.66  -0.38 -0.31 -0.21 -0.19 -0.34 -0.14 -
0.41  0.31  -0.73 -0.66 -1.1  -1.09
IMAGp998A05694    IL12RB1     interleukin 12 receptor, beta 1 (IL12RB1),
transcript variant 2, mRNA    NM_153701         0.47  0.2   0.27  0.3   0.18
      0.43  -0.01 0     -0.05 0.5   -0.07 0.07  -0.06 -0.05 -0.05 0.02  -0.4  -
0.56
IMAGp998A02423    INSR  Insulin receptor        3643  0.42  1.2   0.7   1.21
      0.59  1.34  0.41  0.4   -0.05 0.18  -0.01 0.18  -0.38 -0.16 -0.29 0.09
      0.2   -0.34
IMAGp998L16604    JARID1B     Jumonji, AT rich interactive domain 1B (RBP2-like)
(JARID1B), mRNA   NM_006618         0.06  0.54  -0.1  0.82  0.64  0.11  -0.21
      0.12  -0.13 0.18  -0.42 -0.5  -0.15 -0.42 -0.64 -0.22 -0.8  -0.4
IMAGp998I02621    KENAE Kenae       202243      0.13  0.69  0.2   0.49  0.29
      0.56  0.02  -0.17 0.14  0     0.42  -0.26 0     -0.04 -0.03 -0.25 -0.2  -
0.05
IMAGp998K04644    KIAA1982    KIAA1982 protein        170960      0.29  0.49
      0.18  0.4   0     0.55  0.05  -0.19 0.14  0     -0.2  -0.33 -0.05 0.07  -
0.14  -0.33 0.2   -0.22
IMAGp998O24248    KLF2  Kruppel-like factor 2 (lung) (KLF2), mRNA NM_016270
      0.8   0.94  1.13  0.62  0.86  1.4   -0.32 -0.2  -0.47 -0.22 -0.9  -0.11 -
0.48  -0.06 -0.38 -0.1  0.1   -0.08
IMAGp998F0999     LPP   LIM domain containing preferred translocation partner in
lipoma            4026  0.17  0.25  0.13  0.56  0.3   0.28  -0.07 0.03  -0.1
      0.13  -0.34 -0.15 -0.19 -0.16 -0.22 -0.02 0     0.05
IMAGp998N06124    MAK3  Mak3 homolog (S. cerevisiae)        80218 0.1   0.43  -
0.04  0.65  0.79  1.27  -0.22 0.17  -0.27 0     0.45  -0.11 -0.2  -0.1  -0.48 -
0.11  -0.9  -1.38
IMAGp998B11597    MAN2A2      mannosidase, alpha, class 2A, member 2 (MAN2A2),
mRNA  NM_006122         0.1   0.63  0.1   0.74  0.35  0.31  -0.12 0.03  -0.04 -
0.06  -0.08 0.05  -0.24 -0.25 -0.39 -0.19 -1.2  -0.93
IMAGp998B03411    MAP3K8      Mitogen-activated protein kinase kinase kinase 8
            1326  0.38  0.33  0.14  0.42  0.65  0.33  -0.16 -0.12 0.12  0.14
      0.34  0.01  -0.06 -0.06 -0.07 -0.15 -1    -0.61
IMAGp998I091206   MCPH1 Microcephaly, primary autosomal recessive 1
      79648 0.39  0.49  1.02  0.84  1.2   1.25  0.06  -0.25 0.17  -0.27 -0.14 -
0.13  -0.02 0.28  0.14  0.11  1     -0.21
IMAGp998F1793     ME2   malic enzyme 2, NAD(+)-dependent, mitochondrial (ME2),
nuclear gene encoding mitochondr    NM_002396         0.26  0.27  0.05  0.55
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      0.47  0.82  -0.1  0.09  -0.08 -0.12 0     -0.21 -0.13 -0.06 -0.21 -0.04 -
0.6   -0.88
IMAGp998P2179     METTL4      Methyltransferase like 4            64863 0.26
      0.36  0.11  0.59  0.39  0.5   -0.16 0.1   -0.04 0.62  0.12  0.08  -0.1  -
0.09  -0.19 -0.06 -0.2  -0.81
IMAGp998H08543    MGC26744    Hypothetical protein MGC26744       132989
      0.18  0.55  0.17  0.48  0.28  0.37  0     -0.28 -0.04 -0.16 -0.19 0.15  -
0.08  -0.03 -0.09 -0.3  -0.7  -0.71
IMAGp998E08884    MGC29898    Hypothetical protein MGC29898       133015
      0.2   0.5   0.11  0.35  0.48  0.7   -0.04 0.38  -0.17 0.11  -0.28 -0.3  -
0.18  -0.04 -0.04 0.06  -0.1  -0.56
IMAGp998I1088     MINK1 Misshapen-like kinase 1 (zebrafish)       50488 0.31
      0.3   0.19  0.42  0.43  0.02  -0.28 0.19  -0.17 -0.14 0.15  -0.29 -0.1  -
0.05  -0.2  0.08  0     -0.16
IMAGp998A13664    M-RIP Myosin phosphatase-Rho interacting protein
      23164 0.31  0.23  0.21  0.37  0.41  0.51  -0.15 -0.04 -0.02 0     0.07
      0.04  -0.05 0.06  0.02  -0.35 -0.6  0.17
IMAGp998D243847   MRPL19      Mitochondrial ribosomal protein L19       9801
      0.39  0.11  0.23  0.62  0.26  0.32  -0.13 0.01  -0.11 -0.26 0.13  -0.3  -
0.13  -0.12 -0.48 -0.45 -1.2  -0.34
IMAGp998G142011   MTHFD2L     Methylenetetrahydrofolate dehydrogenase (NADP+
dependent) 2-like       441024      0.55  0.23  0.5   0.76  0.38  0.56  -0.17 -
0.04  0     0.44  0.26  0.26  -0.12 -0.07 -0.34 -0.3  0.4   -0.11
IMAGp998N0586     MYO1D Myosin ID         4642  0.24  0.16  0.01  0.59  0.64
      0.64  -0.13 0     -0.02 -0.24 -0.18 -0.25 -0.05 -0.13 -0.17 -0.1  -0.1  -
0.74
IMAGp998J211113   MYO1E myosin IE (MYO1E), mRNA NM_004998   4643  0.25  0.14
      0.24  0.07  0.28  0.18  -0.29 -0.64 -0.39 -0.48 -0.35 -0.24 -0.21 0.32  -
0.12  -0.31 -0.4  -0.22
IMAGp998L02540    NDRG1 N-myc downstream regulated gene 1 (NDRG1), mRNA
      NM_006096   10397 0.58  0.5   0.32  0.67  1.22  1.42  -0.02 0.2   -0.51 -
0.23  -0.01 -0.54 -0.54 0.39  -0.23 -0.42 -0.7  -0.88
IMAGp998B1793     NEDD1 Neural precursor cell expressed, developmentally down-
regulated 1       121441      0.16  0.45  0.08  0.61  0.35  0.42  -0.21 0.07  -
0.25  0.19  0.32  0.24  -0.16 -0.1  -0.26 -0.13 -1    -0.98
IMAGp998P0888     NFIA  Nuclear factor I/A            4774  0.05  0.59  0.37
      0.9   0.35  0.33  -0.09 0.04  -0.17 -0.14 -0.34 -0.06 -0.12 -0.11 -0.53 -
0.24  -0.6  -0.95
IMAGp998M06127    NT5C2 5'-nucleotidase, cytosolic II       22978 0.15  0.21
      0.13  0.64  0.54  0.24  -0.09 0.05  -0.04 -0.09 0.27  -0.22 -0.22 0.06  -
0.47  -0.09 -0.1  -0.45
IMAGp998P17131    OIT3  Oncoprotein induced transcript 3          170392
      0.45  0.16  0.33  0.42  0.59  0.64  0.07  -0.08 0.06  -0.05 -0.2  0.17  -
0.08  0.14  -0.02 -0.15 0.3   -0.48
IMAGp998M232973   PAIP2 Poly(A) binding protein interacting protein 2
      51247 0.5   0.73  0.48  0.76  0.75  1.04  0.25  0.19  0.01  -0.05 -0.14
      0.46  -0.08 0.04  0.21  0.06  -0.5  -0.23
IMAGp998I09473    PARD3 Par-3 partitioning defective 3 homolog (C. elegans)
      56288 0     0.72  -0.08 0.67  0.49  0.7   -0.15 0.08  -0.14 0.1   0.07
      0.05  -0.17 -0.17 -0.9  -0.16 -1.6  -1.13
IMAGp998I18782    PDE5A Phosphodiesterase 5A, cGMP-specific       8654  0.3
      0.73  0.5   0.54  0.28  0.5   0     -0.02 -0.04 -0.23 -0.17 0.21  -0.14 -
0.31  -0.59 -0.35 0.2   0.18
IMAGp998K05397    PIP3AP      phosphatidylinositol-3-phosphate associated
protein (PIP3AP), mRNA  NM_019061         0.55  0.04  0.28  0.11  0.15  0.71  -
0.02  0     -0.11 -0.1  -0.2  -0.15 0.01  0.02  0.05  -0.09 0     -0.1
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IMAGp998E22463    PLXNA2      Plexin A2         5362  -0.12 0.81  0.32  0.8
      0.79  0.94  -0.69 0.04  -0.15 -0.21 -1.67 -0.31 -0.38 -0.14 -0.38 0.05  -
0.1   -0.39
IMAGp998N0583     PPID  peptidylprolyl isomerase D (cyclophilin D) (PPID), mRNA
      NM_005038         0.3   0.22  0.1   0.47  0.31  0.45  -0.15 0.09  -0.03
      0.32  0.19  0.01  -0.15 0.03  -0.1  -0.06 -0.4  -0.82
IMAGp998F235575   PSEN1 Presenilin 1 (Alzheimer disease 3)        5663  0.25
      0.15  0.74  0.84  1.16  0.63  -0.04 0.28  -0.13 -0.03 -0.11 -0.24 -0.2  -
0.07  0.15  -0.25 -0.2  -0.85
IMAGp998C1818     PSMD3 Proteasome (prosome, macropain) 26S subunit, non-ATPase,
3           5709  0.36  0.32  0.22  0.4   0.5   1.05  -0.07 -0.07 0.14  0.06  -
0.64  -0.25 0.03  -0.01 -0.17 -0.2  -0.4  -0.36
IMAGp998B24243    RAI   RelA-associated inhibitor (RAI), mRNA     NM_006663
      2817  -0.23 0.85  -0.15 0.75  1.44  1.15  -0.44 -0.06 -0.85 -0.46 -1.47 -
0.39  -0.26 -0.49 -0.1  -0.27 -0.5  -1.06
IMAGp998G24524    RBM5  RNA binding motif protein 5         10181 0.08  0.8
      0.11  0.7   0.51  0.63  -0.19 0.05  0.14  0.19  -0.36 0.26  -0.09 -0.1  -
0.31  -0.06 -0.2  -0.02
IMAGp998A211017   RERG  RAS-like, estrogen-regulated, growth inhibitor
      85004 -0.14 0.93  0.24  1.03  0.32  0.93  -0.15 0.34  0     0.23  -0.24
      0.11  -0.29 -0.08 -0.72 -0.31 0     -1.2
IMAGp998E161159   RGC32 response gene to complement 32 (RGC32), mRNA
      NM_014059   28984 0.59  0.82  0.73  0.68  0.74  0.58  -0.39 -0.23 -0.42
      0.15  0.36  -0.03 -0.11 0.21  -0.34 -0.43 0     -0.34
IMAGp998H184004   RHBDF1      rhomboid family 1 (Drosophila) (RHBDF1), mRNA
      NM_022450   64285 0.47  0.64  0.39  0.85  0.82  1.1   -0.1  0.53  0.16  -
0.19  0.43  0.52  -0.4  -0.04 -0.19 -0.04 0.3   0.19
IMAGp998N03471    ROD1  ROD1 regulator of differentiation 1 (S. pombe)
      9991  0.02  0.56  0.4   0.43  0.1   0.54  0.12  -0.1  0.14  0.06  -0.46
      0.07  -0.03 -0.14 -0.14 -0.24 0     -0.21
IMAGp998A23415    RPE   Ribulose-5-phosphate-3-epimerase          6120  0.17
      0.33  0.08  0.23  0.46  0.15  -0.17 -0.04 0.17  -0.13 0.19  0.03  -0.13 -
0.01  -0.06 -0.09 -0.5  -0.31
IMAGp998N11599    SART2 Squamous cell carcinoma antigen recognized by T cells 2
            29940 0.14  0.42  0.11  0.35  0.3   0.54  -0.14 0.11  -0.01 0.06
      0.02  0.07  -0.2  -0.09 -0.18 -0.08 -0.7  -0.74
IMAGp998B01571    SEC22L3     SEC22 vesicle trafficking protein-like 3 (S.
cerevisiae)       9117  0.29  0.41  0.28  0.51  0.21  0.95  -0.19 -0.02 -0.01
      0.51  -0.24 -0.45 -0.08 -0.11 -0.15 -0.08 -0.4  -0.11
IMAGp998F0289     SENP5 SUMO1/sentrin specific peptidase 5        205564
      0.12  0.48  0.11  0.4   0.36  0.77  -0.1  0.09  -0.01 0.15  -0.55 -0.41 -
0.03  -0.03 0.07  -0.05 -0.3  -0.18
IMAGp998G19373    SH3MD1      SH3 multiple domains 1        9644  0.14  0.62
      0.04  0.76  0.75  0.94  -0.18 0.25  -0.18 -0.24 -0.62 0     -0.26 -0.22 -
0.59  -0.24 -0.4  0.37
IMAGp998E0481     SH3TC2      SH3 domain and tetratricopeptide repeats 2
      79628 0.76  0.5   0.16  0.98  0.3   1.23  -0.11 -0.03 -0.07 0.12  -0.17 -
0.05  -0.15 -0.18 -0.64 -0.48 -0.4  -0.16
IMAGp998A18186    SLC2A11     solute carrier family 2 (facilitated glucose
transporter), member 11 (SLC2A11), mRNA   NM_030807   66035 0.2   0.48  0.29
      0.57  0.46  0.44  0.09  -0.11 0.04  0.03  0.13  -0.42 -0.09 -0.1  -0.14 -
0.19  -0.5  -0.53
IMAGp998K16661    SLC35A1     Solute carrier family 35 (CMP-sialic acid
transporter), member A1       10559 0.18  0.55  0.17  0.52  0.46  0.94  -0.11
      0.07  -0.07 -0.12 0.56  -0.11 -0.15 -0.06 -0.08 -0.03 -0.1  -0.06
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IMAGp998B11375    SLC38A2     Solute carrier family 38, member 2        54407 -
0.14  0.91  0.01  0.67  0.67  0.54  -0.1  0.02  0.08  0.18  0.27  -0.4  -0.19 -
0.38  -0.43 -0.44 -1.7  -0.44
IMAGp998O16368    SLC6A16     Solute carrier family 6, member 16        28968
      0.55  0.1   0.21  0.22  0.25  0.51  -0.08 0.01  -0.09 0.11  0.14  -0.3  -
0.14  -0.13 -0.24 -0.06 0.1   0.07
IMAGp998K13329    SMC6L1      SMC6 structural maintenance of chromosomes 6-like
1 (yeast)         79677 0.16  0.56  0.03  0.45  0.19  0.64  -0.14 0.04  -0.07
      0.16  -0.16 -0.42 -0.08 -0.08 -0.07 -0.08 0     -0.04
IMAGp998J18119    SNAPC3      Small nuclear RNA activating complex, polypeptide
3, 50kDa          6619  0.27  0.36  0.04  0.46  0.58  0.04  -0.18 -0.04 0.01  -
0.05  -0.01 -0.08 -0.16 0     -0.29 -0.02 -0.4  -0.46
IMAGp998F2189     STK38 Serine/threonine kinase 38          11329 0.39  0.25
      0.2   0.46  0.57  0.5   -0.05 -0.09 0.12  0.05  -0.02 0.02  -0.11 0.1   -
0.04  -0.05 -0.5  -0.22
IMAGp998K032011   SYNE2 spectrin repeat containing, nuclear envelope 2 (SYNE2),
transcript variant 1, mRNA    NM_015180         0.4   0.3   0.17  0.65  0.6
      1.04  0.01  -0.11 0.16  0.08  0.6   0.67  -0.04 -0.01 -0.12 -0.21 -0.7  -
0.43
IMAGp998G06652    TF    transferrin (TF), mRNA  NM_001063         0.22  0.47  -
0.03  0.75  0.27  0.42  -0.09 0.04  -0.14 0.22  -0.32 -0.46 -0.12 -0.18 0.01  -
0.32  0     -0.53
IMAGp998O2195     THBS2 thrombospondin 2  NM_003247   7058  0.21  0.4   -0.11
      0.7   0.58  0.59  -0.37 0.15  -0.23 -0.27 -0.4  -0.35 -0.15 -0.1  -0.42 -
0.18  0.2   -0.08
IMAGp998M16110    TIRAP toll-interleukin 1 receptor (TIR) domain containing
adaptor protein (TIRAP), transcript NM_052887         0.27  0.21  -0.02 0.61
      0.1   0.37  -0.02 0.27  -0.02 -0.17 -0.05 -0.37 -0.28 -0.15 -0.57 -0.55 -
1.4   -1.19
IMAGp998M081088   TPX2  TPX2, microtubule-associated, homolog (Xenopus laevis)
            22974 0.09  0.62  -0.05 0.83  0.48  0.15  -0.26 0.19  -0.09 -0.07 -
0.25  0.02  -0.17 0.01  -0.55 -0.05 -0.6  -0.76
IMAGp998P051746   TTC5  tetratricopeptide repeat domain 5 (TTC5), mRNA
      NM_138376         0.32  0.67  0.48  0.82  1.07  0.63  -0.13 -0.04 -0.23
      0.35  -0.03 0     0.11  -0.21 -1.29 -0.98 -0.2  -0.79
IMAGp998E15834    TTC8  Tetratricopeptide repeat domain 8         123016
      0.15  0.43  -0.04 0.37  0.37  0.5   -0.03 -0.06 -0.02 0.14  -0.16 -0.21 -
0.19  0.01  0.02  0.04  -0.3  0.13
IMAGp998E01600    TXNRD3      Thioredoxin reductase 3       114112      0.45
      0.37  0.34  0.58  0.22  1.05  -0.11 -0.14 0.01  0.05  -0.13 -0.48 -0.09
      0.04  -0.17 -0.21 -0.9  -0.9
IMAGp998I17587    TYR   Tyrosinase (oculocutaneous albinism IA)         7299
      0.3   0.52  0.06  0.56  0.26  0.53  -0.01 -0.08 0.09  0.13  0.01  -0.08
      0.03  0.01  -0.37 -0.13 -0.4  -0.33
IMAGp998D03381    UACA  Uveal autoantigen with coiled-coil domains and ankyrin
repeats          55075 0.04  0.58  0.25  0.68  0.61  0.77  -0.2  0.11  -0.18 -
0.02  -0.45 -0.06 -0.19 -0.12 -0.52 -0.17 0.3   -0.86
IMAGp998J19112    WSB1  WD repeat and SOCS box-containing 1       26118 0.15
      0.32  0.23  0.53  0.29  0.33  -0.16 -0.08 -0.22 -0.11 0.11  -0.37 -0.14
      0.03  -0.48 -0.03 -0.7  -0.51
IMAGp998I11419    ZBTB1 Zinc finger and BTB domain containing 1         22890
      0.58  0.12  0.24  0.18  0.27  0.78  0     -0.11 0.13  0.06  -0.24 0.12  -
0.02  -0.01 -0.72 -0.13 -0.5  -0.82
IMAGp998M17783    ZNF136      zinc finger protein 136 (clone pHZ-20) (ZNF136),
mRNA  NM_003437   7695  0.09  0.6   0.31  0.58  0.32  0.72  -0.01 -0.08 0.08
      0.08  -0.16 -0.12 -0.1  -0.03 -0.08 -0.24 -0.5  -0.26
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IMAGp998B21281	ZNF533	Zinc finger protein 533	151126	1.21	0.73	0.55	0.71	0.6	0.68	0.65	-0.08	0.27	0.44	-0.75	-0.07	-0.15	-0.21	-0.2	-0.19	-0.4	-1.33
IMAGp998B052305	ZNF563	zinc finger protein 563 (ZNF563), mRNA	NM_145276	-0.07	0.24	0.37	0.49	0.56	0.78	-0.18	-0.44	-0.34	-0.13	-0.38	-0.33	-0.35	0.3	-0.54	-0.48	-0.4	0.03