

Supplementary files

Figure S1: Read count distribution. Total (A) and unique (B) read counts are shown for each biological replicate. On average, 150,000 reads corresponding to approximately 1700 to 2900 unique miRNAs with a minimum of 5 read counts, were identified across all samples.

Figure S2: Side by side comparison of canonical and variant miRNA expression reveal consistent response to nanoparticles. A slightly better distinction of exposure duration was observed for the variant containing miRNAs (isomiRs). The dotted red square includes all samples (coloured symbols) exposed for 6h and the dotted black square all the samples exposed to nanoparticles for 24h.

Figure S3: Integrative miR:mRNA transcriptome correlation-based miRNA target prediction. (A) Heatmap of correlated (cutoff $>|0.7|$) miR:gene pairs, for 6 hours and 24 hours exposures. (B) Venn comparisons of correlated miRs and genes between time points. (C) Biological processes enriched by correlated genes that were common to 6h and 24 exposures (red box), unique to 24h exposures (blue box) or unique to 6h exposures (black box).

Figure S4: Side by side heatmaps of correlated miRs (left) and genes (right). MiR and mRNA transcriptome were profiled in same total RNA pool obtained from unexposed (Ctrl) THP-1 cells or THP-1 cells exposed to titanium dioxide (nTi), zinc oxide (nZn) and silver (nAg) nanoparticles, for 6h or 24h.

Figure S5: Venn comparison between miRs (A) identified to have a high correlation (cutoff $>|0.7|$) with mRNA expression and those identified as differentially expressed following 24h exposure to silver nanoparticles (nAg). Similarly, mRNAs that correlated with miR expression (cutoff $>|0.7|$) were compared to those that were differentially expressed as a result of 24h exposure to silver nanoparticles (B). The topmost enriched biological processes, represented by the unique mRNAs from the set of compared mRNAs in (B), are depicted in (C) and (D). FDR is the false discovery rate.

Figure S6: Venn comparison of differentially expressed genes (*Benjamini-Hochberg* $FDR < 0.05$, \log_2 difference > 0.58) in cells exposed to bulk-sized ZnO particles (bZnO – 300 nm), nano-sized ZnO particles (nZnO – 20 nm), Ag nanoparticles (nAg – 20 nm) and non-particulate nitric acid silver [Ag (1+)] is shown in (A). Response to metal (zinc, copper, cadmium) ion is the most enriched pathway represented by shared (10 genes in all exposures and 37 genes particle-based exposures) differentially expressed genes (B). Metal ion response related pathways are highlighted in green.

Figure S7: Relative expression of selected miRNAs, as quantified by RT-PCR. Seq denotes expression as determined by small RNA sequencing while qPCR denotes the relative expression determined via real time PCR. Real time PCR expression was determined relative to endogenous RNU48 expression. Y-axis is \log_2 -transformed, normalized count data from small RNAseq, and \log_2 -transformed relative qPCR expression using the ddCt method. Error bars indicate mean and SEM from three (smallRNAseq) or four (qPCR) replicates.

Sequence	log2 FC.Ctrl6h/nAg6h	log2 FC.Ctrl6h/nTiO2-6h
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AACATAGCGAGACCCCGTCTCCT	1.48	NaN
AACATAGCGAGACCCCGTCTCTTT	1.54	NaN
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ACTCCCACTGCTTCACTTGACT	1.06	NaN
AGAGGTAGTAGGTTGCATAGT	NaN	NaN
AGAGGTAGTAGGTTGCATAGTT	NaN	-0.55
ATAGCGAGACCCCGTCTCC	1.35	NaN
ATAGCGAGACCCCGTCTCCT	1.39	NaN
ATAGCGAGACCCCGTCTCTG	1.37	NaN
ATATAATACAACCTGCT	NaN	NaN
ATATAATACAACCTGCTAAGC	NaN	NaN
ATATAATACAACCTGCTAAGT	NaN	NaN
ATCACATTGCCAGGGATTTCAG	NaN	NaN
ATCATATTTACCAACC	-0.91	NaN
ATCCCACCACTGCCACC	NaN	NaN
ATCCCACCGCTGCCAC	NaN	NaN
ATCCCACCGCTGCCACC	0.4	0.45
ATCCCACCGCTGCCATC	NaN	NaN
ATCCCACCTCCTGACAC	NaN	NaN
ATCCCAGCGGGGCCTCC	0.9	0.63
ATCCCAGCGGTGCCTCC	0.97	0.7
ATCCCAGTAGAGCCTCC	NaN	NaN
ATCCCATCCTCGTCGC	NaN	NaN
ATTCTCAGCGCGGCTG	1.44	NaN
ATTCTCAGCGCGGCTGT	1.41	NaN
CAAAACGTGAGGCGCTGCT	NaN	NaN
CAAAACGTGAGGCGCTGCTAT	NaN	NaN
CATAAAGTAGAAAGCACTAC	NaN	NaN
CCATAAAGTAGAAAGC	NaN	NaN
CCCACCCAGGGACGCC	NaN	NaN
CCCACGTTGGGCGCCG	-1.07	NaN
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CCCCACCGCTGCCACC	NaN	NaN
CCCCACTCCTGGTACC	NaN	NaN
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CCCCGTCCGTGCCTCC	NaN	NaN
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CCCGGGGAGCCCGGCGGGC	NaN	NaN
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CTATACAATCTACTGTCTTTCT	NaN	NaN
CTCCCACTGCTTCACTTGACT	NaN	NaN

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9	GAGGCGGGGGGCGAG	NaN	NaN
10	GAGGCGGGGGGCGAGC	NaN	NaN
11	GAGGCGGGGGGCGAGCC	NaN	NaN
12	GAGGCGGGGGGCGAGCCC	NaN	NaN
13	GATCCACCGCTGCCACC	NaN	NaN
14	GCCACCCAGGGACGCC	NaN	NaN
15	GCCCGCATCCTCCACC	NaN	NaN
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17	GGGGGGAGAGAAGGGTCG	NaN	NaN
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22	GTGGCCTGTGACTTTC	NaN	NaN
23	GTGGGGGAGAGGCTGT	0.87	NaN
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26	TCCCACTGCTTCACTTGACT	NaN	NaN
27	TCCCCAGCATCTCCACC	NaN	NaN
28	TCCCGGCCAACGCACC	NaN	NaN
29	TCCCGGCCAATGCACC	NaN	NaN
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34	TCCTCGCTGGGGCCTCC	NaN	NaN
35	TCTCACACAGAAATCGCACCC	-0.45	NaN
36	TCTCACACAGAAATCGCACCCGTC	NaN	NaN
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12	NaN	NaN	-1
13	NaN	NaN	-0.82
14	NaN	NaN	-1.13
15	NaN	NaN	-1.08
16	NaN	NaN	-1.07
17	NaN	NaN	-1.04
18	NaN	NaN	-1.02
19	NaN	NaN	-1.05
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	log2 FC.Ctrl24h/nZnO-24h	Annotation: isomiR	Annotation: miRNA
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6	NaN	hsa-miR-4284.SNPC	
7	NaN	hsa-miR-4301	
8	NaN		hsa-let-7d-5p
9	NaN		hsa-let-7d-5p
10	NaN		
11	NaN	hsa-miR-1303	
12	NaN	hsa-miR-1303	
13	NaN	hsa-miR-1303	
14	NaN		hsa-miR-374b-5p
15	NaN	hsa-miR-374b-5p	
16	NaN		hsa-miR-374b-5p
17	NaN	hsa-miR-23b-3p	
18	NaN	hsa-miR-5007-3p	
19	NaN		hsa-miR-1260b
20	NaN	hsa-miR-4695-3p	
21	NaN	hsa-miR-1260b	
22	0.39	hsa-miR-1260a	
23	NaN	hsa-miR-3692-5p	
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26	1.65	hsa-miR-4746-5p	
27	NaN	hsa-miR-4776-5p	
28	1.02	hsa-miR-4482-3p	
29	NaN	hsa-miR-4482-3p	
30	NaN		hsa-miR-424-3p
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32	NaN		hsa-miR-142-5p
33	NaN		hsa-miR-142-5p
34	NaN	hsa-miR-4642	
35	0.75	hsa-miR-2277-3p.SNPC	
36	NaN	hsa-miR-142-5p	
37	NaN		hsa-miR-142-5p
38	NaN	hsa-miR-1260a	
39	1.06		hsa-miR-4286
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42	0.42	hsa-miR-4304	
43	0.76	hsa-miR-4532	
44	NaN	hsa-miR-663b	
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46	NaN	hsa-miR-3178	
47	NaN	hsa-miR-4532	
48	NaN	hsa-miR-597-5p.SNPA	
49	NaN	hsa-miR-4683	
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18	NaN	hsa-miR-548ba	
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3 damage-specific DNA binding protein 2, 48kDa
4 coagulation factor XIII, A1 polypeptide
5 Fanconi anemia, complementation group A
6 galactosylceramidase
7 intercellular adhesion molecule 1
8 integrin, alpha 6
9 integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
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12 protoporphyrinogen oxidase
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17 chemokine (C-X-C motif) ligand 8
18 tumor necrosis factor
19 5-aminolevulinate synthase 1
20 arachidonate 5-lipoxygenase
21 biliverdin reductase B
22 intercellular adhesion molecule 2
23 integrin, beta 7
24 primase, DNA, polypeptide 1 (49kDa)
25 retinoic acid receptor, gamma
26 intersectin 1 (SH3 domain protein)
27 solute carrier family 2 (facilitated glucose transporter), member 9
28 receptor accessory protein 3
29 chemokine (C-C motif) ligand 3-like 3
30 Pim-3 proto-oncogene, serine/threonine kinase
31 microtubule associated tumor suppressor 1
32 hematological and neurological expressed 1
33 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
34 tumor protein D52-like 1
35 numb homolog (Drosophila)
36 inositol hexakisphosphate kinase 2
37 optineurin
38 chemokine (C-X-C motif) receptor 4
39 PHD finger protein 19
40 male-specific lethal 1 homolog (Drosophila)
41 centromere protein P
42 baculoviral IAP repeat containing 5
43 insulin-like growth factor binding protein 3
44 annexin A2 receptor
45 establishment of sister chromatid cohesion N-acetyltransferase 2
46 caspase recruitment domain family, member 16
47 Fanconi anemia, complementation group D2
48 adenosine monophosphate deaminase 3
49 v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog
50 phosphorylase kinase, beta
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SID1 transmembrane family, member 2
N-acylethanolamine acid amidase
nuclear protein, transcriptional regulator, 1
structural maintenance of chromosomes 2
FGR proto-oncogene, Src family tyrosine kinase
Src-like-adaptor
topoisomerase (DNA) II alpha
tubulin, gamma 1
zinc finger protein 697
unc-13 homolog C (C. elegans)
glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
WD repeat domain 62
selenoprotein P, plasma, 1
acid phosphatase, prostate
progesterone and adipoQ receptor family member V
lysosomal-associated membrane protein 2
ATP-binding cassette, sub-family D (ALD), member 3
histone cluster 2, H3d
eukaryotic translation initiation factor 4E
ring finger protein 212
family with sequence similarity 86, member B2
neuralized E3 ubiquitin protein ligase 1B
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
protein phosphatase 1, regulatory subunit 3G
angiopoietin 1
NA
glypican 3
baculoviral IAP repeat containing 3
CD14 molecule
hydroxypyruvate isomerase (putative)
stimulated by retinoic acid 6
ATPase, Ca++ transporting, type 2C, member 1
carbonyl reductase 3
cyclin A2
pre T-cell antigen receptor alpha
PDZ and LIM domain 5
metallothionein 1H
non-SMC condensin II complex, subunit G2
slingshot protein phosphatase 2
tumor necrosis factor, alpha-induced protein 8
uridine phosphorylase 1
uridine phosphorylase 1
early B-cell factor 1
tubulin, beta class I
high mobility group AT-hook 2
metallothionein 1G
cysteine-rich protein 1 (intestinal)
cysteine and glycine-rich protein 2
chemokine (C-X3-C motif) receptor 1
epithelial membrane protein 1

glypican 4
chemokine (C-X-C motif) receptor 3
glutathione S-transferase alpha 4
tumor necrosis factor receptor superfamily, member 9
interleukin-1 receptor-associated kinase 2
aryl hydrocarbon receptor
amphiregulin
caveolin 1, caveolae protein, 22kDa
CD9 molecule
CD19 molecule
CD69 molecule
cyclin-dependent kinase 1
centromere protein A
centromere protein E, 312kDa
CDC28 protein kinase regulatory subunit 1B
clusterin
chemokine (C-C motif) receptor 7
solute carrier family 31 (copper transporter), member 2
endothelin 1
endothelin receptor type A
early growth response 1
epoxide hydrolase 2, cytoplasmic
coagulation factor III (thromboplastin, tissue factor)
Fc fragment of IgA receptor
formyl peptide receptor 1
heme oxygenase 1
heat shock 70kDa protein 6 (HSP70B)
interleukin 3 receptor, alpha (low affinity)
interleukin 7 receptor
inhibin, beta A
integrin, alpha V
killer cell lectin-like receptor subfamily C, member 1
kinesin family member C1
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog G
melanoma antigen family B2
malic enzyme 1, NADP(+)-dependent, cytosolic
marker of proliferation Ki-67
matrix metalloproteinase 1
matrix metalloproteinase 10
matrix metalloproteinase 12
matrix metalloproteinase 19
membrane protein, palmitoylated 1, 55kDa
NA;phosphatidylethanolamine binding protein 1
serpin peptidase inhibitor, clade B (ovalbumin), member 2
protocadherin 1
platelet-derived growth factor alpha polypeptide
Pim-1 proto-oncogene, serine/threonine kinase
mitogen-activated protein kinase kinase 6
pentraxin 3, long
regulator of G-protein signaling 2

1 regulator of G-protein signaling 16
2 replication protein A3, 14kDa
3 S100 calcium binding protein A8
4 chemokine (C-C motif) ligand 3
5 thymidine kinase 1, soluble
6 pleckstrin homology-like domain, family A, member 2
7 TTK protein kinase
8 coronin, actin binding protein, 2A
9 high mobility group AT-hook 2
10 G protein-coupled receptor 68
11 frizzled class receptor 1
12 histone cluster 2, H2ac
13 histone cluster 1, H3b
14 RAD54-like (S. cerevisiae)
15 tyrosylprotein sulfotransferase 1
16 HIRA interacting protein 3
17 semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
18 basic helix-loop-helix family, member e40
19 exonuclease 1
20 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
21 ATP-binding cassette, sub-family C (CFTR/MRP), member 3
22 cathepsin F
23 tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
24 gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase)
25 Fc fragment of IgG binding protein
26 immediate early response 3
27 sequestosome 1
28 ZPR1 zinc finger
29 coagulation factor II (thrombin) receptor-like 3
30 protein regulator of cytokinesis 1
31 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
32 BCL2-related protein A1
33 polo-like kinase 3
34 DNA-damage-inducible transcript 3
35 fms-related tyrosine kinase 3
36 guanine nucleotide binding protein (G protein), gamma 11
37 Ras-related associated with diabetes
38 serine hydroxymethyltransferase 1 (soluble)
39 solute carrier family 1 (glial high affinity glutamate transporter), member 3
40 NA;prolyl 4-hydroxylase, alpha polypeptide II
41 aurora kinase B
42 pituitary tumor-transforming 1
43 fatty acid desaturase 2
44 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
45 nuclear factor, erythroid 2-like 3
46 BUB1 mitotic checkpoint serine/threonine kinase
47 calmeglin
48 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
49 regulator of calcineurin 1
50 dual specificity phosphatase 2

1 dual specificity phosphatase 5
2 fibroblast activation protein, alpha
3 neuregulin 1
4 kinesin family member 11
5 microsomeal glutathione S-transferase 3
6 chemokine (C-C motif) ligand 20
7 sparc/osteonectin, cwcw and kazal-like domains proteoglycan (testican) 1
8 syntaxin 1A (brain)
9 adaptor-related protein complex 3, beta 2 subunit
10 cyclin B2
11 cytokine receptor-like factor 1
12 UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
13 apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
14 myosin binding protein H
15 B-cell CLL/lymphoma 3
16 calmodulin 3 (phosphorylase kinase, delta)
17 cyclin-dependent kinase inhibitor 3
18 E2F transcription factor 1
19 sphingosine-1-phosphate receptor 3
20 cortactin
21 GTP binding protein overexpressed in skeletal muscle
22 histone cluster 1, H1c
23 heat shock 70kDa protein 1A
24 heat shock 70kDa protein 1B
25 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
26 selenoprotein P, plasma, 1
27 solute carrier family 20 (phosphate transporter), member 1
28 vascular endothelial growth factor C
29 chromatin assembly factor 1, subunit B (p60)
30 eomesodermin
31 trophinin associated protein
32 poly (ADP-ribose) polymerase 2
33 ATP-binding cassette, sub-family A (ABC1), member 1
34 immunoglobulin superfamily containing leucine-rich repeat
35 natural killer cell granule protein 7
36 S100 calcium binding protein A12
37 serum/glucocorticoid regulated kinase 1
38 smoothened, frizzled class receptor
39 nuclear receptor subfamily 1, group H, member 3
40 peptidylprolyl isomerase F
41 kinesin family member 20A
42 ADP-ribosylation factor-like 4A
43 metallothionein 1A
44 metallothionein 1B;NA
45 metallothionein 1H
46 metallothionein 1X
47 heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
48 ATPase, class II, type 9A
49 tubulin, alpha 1b
50 tubulin, beta 3 class III

1 ST3 beta-galactoside alpha-2,3-sialyltransferase 6
2 NDC80 kinetochore complex component
3 platelet-derived growth factor receptor, alpha polypeptide
4 platelet-derived growth factor receptor-like
5 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
6 tumor necrosis factor, alpha-induced protein 3
7 tumor necrosis factor, alpha-induced protein 2
8 sperm associated antigen 5
9 fibulin 1
10 v-rel avian reticuloendotheliosis viral oncogene homolog B
11 tissue factor pathway inhibitor 2
12 pituitary tumor-transforming 2
13 phosphoglycerate dehydrogenase
14 BTG family, member 2
15 macrophage receptor with collagenous structure
16 EH-domain containing 1
17 chromobox homolog 1
18 kinesin family member 2C
19 ADAM metallopeptidase with thrombospondin type 1 motif, 8
20 WD repeat and HMG-box DNA binding protein 1
21 protease, serine, 23
22 citron rho-interacting serine/threonine kinase
23 nurim (nuclear envelope membrane protein)
24 paraneoplastic Ma antigen 2
25 Opa interacting protein 5
26 breast cancer 1, early onset
27 Wolf-Hirschhorn syndrome candidate 1
28 killer cell lectin-like receptor subfamily C, member 3
29 CD93 molecule
30 TPX2, microtubule-associated
31 methionine sulfoxide reductase B2
32 tubulin tyrosine ligase-like family member 1
33 extra spindle pole bodies like 1, separase
34 kinesin family member 4A
35 v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
36 DnaJ (Hsp40) homolog, subfamily B, member 9
37 glutaminyl-peptide cyclotransferase
38 RAD54 homolog B (*S. cerevisiae*)
39 six transmembrane epithelial antigen of the prostate 1
40 hyaluronan-mediated motility receptor (RHAMM)
41 PSMC3 interacting protein
42 G-protein signaling modulator 2
43 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5
44 SERTA domain containing 1
45 low density lipoprotein receptor-related protein 12
46 WD repeat domain 91
47 ubiquitin-conjugating enzyme E2T
48 inositol(myo)-1(or 4)-monophosphatase 2
49 hematopoietic cell signal transducer
50 integrin beta 3 binding protein (beta3-endonexin)

1 RASD family, member 2
2 protein phosphatase 1, regulatory subunit 15A
3 solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
4 tumor necrosis factor, alpha-induced protein 8
5 RAB26, member RAS oncogene family
6 linker for activation of T cells;NA
7 NIMA-related kinase 6
8 cell death-inducing DFFA-like effector b
9 Rho guanine nucleotide exchange factor (GEF) 10
10 KIAA0408
11 kinetochore associated 1
12 KIAA0101
13 Ras association (RalGDS/AF-6) domain family member 2
14 KIAA0586
15 discs, large (Drosophila) homolog-associated protein 5
16 secernin 1
17 tripartite motif containing 14
18 maternal embryonic leucine zipper kinase
19 kinesin family member 14
20 DnaJ (Hsp40) homolog, subfamily C, member 9
21 activity-regulated cytoskeleton-associated protein
22 tripartite motif containing 2
23 leucine rich repeat containing 8 family, member B;NA
24 lymphocyte antigen 96
25 mitochondrial pyruvate carrier 2
26 transmembrane protein 158 (gene/pseudogene)
27 zinc finger protein 521
28 retinoic acid induced 14
29 PHD finger protein 19
30 RIB43A domain with coiled-coils 2
31 family with sequence similarity 135, member B
32 complement component 1, q subcomponent, A chain
33 N(alpha)-acetyltransferase 20, NatB catalytic subunit
34 androgen-induced 1
35 polycystic kidney disease 2-like 1
36 cytochrome b5 reductase 2
37 prenylcysteine oxidase 1
38 centromere protein F, 350/400kDa
39 nucleolar and spindle associated protein 1
40 G-2 and S-phase expressed 1
41 ABI family, member 3
42 denticleless E3 ubiquitin protein ligase homolog (Drosophila)
43 tumor necrosis factor receptor superfamily, member 12A
44 chloride intracellular channel 5
45 polymerase (DNA directed), alpha 1, catalytic subunit
46 excision repair cross-complementation group 6-like
47 family with sequence similarity 46, member C
48 DEP domain containing 1
49 sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (sem
50 host cell factor C1 regulator 1 (XPO1 dependent)

1 PARP1 binding protein
2 cell division cycle associated 8
3 centrosomal protein 55kDa
4 abnormal spindle microtubule assembly
5 leucine-rich repeat LGI family, member 2
6 prolyl 3-hydroxylase 2
7 transmembrane protein 184C
8 proline rich 11
9 Holliday junction recognition protein
10 spermatogenesis associated 7
11 leucine-rich repeat containing G protein-coupled receptor 4
12 PDZ binding kinase
13 calcium/calmodulin-dependent protein kinase II inhibitor 1
14 cell migration inducing protein, hyaluronan binding
15 ELMO/CED-12 domain containing 1
16 cell division cycle associated 7-like
17 sulfatase 2
18 phosphodiesterase 7B
19 telomeric repeat binding factor 2, interacting protein
20 glucose-fructose oxidoreductase domain containing 1
21 Ras and Rab interactor 2
22 pseudouridylate synthase 7 (putative)
23 DNA-damage-inducible transcript 4
24 SLAM family member 8
25 kinesin family member 15
26 G protein-coupled receptor 84
27 apoptosis, caspase activation inhibitor
28 mannosidase, alpha, class 1C, member 1
29 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
30 pellino E3 ubiquitin protein ligase 1
31 SPC25, NDC80 kinetochore complex component
32 adenosine A3 receptor
33 heart development protein with EGF-like domains 1
34 tRNA methyltransferase 5
35 neuromedin B
36 hes family bHLH transcription factor 4
37 SLAM family member 7
38 solute carrier family 30 (zinc transporter), member 1
39 NLR family, CARD domain containing 4
40 AXL receptor tyrosine kinase
41 prokineticin 2
42 thymosin beta 15a
43 G protein-coupled receptor 88
44 potassium channel, two pore domain subfamily K, member 12
45 family with sequence similarity 111, member A
46 cell death-inducing DFFA-like effector c
47 ribokinase
48 SAM domain, SH3 domain and nuclear localization signals 1
49 chromosome 10 open reading frame 54
50 non-SMC condensin I complex, subunit G

1 popeye domain containing 3
2 regulatory factor X, 7
3 ZFP69 zinc finger protein B
4 membrane-spanning 4-domains, subfamily A, member 4A
5 transmembrane protein 106C
6 ChaC glutathione-specific gamma-glutamylcyclotransferase 1
7 human immunodeficiency virus type I enhancer binding protein 3
8 ATPase type 13A3
9 acyl-CoA synthetase short-chain family member 3
10 yrdC N(6)-threonylcarbamoyltransferase domain containing
11 E2F transcription factor 8
12 SHC SH2-domain binding protein 1
13 CXADR-like membrane protein
14 ubiquitin-like modifier activating enzyme 5
15 DENN/MADD domain containing 2D
16 pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
17 dedicator of cytokinesis 5
18 PIF1 5-to-3 DNA helicase
19 coiled-coil domain containing 170
20 Fraser extracellular matrix complex subunit 1
21 tribbles pseudokinase 1
22 cytoplasmic polyadenylation element binding protein 4
23 endonuclease/exonuclease/phosphatase family domain containing 1
24 apolipoprotein L, 6
25 chromatin licensing and DNA replication factor 1
26 protein phosphatase 1, regulatory (inhibitor) subunit 14C
27 cytochrome P450, family 19, subfamily A, polypeptide 1
28 cell division cycle associated 3
29 MAX dimerization protein 3
30 APH1B gamma secretase subunit
31 katanin p60 subunit A-like 2
32 cyclin B1
33 MYCBP associated protein
34 PML-RARA regulated adaptor molecule 1
35 acyl-CoA dehydrogenase family, member 11
36 anthrax toxin receptor 1
37 plexin A1
38 zinc finger, MYND-type containing 12
39 polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like
40 family with sequence similarity 213, member A
41 zinc finger, BED-type containing 3
42 junctophilin 4
43 aspartate beta-hydroxylase
44 acyl-CoA synthetase short-chain family member 1
45 lysyl oxidase-like 3
46 proline/serine-rich coiled-coil 1
47 tubulin, alpha 1c
48 glycerol-3-phosphate acyltransferase 3
49 internexin neuronal intermediate filament protein, alpha
50 Fc receptor-like A
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1 chromosome 1 open reading frame 198
2 Rho guanine nucleotide exchange factor (GEF) 39
3 ZW10 interacting kinetochore protein
4 NIMA-related kinase 9
5 naked cuticle homolog 2 (Drosophila)
6 scinderin
7 urocortin 2
8 autophagy related 16-like 2
9 HAUS augmin-like complex, subunit 8
10 tripartite motif containing 47
11 ethanolaminephosphotransferase 1
12 sialic acid binding Ig-like lectin 11
13 transmembrane protein 200A
14 retinol binding protein 7, cellular
15 myosin light chain kinase
16 ANKH inorganic pyrophosphate transport regulator
17 calcium and integrin binding family member 3
18 anthrax toxin receptor 2;NA
19 phosphoserine aminotransferase 1
20 cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
21 oxysterol binding protein-like 1A
22 cell division cycle associated 5
23 phosphatase and actin regulator 3
24 collagen, type XI, alpha 2
25 osteoclast stimulatory transmembrane protein
26 Jun dimerization protein 2
27 cAMP responsive element binding protein 3-like 4
28 potassium channel tetramerization domain containing 12
29 toll-like receptor 4
30 kinesin family member 23
31 high mobility group nucleosomal binding domain 3
32 myeloma overexpressed
33 guanidinoacetate N-methyltransferase
34 secretory carrier membrane protein 5
35 bridging integrator 1
36 SPOC domain containing 1
37 ankyrin repeat domain 35
38 mitogen-activated protein kinase kinase 3
39 microsomal glutathione S-transferase 1
40 centrosomal protein 128kDa
41 cell division cycle associated 2
42 NA;zinc finger protein 366
43 interleukin 4 induced 1
44 KN motif and ankyrin repeat domains 1
45 NIM1 serine/threonine protein kinase
46 SH2 domain containing 3C
47 tachykinin 4 (hemokinin)
48 aldehyde dehydrogenase 1 family, member A2
49 retinol dehydrogenase 10 (all-trans)
50 DCN1, defective in cullin neddylation 1, domain containing 3
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1 lamin tail domain containing 2
2 transmembrane protein 145
3 solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9
4 interleukin 1 receptor antagonist
5 chromosome 1 open reading frame 162
6 Rho GTPase activating protein 27
7 metallothionein 1E;NA
8 formin-like 3
9 spermine oxidase
10 transmembrane and tetratricopeptide repeat containing 1
11 metallothionein 1M
12 nicotinamide nucleotide adenylyltransferase 3
13 gliomedin
14 ubiquitin-conjugating enzyme E2C
15 actin-related protein 2/3 complex inhibitor
16 protein kinase, membrane associated tyrosine/threonine 1
17 family with sequence similarity 101, member B
18 sphingosine kinase 1
19 TSC22 domain family, member 1
20 nebulin-related anchoring protein
21 ribonuclease, RNase A family, 1 (pancreatic)
22 aurora kinase A
23 LON peptidase N-terminal domain and ring finger 2
24 energy homeostasis associated
25 family with sequence similarity 111, member B
26 polymerase (DNA directed), theta
27 adhesion G protein-coupled receptor G1
28 forkhead box M1
29 myoglobin
30 stathmin 1
31 retinoic acid receptor responder (tazarotene induced) 1
32 chromosome 15 open reading frame 52
33 ATP-binding cassette, sub-family G (WHITE), member 1
34 metallothionein 1L (gene/pseudogene)
35 MIR155 host gene
36 growth arrest-specific 5 (non-protein coding);NA
37 pituitary tumor-transforming 3, pseudogene
38 hect domain and RLD 2 pseudogene 2
39 sialic acid binding Ig-like lectin 16 (gene/pseudogene)
40 NA;sperm acrosome associated 6, pseudogene
41 NA
42 ZMIZ1 antisense RNA 1
43 NA;THUMPD3 antisense RNA 1
44 NmrA-like family domain containing 1 pseudogene
45 NA
46 NA;STXBP5 antisense RNA 1
47 NA
48 NA
49 NA
50 long intergenic non-protein coding RNA 892;NA

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2	long intergenic non-protein coding RNA 1137
3	long intergenic non-protein coding RNA 941;NA
4	NA
5	NA
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Transcript ID
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Inc-KATNAL2-4:1
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7	NM_032208
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10	NM_033452
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18	NM_175618
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21	NM_182965
22	NM_2156
23	NM_25060
24	NM_5948
25	NR_001447
26	NR_002825
27	NR_033752
28	NR_038216
29	NR_046696
30	NR_103548
31	NR_103549
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Name
NA
NA
NA
MIR146A host gene
NA
NA
NA
myristoylated alanine-rich protein kinase C substrate
NA
NA
NA
NA
collagen, type IV, alpha 4
intercellular adhesion molecule 1
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
MET proto-oncogene, receptor tyrosine kinase
low density lipoprotein receptor
chemokine (C-X-C motif) ligand 8
5-aminolevulinate synthase 1
chemokine (C-C motif) ligand 3-like 3
chemokine (C-X-C motif) receptor 4
PHD finger protein 19
adenosine monophosphate deaminase 3
nuclear protein, transcriptional regulator, 1
topoisomerase (DNA) II alpha
selenoprotein P, plasma, 1
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
baculoviral IAP repeat containing 3
CD14 molecule
ATPase, Ca++ transporting, type 2C, member 1
metallothionein 1H
metallothionein 1G
chemokine (C-X3-C motif) receptor 1
interleukin-1 receptor-associated kinase 2
clusterin
chemokine (C-C motif) receptor 7
endothelin receptor type A
heme oxygenase 1
heat shock 70kDa protein 6 (HSP70B)
killer cell lectin-like receptor subfamily C, member 1
melanoma antigen family B2
malic enzyme 1, NADP(+)-dependent, cytosolic
matrix metalloproteinase 1
matrix metalloproteinase 12
matrix metalloproteinase 19
Pim-1 proto-oncogene, serine/threonine kinase
S100 calcium binding protein A8
chemokine (C-C motif) ligand 3
high mobility group AT-hook 2

1 G protein-coupled receptor 68
2 basic helix-loop-helix family, member e40
3 ATP-binding cassette, sub-family C (CFTR/MRP), member 3
4 Fc fragment of IgG binding protein
5 immediate early response 3
6 sequestosome 1
7 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
8 polo-like kinase 3
9 Ras-related associated with diabetes
10 solute carrier family 1 (glial high affinity glutamate transporter), member 3
11 nuclear factor, erythroid 2-like 3
12 dual specificity phosphatase 2
13 chemokine (C-C motif) ligand 20
14 adaptor-related protein complex 3, beta 2 subunit
15 B-cell CLL/lymphoma 3
16 GTP binding protein overexpressed in skeletal muscle
17 heat shock 70kDa protein 1A
18 heat shock 70kDa protein 1B
19 selenoprotein P, plasma, 1
20 vascular endothelial growth factor C
21 serum/glucocorticoid regulated kinase 1
22 metallothionein 1A
23 metallothionein 1B;NA
24 metallothionein 1H
25 metallothionein 1X
26 tubulin, beta 3 class III
27 tumor necrosis factor, alpha-induced protein 3
28 tumor necrosis factor, alpha-induced protein 2
29 v-rel avian reticuloendotheliosis viral oncogene homolog B
30 tissue factor pathway inhibitor 2
31 paraneoplastic Ma antigen 2
32 CD93 molecule
33 v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
34 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5
35 low density lipoprotein receptor-related protein 12
36 protein phosphatase 1, regulatory subunit 15A
37 solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
38 KIAA0408
39 activity-regulated cytoskeleton-associated protein
40 family with sequence similarity 135, member B
41 leucine-rich repeat LGI family, member 2
42 transmembrane protein 184C
43 PDZ binding kinase
44 Ras and Rab interactor 2
45 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
46 tRNA methyltransferase 5
47 hes family bHLH transcription factor 4
48 SLAM family member 7
49 solute carrier family 30 (zinc transporter), member 1
50 AXL receptor tyrosine kinase

1	
2	prokineticin 2
3	G protein-coupled receptor 88
4	popeye domain containing 3
5	CXADR-like membrane protein
6	coiled-coil domain containing 170
7	anthrax toxin receptor 1
8	glycerol-3-phosphate acyltransferase 3
9	urocortin 2
10	tripartite motif containing 47
11	sialic acid binding Ig-like lectin 11
12	
13	
14	
15	bridging integrator 1
16	mitogen-activated protein kinase kinase 3
17	NA;zinc finger protein 366
18	interleukin 4 induced 1
19	metallothionein 1E;NA
20	
21	
22	metallothionein 1M
23	family with sequence similarity 101, member B
24	sphingosine kinase 1
25	
26	
27	
28	
29	metallothionein 1L (gene/pseudogene)
30	sialic acid binding Ig-like lectin 16 (gene/pseudogene)
31	NmrA-like family domain containing 1 pseudogene
32	NA
33	NA
34	NA
35	NA
36	
37	
38	
39	
40	
41	
42	
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Exposure: 24h Silver nanoparticles (20 nm)

Probe ID	TargetID	GeneSymbol
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A_23_P86470	NM_003956	CH25H
A_23_P150316	NM_002426	MMP12
A_33_P3412087	NM_025059	CCDC170
A_23_P151046	NM_002259	KLRC1
A_24_P347378	NM_001629	ALOX5AP
A_23_P35995	NM_024769	CLMP
A_23_P256107	NM_006665	HPSE
A_23_P121926	NM_005410	SEPP1
A_23_P95930	NM_003483	HMGA2
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A_24_P931443	NM_003485	GPR68
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A_23_P211957	NM_001024847	TGFBR2
A_33_P3364268	NM_030915	LBH
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21	A_23_P145024	NM_000024	ADRB2
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44	A_23_P376799	NM_015262	FAM21C
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4	A_33_P7476087	NR_027007	THUMPD3-AS1
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6	A_23_P118427	NM_145109	MAP2K3
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22	A_32_P80741	NM_001007176	C8orf22
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28	A_23_P30603	NM_003649	DDO
29	A_32_P42574	NM_032800	C1orf198
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38	A_23_P214766	NM_006734	HIVEP2
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42	A_23_P208389	NM_021913	AXL
43	A_33_P3544856	Inc-ERC1-1:2	Inc-ERC1-1
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51	A_23_P34744	NM_000396	CTSK

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5	A_23_P411296	NM_005194	CEBPB
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7	A_24_P173754	NM_030806	C1orf21
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24	A_23_P341223	NM_014851	KLHL21
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27	A_33_P3352970	NM_001570	IRAK2
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30	A_24_P22050	NM_017817	RAB20
31	A_24_P226008	NM_007283	MGLL
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34	A_23_P146572	NM_015392	NPDC1
35	A_24_P941268	NM_007220	CA5B
36	A_24_P96961	NM_025106	SPSB1
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43	A_22_P00018123	lnc-ZNF484-1:1	lnc-ZNF484-1
44	A_23_P50535	NM_004409	DMPK
45	A_24_P145066	NM_183416	KIF1B
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47	A_24_P318656	NM_000212	ITGB3
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51	A_33_P3390172	NM_001145271	ADAMDEC1
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50	A_23_P202156	NM_001288724	NFKB2
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40	A_23_P106844	NM_005953	MT2A
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44	A_22_P00004191	XR_246017	LOC101928617
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47	A_24_P63522	NM_002130	HMGCS1
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58	A_21_P0005747	ENST00000523572	
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60	A_33_P3364864	NM_005746	NAMPT

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11	A_24_P212539	NM_138801	GALM
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16	A_33_P3413671	NM_007314	ABL2
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35	A_23_P121064	NM_002852	PTX3
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41	A_33_P3224800	ENST00000435988	NCF1B
42	A_23_P213959	NM_133263	PPARGC1B
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44	A_21_P0013032	ENST00000368966	CCDC162P
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50	A_33_P3222367	NR_002988	SNORA74B
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52	A_23_P253321	NM_006228	PNOC
53	A_33_P3352407	ENST00000434913	
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55	A_21_P0003882	Inc-CTBP1-1:1	Inc-CTBP1-1
56	A_23_P132277	NM_006739	MCM5
57	A_23_P60146	NM_006207	PDGFRL
58	A_33_P3270636	NM_001272068	SHISA5
59	A_21_P0011522	TCONS_I2_000106(XLOC_I2_005692	
60	A_23_P67971	NM_138801	GALM

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3	A_24_P323598	NM_001017420	ESCO2
4	A_33_P3224803	NM_000265	NCF1
5	A_23_P320897	NM_001195215	DENND1B
6	A_23_P60591	NM_003315	DNAJC7
7	A_24_P295245	NM_032467	ASPH
8	A_22_P00012499	NR_015377	PAX8-AS1
9	A_23_P97623	NM_022157	RRAGC
10	A_23_P153562	NM_001736	C5AR1
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12	A_33_P3336696	ENST00000361335	ND4L
13	A_23_P69179	NM_018192	P3H2
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15	A_23_P360754	NM_005099	ADAMTS4
16	A_33_P3408054	ENST00000602906	
17	A_21_P0014273	ENST00000532805	CYP2R1
18	A_32_P342064	NM_002032	FTH1
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20	A_23_P215634	NM_001013398	IGFBP3
21	A_33_P3258046	NM_170685	TAC4
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23	A_23_P368886	NM_175856	CHSY3
24	A_21_P0000108	NM_001190702	MTRNR2L8
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26	A_33_P3347040	NM_001242901	DPP9-AS1
27	A_33_P3849600	M30627	HSP90AA2P
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description	adj. p value	log 2 FC
limb bud and heart development	0	-2.18
roundabout guidance receptor 4	0	-1.62
lysyl oxidase-like 4	0	-1.48
HOP homeobox	0	-1.47
Ras and Rab interactor 2	0	-1.45
Fc fragment of IgG binding protein	0	-1.42
MIR503 host gene	0	-1.39
cholesterol 25-hydroxylase	0	-1.38
matrix metalloproteinase 12	0	-1.35
coiled-coil domain containing 170	0	-1.35
killer cell lectin-like receptor subfamily C, member 1	0	-1.33
arachidonate 5-lipoxygenase-activating protein	0	-1.22
CXADR-like membrane protein	0	-1.18
heparanase	0	-1.17
selenoprotein P, plasma, 1	0	-1.16
high mobility group AT-hook 2	0	-1.16
collagen, type IV, alpha 4	0	-1.16
G protein-coupled receptor 68	0	-1.13
bone morphogenetic protein 4	0	-1.1
cholinergic receptor, muscarinic 2	0	-1.09
selenoprotein W, 1	0	-1.08
neurotensin receptor 1 (high affinity)	0	-1.06
cathepsin C	0	-1.06
neurogranin (protein kinase C substrate, RC3)	0	-1.05
protein tyrosine phosphatase type IVA, member 3	0	-1.05
chemokine (C-X3-C motif) receptor 1	0	-1.03
sialic acid binding Ig-like lectin 11	0	-1.02
protein kinase domain containing, cytoplasmic	0	-1.01
sortilin-related receptor, L(DLR class) A repeats containing	0	-1
integral membrane protein 2C	0	-1
multimerin 2	0	-0.99
5-nucleotidase, ecto (CD73)	0	-0.99
enabled homolog (Drosophila)	0	-0.98
protein kinase domain containing, cytoplasmic	0	-0.98
NA	0	-0.97
transmembrane protein 184C	0	-0.97
cholinergic receptor, muscarinic 3	0	-0.96
CD93 molecule	0	-0.96
cathepsin C	0	-0.96
transforming growth factor, beta receptor II (70/80kDa)	0	-0.95
limb bud and heart development	0	-0.93
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	0	-0.92
family with sequence similarity 101, member B	0	-0.92
family with sequence similarity 135, member B	0	-0.92
wntless Wnt ligand secretion mediator	0	-0.88
TOX high mobility group box family member 2	0	-0.85
selenoprotein W, 1	0	-0.84

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2	spermine oxidase	0	-0.82
3	out at first homolog	0	-0.82
4	transforming growth factor, beta-induced, 68kDa	0	-0.8
5	adenosine deaminase, RNA-specific, B1	0	-0.8
6	sortilin 1	0	-0.8
7			
8	pyridine nucleotide-disulphide oxidoreductase domain 2	0	-0.79
9	matrix metalloproteinase 7	0	-0.79
10	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	0	-0.78
11	sprouty-related, EVH1 domain containing 1	0	-0.78
12	glutathione peroxidase 1	0	-0.78
13			
14	carcinoembryonic antigen-related cell adhesion molecule 6 (non	0	-0.77
15	NA	0	-0.77
16	ATPase, aminophospholipid transporter, class I, type 8B, membe	0	-0.76
17	NA	0	-0.75
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19	sema domain, immunoglobulin domain (Ig), transmembrane don	0	-0.75
20	long intergenic non-protein coding RNA 341	0	-0.75
21	pleckstrin 2	0	-0.75
22	NA	0	-0.74
23	limb bud and heart development	0	-0.74
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25	adrenoceptor beta 2, surface	0	-0.73
26	mast cell-expressed membrane protein 1	0	-0.73
27	PHD finger protein 19	0	-0.73
28	NA	0	-0.72
29	tubulin, alpha 4a	0	-0.72
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31	polymeric immunoglobulin receptor	0	-0.72
32	S100 calcium binding protein A4	0	-0.71
33	protoporphyrinogen oxidase	0	-0.69
34	integrin, beta 7	0	-0.69
35	Tctex1 domain containing 1	0	-0.68
36	sialic acid binding Ig-like lectin 16 (gene/pseudogene)	0	-0.68
37			
38	sterile alpha motif and leucine zipper containing kinase AZK	0	-0.67
39	leukocyte immunoglobulin-like receptor, subfamily B (with TM al	0	-0.67
40	NA	0	-0.66
41	cysteinyl leukotriene receptor 1	0	-0.66
42	G protein-coupled receptor 84	0	-0.65
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44	RecQ mediated genome instability 2	0	-0.65
45	small cell adhesion glycoprotein	0	-0.65
46	RAS protein activator like 3	0	-0.64
47	chromosome 2 open reading frame 91	0	-0.6
48	pecanex-like 2 (Drosophila)	0	-0.58
49			
50	ankyrin repeat domain 1 (cardiac muscle)	0	0.58
51	vesicle amine transport 1	0	0.58
52	family with sequence similarity 21, member C	0	0.58
53	CDK5 regulatory subunit associated protein 2	0	0.58
54	cathepsin Z	0	0.58
55			
56	von Willebrand factor A domain containing 5A	0	0.58
57	claudin 23	0	0.59
58	PR domain containing 13	0	0.59
59	NCK-associated protein 1	0	0.59
60	sialidase 1 (lysosomal sialidase)	0	0.59

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2	NA	0	0.6
3	NA	0	0.6
4	NA	0	0.6
5	NA	0	0.61
6	mitogen-activated protein kinase kinase 3	0	0.62
7	ubiquilin 1	0	0.63
8	NA	0	0.64
9	NA	0	0.64
10	NA	0	0.64
11	Niemann-Pick disease, type C1	0	0.64
12	neuropeptide FF receptor 2	0	0.64
13	phosphodiesterase 4D interacting protein	0	0.64
14	apolipoprotein C-I	0	0.64
15	zinc finger, AN1-type domain 5	0	0.64
16	transmembrane protein 167B	0	0.64
17	N-myristoyltransferase 2	0	0.65
18	claudin 14	0	0.65
19	ATPase, H ⁺ transporting, lysosomal 14kDa, V1 subunit F	0	0.65
20	coiled-coil domain containing 77	0	0.65
21	pleckstrin homology domain containing, family B (evectins) mem	0	0.65
22	zinc finger protein 746	0	0.65
23	chromosome 8 open reading frame 22	0	0.65
24	ZMIZ1 antisense RNA 1	0	0.66
25	glucan (1,4-alpha-), branching enzyme 1	0	0.66
26	abhydrolase domain containing 6	0	0.66
27	Cbl proto-oncogene B, E3 ubiquitin protein ligase	0	0.66
28	interferon-induced protein with tetratricopeptide repeats 2	0	0.66
29	D-aspartate oxidase	0	0.66
30	chromosome 1 open reading frame 198	0	0.66
31	uncharacterized LOC153811	0	0.66
32	lactate dehydrogenase A-like 6B	0	0.67
33	Pim-3 proto-oncogene, serine/threonine kinase	0	0.67
34	ras homolog family member Q	0	0.67
35	acyl-CoA synthetase long-chain family member 1	0	0.68
36	solute carrier family 11 (proton-coupled divalent metal ion trans	0	0.68
37	cathepsin V	0	0.68
38	thyroid hormone receptor, alpha	0	0.68
39	human immunodeficiency virus type I enhancer binding protein	0	0.68
40	ras homolog family member Q	0	0.68
41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0	0.68
42	oncostatin M	0	0.69
43	AXL receptor tyrosine kinase	0	0.69
44	long intergenic non-protein coding RNA 942	0	0.69
45	long intergenic non-protein coding RNA, p53 induced transcript	0	0.7
46	complement factor H	0	0.7
47	transmembrane protein 251	0	0.7
48	phosphatidic acid phosphatase type 2A	0	0.7
49	transmembrane protein 144	0	0.7
50	NA	0	0.71
51	WW domain binding protein 5	0	0.71
52	cathepsin K	0	0.71

1			
2	solute carrier family 1 (glial high affinity glutamate transporter),	0	0.71
3	solute carrier family 36 (proton/amino acid symporter), member	0	0.71
4	NA	0	0.72
5	CCAAT/enhancer binding protein (C/EBP), beta	0	0.72
6	atlastin GTPase 1	0	0.72
7	chromosome 1 open reading frame 21	0	0.72
8	synaptophysin-like 2	0	0.72
9	receptor-interacting serine-threonine kinase 2	0	0.73
10	oxidation resistance 1	0	0.73
11	NA	0	0.73
12	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	0	0.73
13	solute carrier family 38, member 6	0	0.73
14	NA	0	0.74
15	NA	0	0.74
16	NA	0	0.74
17	NA	0	0.74
18	transmembrane protein 255A	0	0.74
19	regulator of G-protein signaling 4	0	0.74
20	coiled-coil domain containing 88A	0	0.74
21	solute carrier family 11 (proton-coupled divalent metal ion trans	0	0.74
22	fatty acid binding protein 3, muscle and heart	0	0.74
23	NA	0	0.74
24	glucagon	0	0.74
25	interleukin 15	0	0.75
26	lactamase, beta	0	0.75
27	apoptosis-inducing factor, mitochondrion-associated, 2	0	0.75
28	nuclear receptor subfamily 1, group H, member 3	0	0.75
29	NAD(P)H dehydrogenase, quinone 1	0	0.76
30	phospholipase D family, member 6	0	0.76
31	mitogen-activated protein kinase kinase 3	0	0.76
32	GM2 ganglioside activator	0	0.76
33	sterile alpha motif domain containing 9-like	0	0.77
34	cystatin B (stefin B)	0	0.77
35	methyltransferase like 1	0	0.77
36	5-aminolevulinate synthase 1	0	0.77
37	Myb/SANT-like DNA-binding domain containing 3	0	0.77
38	NA	0	0.77
39	NA	0	0.78
40	Pim-1 proto-oncogene, serine/threonine kinase	0	0.78
41	NA	0	0.78
42	zinc finger protein 365	0	0.78
43	serum/glucocorticoid regulated kinase 1	0	0.79
44	chemokine (C-C motif) receptor-like 2	0	0.79
45	myosin X	0	0.79
46	NA	0	0.8
47	NA	0	0.8
48	NA	0	0.8
49	glutaredoxin (thioltransferase)	0	0.8
50	kinesin family member 1B	0	0.8
51	sterile alpha motif domain containing 9-like	0	0.8

1			
2	NA	0	0.81
3	tumor protein D52-like 1	0	0.81
4	activating transcription factor 3	0	0.81
5	galactosidase, alpha	0	0.81
6	deafness, autosomal dominant 5	0	0.81
7	family with sequence similarity 21, member C	0	0.81
8	NA	0	0.82
9	troponin I type 2 (skeletal, fast)	0	0.82
10	heat shock 105kDa/110kDa protein 1	0	0.82
11	perilipin 4	0	0.82
12	NA	0	0.83
13	protein C (inactivator of coagulation factors Va and VIIIa)	0	0.83
14	ATPase, H ⁺ transporting, lysosomal 50/57kDa, V1 subunit H	0	0.83
15	ATPase, H ⁺ transporting, lysosomal 70kDa, V1 subunit A	0	0.83
16	pleckstrin homology domain containing, family M, member 3	0	0.83
17	jun proto-oncogene	0	0.84
18	ghrelin/obestatin prepropeptide	0	0.85
19	lectin, galactoside-binding, soluble, 8	0	0.85
20	NA	0	0.86
21	NA	0	0.86
22	glutathione S-transferase mu 3 (brain)	0	0.86
23	microsomal glutathione S-transferase 1	0	0.86
24	interferon induced with helicase C domain 1	0	0.86
25	N(alpha)-acetyltransferase 50, NatE catalytic subunit	0	0.86
26	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 1	0	0.87
27	nuclear factor, erythroid 2-like 3	0	0.87
28	dendritic cell-associated nuclear protein	0	0.87
29	growth arrest and DNA-damage-inducible, gamma	0	0.87
30	urocortin 2	0	0.87
31	neurolysin (metallopeptidase M3 family)	0	0.87
32	ubiquitin protein ligase E3 component n-recogin 4	0	0.87
33	NA	0	0.88
34	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	0	0.88
35	SH3-domain binding protein 5 (BTK-associated)	0	0.88
36	prokineticin 2	0	0.88
37	ribosomal protein S6 kinase, 90kDa, polypeptide 2	0	0.88
38	NA	0	0.89
39	NA	0	0.9
40	NA	0	0.9
41	tripartite motif family-like 2	0	0.9
42	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	0	0.9
43	NA	0	0.91
44	NA	0	0.91
45	NA	0	0.91
46	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog	0	0.91
47	leupaxin	0	0.91
48	cytoplasmic polyadenylation element binding protein 1	0	0.91
49	NA	0	0.92
50	NA	0	0.92
51	melanoregulin	0	0.92

1			
2	tubulin, beta 2A class IIa	0	0.92
3	low density lipoprotein receptor	0	0.92
4	hexokinase 2	0	0.92
5	sphingosine kinase 1	0	0.92
6	transcription factor EC	0	0.92
7	nuclear receptor interacting protein 3	0	0.92
8	tubulin tyrosine ligase-like family member 4	0	0.92
9	mannose-P-dolichol utilization defect 1	0	0.92
10	glutathione reductase	0	0.93
11	adaptor-related protein complex 3, beta 2 subunit	0	0.93
12	NA	0	0.94
13	NA	0	0.94
14	glycerol-3-phosphate acyltransferase 3	0	0.94
15	heat shock 27kDa protein 3	0	0.94
16	NA	0	0.95
17	endothelial PAS domain protein 1	0	0.95
18	aldo-keto reductase family 1, member B10 (aldose reductase)	0	0.95
19	serine dehydratase-like	0	0.95
20	spire-type actin nucleation factor 1	0	0.95
21	amidohydrolase domain containing 2	0	0.95
22	NA	0	0.96
23	chromosome 1 open reading frame 226	0	0.96
24	epithelial stromal interaction 1 (breast)	0	0.96
25	mitogen-activated protein kinase 10	0	0.96
26	CD83 molecule	0	0.96
27	vestigial-like family member 2	0	0.96
28	monoglyceride lipase	0	0.96
29	phosphodiesterase 4D interacting protein	0	0.96
30	MIR146A host gene	0	0.96
31	F-box protein 30	0	0.97
32	protein C (inactivator of coagulation factors Va and VIIIa)	0	0.97
33	ATPase, Ca ⁺⁺ transporting, type 2C, member 1	0	0.98
34	intercellular adhesion molecule 1	0	0.98
35	melanoma antigen family B2	0	0.98
36	protein phosphatase 1, regulatory subunit 15A	0	0.98
37	phosphodiesterase 4D interacting protein	0	0.98
38	solute carrier family 48 (heme transporter), member 1	0	0.98
39	tRNA methyltransferase 5	0	0.98
40	NA	0	0.99
41	NA	0	0.99
42	methylenetetrahydrofolate dehydrogenase (NADP ⁺ dependent)	0	0.99
43	nuclear receptor interacting protein 3	0	0.99
44	interleukin 13 receptor, alpha 2	0	0.99
45	basic helix-loop-helix family, member e40	0	0.99
46	transaldolase 1	0	0.99
47	pannexin 2	0	0.99
48	NA	0	1
49	metallothionein 1E	0	1.01
50	v-rel avian reticuloendotheliosis viral oncogene homolog B	0	1.01
51	tumor necrosis factor, alpha-induced protein 3	0	1.01
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2	NA	0	1.02
3	glucosidase, beta, acid 3 (gene/pseudogene)	0	1.02
4	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	0	1.02
5	NA	0	1.03
6	KIAA0408	0	1.03
7	arrestin domain containing 4	0	1.03
8	phospholipase A2, group IVC (cytosolic, calcium-independent)	0	1.03
9	Rho-related BTB domain containing 3	0	1.03
10	NA	0	1.04
11	V-set and immunoglobulin domain containing 10 like	0	1.04
12	tumor necrosis factor, alpha-induced protein 2	0	1.04
13	BCL2-associated athanogene 3	0	1.04
14	TRAF-interacting protein with forkhead-associated domain, family 1	0	1.04
15	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0	1.05
16	tubulin, beta 3 class III	0	1.05
17	SLAM family member 7	0	1.05
18	NA	0	1.06
19	NA	0	1.06
20	somatostatin receptor 2	0	1.06
21	outer dense fiber of sperm tails 3B	0	1.06
22	NA	0	1.07
23	kelch-like family member 21	0	1.07
24	transmembrane 4 L six family member 19	0	1.07
25	phosphodiesterase 4D interacting protein	0	1.07
26	interleukin-1 receptor-associated kinase 2	0	1.07
27	interferon induced transmembrane protein 10	0	1.07
28	family with sequence similarity 189, member A2	0	1.08
29	RAB20, member RAS oncogene family	0	1.08
30	monoglyceride lipase	0	1.08
31	NA	0	1.08
32	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	0	1.08
33	folliculin interacting protein 2	0	1.08
34	NA	0	1.09
35	dual specificity phosphatase 13	0	1.09
36	leucine rich repeat containing 3B	0	1.09
37	hydroxycarboxylic acid receptor 3	0	1.09
38	phosphodiesterase 4D interacting protein	0	1.09
39	ribosomal protein S6 kinase, 90kDa, polypeptide 2	0	1.09
40	2-5-oligoadenylate synthetase-like	0	1.1
41	tumor necrosis factor, alpha-induced protein 6	0	1.1
42	DnaJ (Hsp40) homolog, subfamily A, member 4	0	1.1
43	interleukin 36, beta	0	1.1
44	NA	0	1.11
45	cytotoxic and regulatory T cell molecule	0	1.11
46	tissue factor pathway inhibitor 2	0	1.11
47	BMP and activin membrane-bound inhibitor	0	1.11
48	C-type lectin domain family 19, member A	0	1.11
49	matrix metalloproteinase 19	0	1.12
50	microtubule-associated protein 1B	0	1.12
51	immediate early response 5	0	1.13

1			
2	growth arrest and DNA-damage-inducible, beta	0	1.13
3	dual specificity phosphatase 1	0	1.14
4	peroxiredoxin 1	0	1.14
5	aquaporin 1 (Colton blood group)	0	1.14
6	NA	0	1.15
7	dihydropyrimidinase-like 3	0	1.15
8	interferon-induced protein 44-like	0	1.16
9	nuclear protein, transcriptional regulator, 1	0	1.16
10	coiled-coil domain containing 85A	0	1.16
11	NA	0	1.17
12	NA	0	1.17
13	NA	0	1.17
14	homogentisate 1,2-dioxygenase	0	1.18
15	kelch-like family member 6	0	1.18
16	peroxiredoxin 1	0	1.18
17	NA	0	1.2
18	chromosome 11 open reading frame 96	0	1.2
19	NA	0	1.21
20	regulating synaptic membrane exocytosis 3	0	1.22
21	basic helix-loop-helix family, member e41	0	1.23
22	Rho family GTPase 3	0	1.24
23	corepressor interacting with RBPJ, 1	0	1.24
24	NA	0	1.25
25	MX dynamin-like GTPase 1	0	1.25
26	Ras-related associated with diabetes	0	1.25
27	nuclear factor of kappa light polypeptide gene enhancer in B-cell	0	1.26
28	malic enzyme 1, NADP(+)-dependent, cytosolic	0	1.26
29	PAX8 antisense RNA 1	0	1.27
30	muscle RAS oncogene homolog	0	1.27
31	low density lipoprotein receptor-related protein 12	0	1.28
32	growth arrest and DNA-damage-inducible, gamma	0	1.29
33	NA	0	1.31
34	chemokine (C-C motif) ligand 15	0	1.31
35	NA	0	1.32
36	long intergenic non-protein coding RNA 942	0	1.33
37	DnaJ (Hsp40) homolog, subfamily C, member 6	0	1.33
38	sialic acid binding Ig-like lectin 15	0	1.34
39	synaptophysin-like 2	0	1.34
40	sequestosome 1	0	1.35
41	tripartite motif containing 47	0	1.35
42	MET proto-oncogene, receptor tyrosine kinase	0	1.37
43	NA	0	1.38
44	NA	0	1.38
45	purinergic receptor P2X, ligand gated ion channel, 7	0	1.38
46	neuronal cell adhesion molecule	0	1.39
47	NA	0	1.4
48	calcium channel, voltage-dependent, T type, alpha 1G subunit	0	1.4
49	hemicentin 1	0	1.4
50	solute carrier family 30 (zinc transporter), member 2	0	1.4
51	NA	0	1.41

1			
2	interleukin 4 induced 1	0	1.41
3	NA	0	1.44
4	small glutamine-rich tetratricopeptide repeat (TPR)-containing, t	0	1.45
5	radical S-adenosyl methionine domain containing 2	0	1.46
6	nuclear receptor subfamily 4, group A, member 3	0	1.48
7	glutamate-cysteine ligase, catalytic subunit	0	1.49
9	chromogranin A	0	1.49
10	NA	0	1.5
11	NA	0	1.5
12	tripartite motif containing 16-like	0	1.5
14	storkhead box 2	0	1.5
15	NA	0	1.52
16	NA	0	1.53
17	interferon-induced protein with tetratricopeptide repeats 1	0	1.54
18	Epstein-Barr virus induced 3	0	1.55
19	zinc finger protein 365	0	1.55
20	NA	0	1.55
21	NA	0	1.55
22	NA	0	1.57
23	DnaJ (Hsp40) homolog, subfamily B, member 1	0	1.57
24	NA	0	1.59
25	spermidine/spermine N1-acetyltransferase 1	0	1.59
26	testis expressed 19	0	1.59
27	hepcidin antimicrobial peptide	0	1.6
28	spermidine/spermine N1-acetyltransferase 1	0	1.6
29	solute carrier family 30 (zinc transporter), member 1	0	1.61
30	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	0	1.62
31	KIT ligand	0	1.63
32	chromosome 22 open reading frame 42	0	1.65
33	TBC1 domain family, member 2	0	1.65
34	solute carrier family 26 (anion exchanger), member 11	0	1.66
35	uncharacterized LOC283485	0	1.66
36	pirin (iron-binding nuclear protein)	0	1.67
37	thioredoxin reductase 1	0	1.67
38	CD86 molecule	0	1.68
39	NA	0	1.69
40	NA	0	1.69
41	musculin	0	1.69
42	coiled-coil domain containing 85A	0	1.7
43	cytochrome P450, family 27, subfamily A, polypeptide 1	0	1.7
44	uncharacterized LOC400958	0	1.71
45	chemokine (C-C motif) ligand 20	0	1.71
46	chromosome 12 open reading frame 50	0	1.71
47	NA	0	1.73
48	NA	0	1.74
49	adenylate kinase 8	0	1.75
50	zinc finger, AN1-type domain 2A	0	1.77
51	NA	0	1.78
52	clusterin	0	1.78
53	crystallin, alpha B	0	1.78
54	adrenomedullin	0	1.79
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2	tetraspanin 10	0	1.8
3	chemokine (C-C motif) ligand 4	0	1.81
4	cancer susceptibility candidate 15 (non-protein coding)	0	1.82
5	peptidase inhibitor 3, skin-derived	0	1.82
6	NA	0	1.84
7	beta-1,4-N-acetyl-galactosaminyl transferase 1	0	1.84
8	chemokine (C-X-C motif) receptor 4	0	1.85
9	serine dehydratase	0	1.85
10	chemokine (C-C motif) ligand 4	0	1.98
11	NmrA-like family domain containing 1 pseudogene	0	1.98
12	NA	0	1.99
13	chemokine (C-C motif) receptor 7	0	1.99
14	neuralized E3 ubiquitin protein ligase 3	0	2
15	dehydrogenase/reductase (SDR family) member 2	0	2.02
16	tryptophan 2,3-dioxygenase	0	2.04
17	NA	0	2.06
18	long intergenic non-protein coding RNA 520	0	2.07
19	hes family bHLH transcription factor 4	0	2.08
20	superoxide dismutase 2, mitochondrial	0	2.09
21	chemokine (C-X-C motif) ligand 3	0	2.18
22	VGF nerve growth factor inducible	0	2.32
23	chemokine (C-C motif) ligand 18 (pulmonary and activation-regu	0	2.34
24	phospholipase A2, group VII (platelet-activating factor acetylhyd	0	2.35
25	NA	0	2.37
26	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating	0	2.46
27	NA	0	2.48
28	oxidative stress induced growth inhibitor 1	0	2.49
29	coiled-coil domain containing 30	0	2.52
30	sulfiredoxin 1	0	2.56
31	popeye domain containing 3	0	2.57
32	chemokine (C-X-C motif) ligand 2	0	2.62
33	serine peptidase inhibitor, Kazal type 1	0	2.73
34	NA	0	2.8
35	chemokine (C-C motif) ligand 3-like 3	0	3.02
36	chemokine (C-C motif) ligand 3-like 3	0	3.11
37	heme oxygenase 1	0	3.15
38	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating	0	3.28
39	chemokine (C-C motif) ligand 3	0	3.29
40	solute carrier family 7 (anionic amino acid transporter light chain	0	3.38
41	heat shock 70kDa protein 1A	0	3.41
42	chemokine (C-X-C motif) ligand 2	0	3.5
43	metallothionein 1A	0	3.57
44	activity-regulated cytoskeleton-associated protein	0	3.71
45	metallothionein 1F	0	3.84
46	heat shock 70kDa protein 1B	0	3.93
47	NA	0	3.95
48	metallothionein 1L (gene/pseudogene)	0	4.03
49	metallothionein 1B	0	4.05
50	metallothionein 1H	0	4.07
51	NA	0	4.25

1			
2	chemokine (C-X-C motif) ligand 8	0	4.29
3	NA	0	4.43
4	metallothionein 1E	0	4.49
5	heat shock 70kDa protein 6 (HSP70B)	0	4.73
6	metallothionein 1H	0	5.03
7	metallothionein 1X	0	5.53
8	metallothionein 1M	0	5.54
9	metallothionein 1G	0	6.83
10	heat shock 70kDa protein 6 (HSP70B)	0	7.33
11	5-nucleotidase domain containing 2	0.000001	-1.34
12	coiled-coil domain containing 170	0.000001	-1.05
13	JAZF zinc finger 1	0.000001	-0.88
14	coiled-coil domain containing 109B	0.000001	-0.76
15	oxysterol binding protein-like 3	0.000001	-0.73
16	ankyrin 1, erythrocytic	0.000001	-0.72
17	MIR503 host gene	0.000001	-0.69
18	protein tyrosine kinase 2	0.000001	-0.69
19	NA	0.000001	-0.67
20	pleiomorphic adenoma gene 1	0.000001	-0.67
21	family with sequence similarity 64, member A	0.000001	-0.67
22	asialoglycoprotein receptor 2	0.000001	-0.66
23	Rho guanine nucleotide exchange factor (GEF) 3	0.000001	-0.66
24	adenosine A3 receptor	0.000001	-0.61
25	internexin neuronal intermediate filament protein, alpha	0.000001	-0.61
26	transcobalamin I (vitamin B12 binding protein, R binder family)	0.000001	-0.58
27	NA	0.000001	0.59
28	neuropeptide Y	0.000001	0.59
29	adaptor-related protein complex 5, zeta 1 subunit	0.000001	0.6
30	nicotinamide phosphoribosyltransferase	0.000001	0.6
31	BCL2-related protein A1	0.000001	0.62
32	thioredoxin	0.000001	0.62
33	interferon-induced protein with tetratricopeptide repeats 5	0.000001	0.63
34	CAP-GLY domain containing linker protein family, member 4	0.000001	0.64
35	hydroxysteroid (11-beta) dehydrogenase 1	0.000001	0.64
36	complement component 8, gamma polypeptide	0.000001	0.64
37	NA	0.000001	0.64
38	erythrocyte membrane protein band 4.1-like 2	0.000001	0.65
39	NA	0.000001	0.65
40	NA	0.000001	0.66
41	ankyrin repeat domain 37	0.000001	0.66
42	solute carrier family 17 (acidic sugar transporter), member 5	0.000001	0.66
43	family with sequence similarity 89, member A	0.000001	0.67
44	calcium channel, voltage-dependent, R type, alpha 1E subunit	0.000001	0.67
45	polyamine modulated factor 1 binding protein 1	0.000001	0.68
46	leucine rich repeat containing 2	0.000001	0.7
47	paraneoplastic Ma antigen 2	0.000001	0.7
48	aspartate beta-hydroxylase	0.000001	0.75
49	NA	0.000001	0.77
50	N-acylsphingosine amidohydrolase (acid ceramidase) 1	0.000001	0.79
51	guanylate binding protein 5	0.000001	0.8

1			
2	zinc finger protein 366	0.000001	0.9
3	GTP binding protein overexpressed in skeletal muscle	0.000001	0.91
4	NA	0.000001	0.94
5	uncharacterized LOC644727	0.000001	0.97
6	MX dynamin-like GTPase 2	0.000001	1
7	heat shock 105kDa/110kDa protein 1	0.000001	1.03
8	G protein-coupled receptor 35	0.000001	1.03
9	NA	0.000001	1.08
10	insulin induced gene 1	0.000001	1.14
11	NA	0.000001	1.16
12	bridging integrator 1	0.000002	-0.97
13	protein tyrosine phosphatase type IVA, member 3	0.000002	-0.88
14	crystallin, beta B1	0.000002	-0.75
15	leucine rich repeat containing 4	0.000002	-0.74
16	reversion-inducing-cysteine-rich protein with kazal motifs	0.000002	-0.72
17	transmembrane channel-like 8	0.000002	-0.69
18	PHD finger protein 19	0.000002	-0.67
19	rhopilin, Rho GTPase binding protein 1	0.000002	-0.67
20	G-2 and S-phase expressed 1	0.000002	-0.65
21	ret proto-oncogene	0.000002	-0.62
22	chromobox homolog 7	0.000002	-0.61
23	reticulocalbin 2, EF-hand calcium binding domain	0.000002	-0.61
24	STE20-related kinase adaptor beta	0.000002	-0.6
25	meteorin, glial cell differentiation regulator	0.000002	-0.59
26	pleckstrin homology domain containing, family B (evectins) mem	0.000002	0.58
27	NA	0.000002	0.59
28	NA	0.000002	0.61
29	sperm associated antigen 9	0.000002	0.63
30	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.000002	0.65
31	NA	0.000002	0.66
32	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	0.000002	0.68
33	NA	0.000002	0.71
34	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.000002	0.76
35	FK506 binding protein 4, 59kDa	0.000002	0.77
36	NA	0.000002	0.78
37	NA	0.000002	0.81
38	baculoviral IAP repeat containing 3	0.000002	0.85
39	unkempt family zinc finger-like	0.000002	0.91
40	long intergenic non-protein coding RNA 1010	0.000002	0.94
41	neutrophil cytosolic factor 2	0.000002	1.01
42	coiled-coil domain containing 172	0.000002	1.19
43	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d2	0.000002	1.22
44	transmembrane protein 158 (gene/pseudogene)	0.000003	-0.8
45	uncharacterized LOC100130417	0.000003	-0.77
46	eomesodermin	0.000003	-0.64
47	cadherin 2, type 1, N-cadherin (neuronal)	0.000003	-0.63
48	NA	0.000003	-0.6
49	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	0.000003	0.59
50	CD5 molecule-like	0.000003	0.62
51	mitogen-activated protein kinase kinase kinase 8	0.000003	0.62

1			
2	spire-type actin nucleation factor 1	0.000003	0.63
3	diacylglycerol kinase, gamma 90kDa	0.000003	0.63
4	myelin protein zero-like 1	0.000003	0.66
5	glycerol kinase	0.000003	0.68
6	CNKSR family member 3	0.000003	0.69
7	NA	0.000003	0.71
8	long intergenic non-protein coding RNA, p53 induced transcript	0.000003	0.72
9	interferon-induced protein with tetratricopeptide repeats 2	0.000003	0.72
10	integrin, alpha 6	0.000003	0.73
11	NA	0.000003	0.77
12	zinc finger, FYVE domain containing 16	0.000003	0.77
13	solute carrier family 12, member 8	0.000003	0.77
14	variable charge, X-linked 2	0.000003	0.78
15	glutathione reductase	0.000003	0.8
16	MSC antisense RNA 1	0.000003	0.82
17	NA	0.000003	0.93
18	P450 (cytochrome) oxidoreductase	0.000003	1.01
19	NA	0.000004	-1.15
20	secreted phosphoprotein 1	0.000004	-1.14
21	endothelin receptor type A	0.000004	-1.06
22	PDZ binding kinase	0.000004	-0.82
23	frizzled class receptor 1	0.000004	-0.69
24	pleckstrin homology domain containing, family B (evectins) mem	0.000004	0.63
25	solute carrier family 48 (heme transporter), member 1	0.000004	0.64
26	colony stimulating factor 1 (macrophage)	0.000004	0.64
27	interferon regulatory factor 7	0.000004	0.68
28	solute carrier family 2 (facilitated glucose transporter), member	0.000004	0.77
29	chitinase 1 (chitotriosidase)	0.000004	0.8
30	ras homolog family member Q	0.000004	0.86
31	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate syntha	0.000004	0.93
32	B-cell CLL/lymphoma 3	0.000004	1.19
33	platelet derived growth factor D	0.000005	-0.71
34	kalirin, RhoGEF kinase	0.000005	-0.69
35	synaptic vesicle glycoprotein 2B	0.000005	-0.61
36	catenin (cadherin-associated protein), alpha-like 1	0.000005	-0.6
37	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	0.000005	0.59
38	poly (ADP-ribose) polymerase family, member 9	0.000005	0.62
39	HECT and RLD domain containing E3 ubiquitin protein ligase 5	0.000005	0.63
40	BEN domain containing 6	0.000005	0.68
41	ISG15 ubiquitin-like modifier	0.000005	0.73
42	NA	0.000005	0.74
43	proenkephalin	0.000005	0.76
44	NA	0.000005	0.8
45	Ras-related GTP binding D	0.000006	0.58
46	transcription factor EC	0.000006	0.63
47	STXBP5 antisense RNA 1	0.000006	0.69
48	adenosine monophosphate deaminase 3	0.000006	0.7
49	thrombospondin 2	0.000007	-1
50	purinergic receptor P2Y, G-protein coupled, 12	0.000007	-0.88
51	anthrax toxin receptor 1	0.000007	-0.84

1			
2	NA	0.000007	-0.79
3	tubulin, alpha 4a	0.000007	-0.72
4	NUAK family, SNF1-like kinase, 2	0.000007	-0.69
5	SPARC-like 1 (hevin)	0.000007	-0.66
6	MAX dimerization protein 3	0.000007	-0.58
7	NA	0.000007	0.58
8	NA	0.000007	0.64
9	cytochrome b5 reductase 1	0.000007	0.65
10	bone morphogenetic protein 6	0.000007	0.67
11	ferritin, light polypeptide	0.000007	0.78
12	signal transducer and activator of transcription 1, 91kDa	0.000007	0.8
13	selenoprotein P, plasma, 1	0.000008	-0.88
14	NA	0.000008	-0.76
15	spinster homolog 3 (Drosophila)	0.000008	-0.65
16	NA	0.000008	0.6
17	trio Rho guanine nucleotide exchange factor	0.000008	0.6
18	lipoma HMGIC fusion partner-like 2	0.000008	0.62
19	nuclear receptor subfamily 4, group A, member 2	0.000008	0.63
20	proteasome 26S subunit, non-ATPase 1	0.000008	0.66
21	activating transcription factor 3	0.000008	0.74
22	ferritin, light polypeptide	0.000008	0.77
23	NA	0.000008	0.92
24	carboxypeptidase E	0.000009	-0.78
25	NA	0.000009	-0.68
26	NA	0.000009	0.66
27	2-5-oligoadenylate synthetase 3, 100kDa	0.000009	0.85
28	caveolin 1, caveolae protein, 22kDa	0.00001	-0.78
29	NA	0.00001	-0.77
30	chromosome 16 open reading frame 74	0.00001	-0.63
31	signal-induced proliferation-associated 1 like 2	0.00001	0.6
32	family with sequence similarity 213, member B	0.00001	0.61
33	pre-B-cell leukemia homeobox 4	0.00001	0.62
34	anoctamin 3	0.00001	0.68
35	methyltransferase like 1	0.000011	0.69
36	transmembrane protein 138	0.000011	0.72
37	zinc finger, AN1-type domain 5	0.000011	0.73
38	interferon, alpha-inducible protein 27	0.000011	0.85
39	NA	0.000012	-0.62
40	tripartite motif containing 22	0.000013	0.66
41	dendrocyte expressed seven transmembrane protein	0.000013	0.71
42	SOGA family member 3	0.000013	0.82
43	NA	0.000013	1.1
44	myristoylated alanine-rich protein kinase C substrate	0.000014	0.83
45	matrix metalloproteinase 1	0.000015	-1.68
46	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	0.000015	0.59
47	NA	0.000015	0.61
48	mastermind-like domain containing 1	0.000015	0.67
49	intraflagellar transport 122 homolog (Chlamydomonas) pseudog	0.000016	0.76
50	chemokine (C-X-C motif) ligand 14	0.000016	0.8
51	CD163 molecule	0.000017	-0.86

1			
2	NA	0.000017	0.77
3	collagen, type VI, alpha 1	0.000017	0.91
4	brain abundant, membrane attached signal protein 1	0.000018	0.58
5	kynureninase	0.000018	0.79
6	NA	0.000018	0.8
7	formimidoyltransferase cyclodeaminase	0.000019	0.74
8	phosphogluconate dehydrogenase	0.000019	1.06
9	chromosome 1 open reading frame 106	0.00002	-0.66
10	oxysterol binding protein-like 3	0.00002	-0.64
11	Ras protein-specific guanine nucleotide-releasing factor 1	0.00002	0.6
12	NA	0.00002	0.62
13	chemokine (C-X-C motif) ligand 10	0.00002	1.18
14	vascular endothelial growth factor C	0.000021	-0.88
15	killer cell lectin-like receptor subfamily C, member 3	0.000021	-0.72
16	gap junction protein, delta 3, 31.9kDa	0.000021	0.75
17	regulator of G-protein signaling 20	0.000021	0.78
18	endothelin 1	0.000023	-0.69
19	V-set and immunoglobulin domain containing 4	0.000024	-0.83
20	biliverdin reductase B	0.000024	0.66
21	polo-like kinase 3	0.000024	0.69
22	discs, large homolog 3 (Drosophila)	0.000026	-0.78
23	cathepsin C	0.000026	-0.66
24	cytoskeleton associated protein 2-like	0.000027	-0.66
25	proteolipid protein 2 (colonic epithelium-enriched)	0.000027	-0.63
26	glutathione peroxidase 1	0.000027	-0.6
27	pleckstrin	0.000027	0.61
28	tyrosyl-DNA phosphodiesterase 2	0.000027	0.61
29	myeloid leukemia factor 1	0.000028	0.58
30	neural proliferation, differentiation and control, 1	0.000029	-0.61
31	carbonic anhydrase VB, mitochondrial	0.00003	-0.59
32	splA/ryanodine receptor domain and SOCS box containing 1	0.00003	0.63
33	N-myristoyltransferase 2	0.00003	0.65
34	CD14 molecule	0.000031	-1.26
35	aldo-keto reductase family 1, member A1 (aldehyde reductase)	0.000031	0.63
36	lymphocyte antigen 96	0.000031	0.65
37	2-5-oligoadenylate synthetase 2, 69/71kDa	0.000032	0.59
38	ferritin, light polypeptide	0.000032	0.71
39	NA	0.000033	-0.66
40	dystrophin myotonia-protein kinase	0.000033	-0.6
41	kinesin family member 1B	0.000033	0.63
42	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	0.000033	0.65
43	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.000034	0.75
44	SAGA complex associated factor 29 pseudogene	0.000034	0.75
45	NA	0.000034	0.94
46	spermatogenesis associated 13	0.000034	0.96
47	ADAM-like, decysin 1	0.000035	1.25
48	integral membrane protein 2C	0.000036	-1
49	NA	0.000037	0.88
50	sphingosine-1-phosphate receptor 1	0.000039	-0.79
51	NA	0.000039	0.61

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2	calmodulin regulated spectrin-associated protein family, member 1	0.000039	0.67
3	sperm associated antigen 9	0.000039	0.69
4	neutrophil cytosolic factor 1	0.000039	0.73
5	interleukin 32	0.000039	1.05
6	neurotensin	0.00004	-1.29
7	optineurin	0.000042	0.62
8	protocadherin 12	0.000043	-0.59
9	tumor necrosis factor receptor superfamily, member 8	0.000043	0.62
10	wntless Wnt ligand secretion mediator	0.000044	-0.66
11	triggering receptor expressed on myeloid cells-like 2	0.000044	-0.59
12	interferon-induced protein with tetratricopeptide repeats 3	0.000044	0.75
13	spermatogenesis associated, serine-rich 1	0.000045	0.63
14	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0.000045	0.71
15	myotubularin related protein 11	0.000046	-0.66
16	low density lipoprotein receptor-related protein 8, apolipoprotein	0.000046	0.58
17	NA	0.000046	0.66
18	lymphoid enhancer-binding factor 1	0.000048	-0.78
19	YME1-like 1 ATPase	0.000048	-0.66
20	retinol binding protein 7, cellular	0.000048	-0.6
21	cytochrome b561 family, member A3	0.000049	0.66
22	NA	0.00005	0.61
23	acid sensing (proton gated) ion channel 1	0.000051	-0.7
24	NA	0.000053	-0.66
25	sialic acid acetyltransferase	0.000057	-0.89
26	killer cell lectin-like receptor subfamily C, member 1	0.000057	-0.77
27	proteasome 26S subunit, non-ATPase 11	0.000059	0.69
28	fibroblast growth factor 13	0.00006	0.63
29	achaete-scute family bHLH transcription factor 2	0.00006	0.68
30	guanine nucleotide binding protein (G protein), alpha inhibiting 2	0.000064	-0.76
31	dual specificity phosphatase 2	0.000064	0.77
32	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1J	0.000067	-0.58
33	topoisomerase (DNA) II alpha	0.00007	-0.69
34	NA	0.00007	0.6
35	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-bu	0.000071	-0.84
36	kinesin family member 23	0.000071	-0.58
37	long intergenic non-protein coding RNA 1160	0.000072	-0.67
38	protein phosphatase methylesterase 1	0.000073	0.59
39	ZFP36 ring finger protein-like 1	0.000074	-0.58
40	NA	0.000074	0.91
41	homer scaffolding protein 2	0.000077	-0.77
42	monocyte to macrophage differentiation-associated	0.000078	-0.65
43	long intergenic non-protein coding RNA 926	0.000079	0.82
44	fibrillin 2	0.000083	-0.68
45	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0.000095	-0.69
46	splA/ryanodine receptor domain and SOCS box containing 1	0.000096	0.66
47	transmembrane protein 38B	0.0001	0.58
48	tripartite motif containing 58	0.000102	-0.63
49	TIMP metalloproteinase inhibitor 1	0.000103	-0.61
50	toll-like receptor 7	0.000105	-0.65
51	family with sequence similarity 26, member F	0.000106	-0.6

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2	syntaxin 1A (brain)	0.000107	-0.61
3	zinc finger protein 385B	0.000108	-0.71
4	tubulin, alpha 4a	0.000108	-0.63
5	NA	0.00011	-0.64
6	leucine-rich repeat LIG family, member 2	0.000112	-1.09
7	transmembrane protein 2	0.000117	-0.73
8	intercellular adhesion molecule 3	0.000119	-0.67
9	receptor tyrosine kinase-like orphan receptor 2	0.000121	0.59
10	cysteine and histidine-rich domain (CHORD) containing 1	0.000121	0.62
11	ATPase, H ⁺ transporting, lysosomal 56/58kDa, V1 subunit B2	0.000122	0.58
12	endothelin receptor type B	0.000123	0.67
13	neutrophil cytosolic factor 1	0.000123	0.9
14	FK506 binding protein 4, 59kDa	0.000133	0.62
15	integrin, alpha 6	0.000133	0.63
16	chondrolectin	0.000135	-0.65
17	mitogen-activated protein kinase kinase kinase 2	0.000135	0.61
18	NA	0.000135	0.8
19	neutrophil cytosolic factor 1	0.000136	0.8
20	prickle homolog 1	0.000137	-0.63
21	NA	0.000144	0.6
22	G protein-coupled receptor 88	0.000145	-0.93
23	T-cell immunoglobulin and mucin domain containing 4	0.000151	-0.63
24	glycoprotein (transmembrane) nmb	0.000153	0.63
25	Myb/SANT-like DNA-binding domain containing 3	0.000154	0.61
26	solute carrier family 38, member 6	0.000161	0.6
27	activating transcription factor 5	0.000162	0.64
28	proline rich 5 like	0.000175	-0.69
29	polo-like kinase 2	0.000176	-1.03
30	interleukin 18 binding protein	0.000177	0.6
31	zinc finger, BED-type containing 3	0.000178	0.65
32	NA	0.000185	0.94
33	leukocyte immunoglobulin-like receptor, subfamily B (with TM a	0.000188	0.64
34	NA	0.000191	-0.61
35	discs, large (Drosophila) homolog-associated protein 5	0.000191	-0.58
36	sulfide quinone reductase-like (yeast)	0.000191	0.67
37	NA	0.000193	-0.6
38	killer cell lectin-like receptor subfamily C, member 4	0.000196	-0.96
39	phosphoribosyl pyrophosphate synthetase 1	0.000198	-0.64
40	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associ	0.000198	-0.58
41	selenoprotein N, 1	0.000206	-0.69
42	oxytocin receptor	0.000212	-0.83
43	NA	0.000212	0.58
44	spermatogenesis associated 13	0.000221	0.59
45	calsyntenin 3	0.000223	-0.78
46	NA	0.000232	0.64
47	Ras-like without CAAX 1	0.000237	1
48	angiopoietin 1	0.00024	-0.66
49	glutamate receptor, metabotropic 8	0.000242	0.68
50	NA	0.000253	0.67
51	NA	0.000257	0.65

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2	immediate early response 3	0.000262	0.67
3	nuclear receptor subfamily 5, group A, member 2	0.000266	-0.69
4	NA	0.000274	0.8
5	DnaJ (Hsp40) homolog, subfamily B, member 4	0.000288	0.58
6	adrenoceptor beta 1	0.000294	-0.62
7	NA	0.000294	0.64
8	four jointed box 1	0.000302	-0.67
9	interferon stimulated exonuclease gene 20kDa	0.000312	0.61
10	CD164 molecule, sialomucin	0.000316	-0.79
11	tescalcin	0.000328	-0.58
12	microphthalmia-associated transcription factor	0.000329	0.72
13	CD19 molecule	0.000342	0.69
14	Fc fragment of IgM receptor	0.000359	-0.67
15	ribonuclease, RNase A family, 1 (pancreatic)	0.00038	-0.66
16	hes-related family bHLH transcription factor with YRPW motif 2	0.000392	-0.99
17	NA	0.000392	0.8
18	small ILF3/NF90-associated RNA A3	0.000393	0.62
19	cell migration inducing protein, hyaluronan binding	0.000398	-0.92
20	myoglobin	0.0004	-0.7
21	activating transcription factor 3	0.000404	0.65
22	RAS p21 protein activator (GTPase activating protein) 1	0.00042	-0.69
23	sestrin 1	0.00042	-0.58
24	Kruppel-like factor 12	0.000426	-0.58
25	NA	0.00045	0.91
26	hexokinase 3 (white cell)	0.000474	-0.59
27	fms-related tyrosine kinase 3	0.00048	-0.61
28	microphthalmia-associated transcription factor	0.000482	0.65
29	absent in melanoma 2	0.000486	-0.63
30	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (te	0.000503	-0.66
31	ferritin, heavy polypeptide-like 17	0.00053	0.67
32	immunoglobulin superfamily, member 6	0.000532	0.71
33	NA	0.000553	-0.59
34	metallothionein 2A	0.000563	2.68
35	complement factor properdin	0.00058	-0.74
36	choroideremia (Rab escort protein 1)	0.000597	0.58
37	NA	0.000599	-0.79
38	integrin, alpha 1	0.000604	-0.69
39	NA	0.000682	0.62
40	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	0.000683	0.65
41	NA	0.000695	0.7
42	LON peptidase N-terminal domain and ring finger 2	0.000704	-0.62
43	RasGEF domain family, member 1B	0.000717	0.83
44	S100 calcium binding protein A9	0.000752	-0.86
45	solute carrier family 4, sodium bicarbonate cotransporter, mem	0.000799	-0.58
46	drebrin 1	0.0008	-0.64
47	immediate early response 3	0.000819	0.59
48	NA	0.00083	0.93
49	NA	0.000916	0.58
50	Rho GTPase activating protein 6	0.000945	-0.66
51	nicotinamide phosphoribosyltransferase	0.000956	0.67

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2	sorting nexin 9	0.000985	0.65
3	neuralized E3 ubiquitin protein ligase 1B	0.001007	-0.58
4	potassium channel, voltage gated KQT-like subfamily Q, member	0.001032	-0.69
5	kelch-like family member 6	0.001129	0.65
6	caveolin 1, caveolae protein, 22kDa	0.001181	-0.68
7	2-5-oligoadenylate synthetase 2, 69/71kDa	0.001205	0.69
8	tRNA methyltransferase 2 homolog B	0.001362	-0.58
9	aldo-keto reductase family 1, member B10 (aldose reductase)	0.001387	0.83
10	galactose mutarotase (aldose 1-epimerase)	0.001479	0.65
11	NA	0.001495	0.62
12	pepsinogen 3, group I (pepsinogen A)	0.001501	-0.58
13	peripheral myelin protein 22	0.001613	0.59
14	ABL proto-oncogene 2, non-receptor tyrosine kinase	0.001921	0.75
15	lamin B1	0.001998	-0.83
16	chemokine (C-X-C motif) ligand 10	0.002036	0.65
17	G0/G1 switch 2	0.002063	0.72
18	ferritin, heavy polypeptide 1	0.00219	0.68
19	acid sensing (proton gated) ion channel family member 4	0.002305	0.63
20	ATP-binding cassette, sub-family A (ABC1), member 1	0.002319	0.66
21	guanylate cyclase 1, soluble, alpha 2	0.002374	0.62
22	centromere protein F, 350/400kDa	0.002394	-0.69
23	matrix metalloproteinase 14 (membrane-inserted)	0.002465	-0.76
24	transmembrane protein 119	0.002488	0.75
25	transmembrane p24 trafficking protein 9	0.003178	-0.63
26	copine II	0.003558	-0.65
27	NA	0.003613	0.59
28	nerve growth factor receptor	0.003769	-0.61
29	solute carrier family 39 (zinc transporter), member 10	0.003797	-0.85
30	pentraxin 3, long	0.003845	0.59
31	NA	0.003925	0.7
32	Rab interacting lysosomal protein-like 1	0.003954	0.59
33	v-ets avian erythroblastosis virus E26 oncogene homolog 1	0.004029	-0.71
34	nuclear factor I/C (CCAAT-binding transcription factor)	0.004148	0.6
35	NA	0.004346	0.63
36	peroxisome proliferator-activated receptor gamma, coactivator 1	0.004535	0.75
37	NA	0.005005	-0.69
38	NA	0.005152	0.7
39	zinc finger, CCHC domain containing 2	0.005204	0.6
40	interferon-induced protein 44	0.005302	0.85
41	S100 calcium binding protein A16	0.005643	-0.58
42	small nucleolar RNA, H/ACA box 74B	0.005844	0.61
43	neuronal regeneration related protein	0.006132	-0.61
44	prepronociceptin	0.006309	-0.72
45	NA	0.006616	0.64
46	NA	0.007861	0.87
47	minichromosome maintenance complex component 5	0.008133	-0.59
48	platelet-derived growth factor receptor-like	0.008204	-0.58
49	shisa family member 5	0.008343	0.62
50	NA	0.008406	1.1
51	galactose mutarotase (aldose 1-epimerase)	0.00868	0.67

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2	poly (ADP-ribose) polymerase family, member 14	0.008894	0.7
3	establishment of sister chromatid cohesion N-acetyltransferase 2	0.009125	-0.58
4	neutrophil cytosolic factor 1	0.00939	0.6
5	DENN/MADD domain containing 1B	0.009701	-0.78
6	DnaJ (Hsp40) homolog, subfamily C, member 7	0.010648	-0.58
7	aspartate beta-hydroxylase	0.012066	0.61
8	NA	0.012068	0.65
9	Ras-related GTP binding C	0.012456	0.63
10	complement component 5a receptor 1	0.013322	0.82
11	NA	0.013763	-0.58
12	NA	0.014242	0.64
13	prolyl 3-hydroxylase 2	0.015349	0.67
14	thymidylate synthetase	0.01648	-0.62
15	ADAM metalloproteinase with thrombospondin type 1 motif, 4	0.017577	-0.62
16	heat shock protein 90kDa alpha (cytosolic), class B member 2, ps	0.018346	0.89
17	NA	0.022499	0.82
18	ferritin, heavy polypeptide 1	0.024846	0.59
19	heat shock protein 90kDa alpha (cytosolic), class A member 1	0.024978	0.73
20	insulin-like growth factor binding protein 3	0.02746	0.58
21	tachykinin 4 (hemokinin)	0.03595	-0.59
22	NA	0.036088	0.58
23	chondroitin sulfate synthase 3	0.039112	-0.6
24	NA	0.039244	0.61
25	CD84 molecule	0.046833	0.68
26	DPP9 antisense RNA 1	0.047776	0.61
27	heat shock protein 90kDa alpha (cytosolic), class A member 2, ps	0.048493	0.78
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Exposure: 24h Silver ions (nitric acid silver)

Probe ID	TargetID	GeneSymbol
A_23_P1691	NM_002421	MMP1
A_23_P324754	NM_018689	CEMIP
A_23_P83579	NM_014862	ARNT2
A_33_P3258046	NM_170685	TAC4
A_33_P3333232	ENST00000621947	CCDC162P
A_23_P20660	ENST00000375765	DIRAS2
A_23_P36882	NM_006183	NTS
A_23_P214080	NM_001964	EGR1
A_23_P95930	NM_003483	HMGA2
A_24_P363408	NM_012259	HEY2
A_33_P3380457	NM_022049	GPR88
A_23_P215060	NM_001018111	PODXL
A_23_P404494	NM_002185	IL7R
A_23_P402765	NM_198060	NRAP
A_23_P120227	NM_030915	LBH
A_23_P320578	NM_002928	RGS16
A_33_P3413741	NM_000916	OXTR
A_23_P50919	NM_006216	SERPINE2
A_23_P114947	NM_002923	RGS2
A_23_P54144	NM_001202	BMP4
A_33_P3361636	NM_001190839	MGP
A_23_P204286	NM_000900	MGP
A_23_P30254	NM_006622	PLK2
A_23_P39931	NM_003494	DYSF
A_33_P3303649	NM_203377	MB
A_23_P360754	NM_005099	ADAMTS4
A_23_P253321	NM_006228	PNOC
A_23_P66948	NM_022751	GAREM
A_23_P97141	NM_002922	RGS1
A_24_P709377	NR_015377	PAX8-AS1
A_23_P103672	NM_006617	NES
A_23_P16523	NM_004864	GDF15
A_32_P190303	NM_198461	LONRF2
A_23_P147918	NM_080388	S100A16
A_23_P254507	NM_139211	HOPX
A_23_P46936	NM_000399	EGR2
A_23_P57277	NM_020152	MAP3K7CL
A_33_P3216442	NM_080680	COL11A2
A_33_P3290394	NM_000206	IL2RG
A_33_P3315906	NM_032611	PTP4A3
A_21_P0000160	NM_138461	TM4SF19
A_24_P406754	NM_032211	LOXL4
A_23_P205031	NM_001846	COL4A2
A_23_P151046	NM_002259	KLRC1
A_24_P208909	NM_015271	TRIM2
A_33_P3358233	NM_006617	NES
A_33_P3391290	NM_001142483	NREP

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2	A_23_P146811	NM_030793	FBXO38
3	A_23_P17663	NM_002462	MX1
4	A_23_P310460	NM_153487	MDGA1
5	A_23_P389897	NM_002507	NGFR
6	A_33_P3372666	NM_033023	PDGFA
7	A_23_P122924	NM_002192	INHBA
8	A_23_P24716	NM_017870	TMEM132A
9	A_23_P43898	NM_173567	EPHX4
10	A_24_P49199	NM_181789	GLDN
11	A_33_P3227375	NM_003247	THBS2
12	A_23_P121665	NM_020777	SORCS2
13	A_23_P150018	NM_004419	DUSP5
14	A_23_P99906	NM_199330	HOMER2
15	A_32_P2452	NM_175861	TMTC1
16	A_23_P128598	NM_006001	TUBA3C
17	A_23_P202837	NM_053056	CCND1
18	A_23_P213562	NM_001992	F2R
19	A_32_P59302	NM_024503	HIVEP3
20	A_33_P3783812	AK022255	C8orf60
21	A_23_P165333	NM_139346	BIN1
22	A_23_P215525	NM_015550	OSBPL3
23	A_23_P76488	NM_001423	EMP1
24	A_23_P86470	NM_003956	CH25H
25	A_24_P12626	NM_001753	CAV1
26	A_32_P83049	NM_014971	EFR3B
27	A_21_P0013034	ENST00000368966	CCDC162P
28	A_23_P112774	NM_032611	PTP4A3
29	A_23_P150693	NM_014344	FJX1
30	A_23_P372946	NM_138461	TM4SF19
31	A_23_P435407	NM_001448	GPC4
32	A_23_P500130	NM_153186	KANK1
33	A_23_P122976	NM_002069	GNAI1
34	A_23_P127495	NM_003986	BBOX1
35	A_23_P167389	NM_022481	ARAP3
36	A_23_P49448	NM_024306	FA2H
37	A_23_P76749	NM_020692	GALNT16
38	A_23_P98410	NM_000073	CD3G
39	A_24_P296587	NM_005220	DLX3
40	A_21_P0001070	ENST00000445339	LOC101927532
41	A_23_P102000	NM_001008540	CXCR4
42	A_23_P137931	NM_000677	ADORA3
43	A_24_P212539	NM_138801	GALM
44	A_24_P252945	NM_032966	CXCR5
45	A_24_P280148	NM_080817	GPR82
46	A_32_P351968	NM_002118	HLA-DMB
47	A_21_P0003164	lnc-KLF15-3:4	lnc-KLF15-3
48	A_22_P00003588	ENST00000415019	
49	A_22_P00002818	NR_126337	LOC101927070
50	A_23_P100711	NM_000304	PMP22
51	A_24_P270728	NM_001042483	NUPR1

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2	A_23_P38795	NM_002029	FPR1
3	A_23_P8571	NM_080744	SSC4D
4	A_24_P354689	NM_004598	SPOCK1
5	A_33_P3323887	ENST00000558436	LOC102723481
6	A_33_P3402091	NM_006343	MERTK
7	A_23_P166087	NM_014737	RASSF2
8	A_23_P169494	NM_000607	ORM1
9	A_23_P42975	NM_002736	PRKAR2B
10	A_24_P402588	NM_018014	BCL11A
11	A_33_P3241984	NM_015967	PTPN22
12	A_33_P3338733	NM_198159	MITF
13	A_24_P188800	NM_017923	37196
14	A_33_P3240532	NM_015149	RGL1
15	A_23_P426663	NM_198159	MITF
16	A_23_P58132	NM_004310	RHOH
17	A_24_P103469	NM_007161	LST1
18	A_21_P0006860	lnc-ZNF33A-4:1	lnc-ZNF33A-4
19	A_23_P129064	NM_001482	GATM
20	A_23_P33723	NM_004244	CD163
21	A_23_P67971	NM_138801	GALM
22	A_23_P7144	NM_001511	CXCL1
23	A_33_P3363637	NM_013314	BLNK
24	A_33_P3691916	NM_014883	FAM13A
25	A_21_P0002075	NR_126337	LOC101927070
26	A_23_P217269	NM_007268	VSIG4
27	A_23_P3014	NM_005615	RNASE6
28	A_24_P274814	NM_030984	TBXAS1
29	A_23_P34644	NM_004001	FCGR2B
30	A_24_P334130	NM_054034	FN1
31	A_23_P9485	NM_000608	ORM2
32	A_33_P3395605	NM_181724	TMEM119
33	A_23_P25566	NM_004951	GPR183
34	A_23_P412562	NM_174896	C1orf162
35	A_33_P3375368	NM_001195381	GPR35
36	A_23_P13753	NM_006163	NFE2
37	A_23_P214627	NM_004847	AIF1
38	A_23_P143526	NM_006272	S100B
39	A_22_P00013493	ENST00000558436	LOC102723481
40	A_23_P387031	NM_173465	COL23A1
41	A_23_P145114	NM_001498	GCLC
42	A_23_P27306	NM_130386	COLEC12
43	A_23_P142424	NM_024660	IGFLR1
44	A_33_P3376971	NM_024111	CHAC1
45	A_23_P206760	NM_005143	HP
46	A_23_P104464	NM_000698	ALOX5
47	A_24_P222655	NM_015991	C1QA
48	A_33_P3242623	NM_014331	SLC7A11
49	A_23_P12554	NM_016112	PKD2L1
50	A_23_P420863	NM_022162	NOD2
51	A_24_P153568	NM_001039396	MPEG1

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2	A_33_P3361422	NM_000784	CYP27A1
3	A_21_P0009596	Inc-AC068473.1-1:1	Inc-AC068473.1-1
4	A_23_P145096	NM_005084	PLA2G7
5	A_23_P120902	NM_006498	LGALS2
6	A_23_P4536	NM_012307	EPB41L3
7			
8	A_33_P3358397	NM_018176	LGI2
9	A_23_P216340	NM_001045556	SLA
10	A_23_P259611	NM_016616	NME8
11	A_33_P3390172	NM_001145271	ADAMDEC1
12			
13	A_33_P3284508	NM_001174104	CD14
14	A_23_P146146	NM_152565	ATP6V0D2
15	A_23_P23048	NM_002965	S100A9
16	A_33_P3236868	NM_005952	MT1X
17	A_23_P209625	NM_000104	CYP1B1
18			
19	A_33_P3290343	NM_000104	CYP1B1
20	A_23_P21485	NM_017933	PID1
21	A_33_P3385785	NM_005621	S100A12
22	A_23_P66241	NM_176870	MT1M
23	A_23_P74001	NM_005621	S100A12
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25	A_33_P3233645	NM_001301267	MT1G
26	A_23_P434809	NM_002964	S100A8
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description	adj. p value	log 2 FC
matrix metallopeptidase 1	0.000566	-1.67
cell migration inducing protein, hyaluronan binding	0.000256	-1.26
aryl-hydrocarbon receptor nuclear translocator 2	0.00062	-1.24
tachykinin 4 (hemokinin)	0.000566	-1.16
NA	0.000566	-1.07
DIRAS family, GTP-binding RAS-like 2	0.002497	-1.06
neurotensin	0.007199	-1.05
early growth response 1	0.013778	-0.99
high mobility group AT-hook 2	0.000205	-0.99
hes-related family bHLH transcription factor with YRPW motif 2	0.00458	-0.99
G protein-coupled receptor 88	0.002102	-0.94
podocalyxin-like	0.000566	-0.92
interleukin 7 receptor	0.016372	-0.92
nebulin-related anchoring protein	0.006199	-0.91
limb bud and heart development	0.001564	-0.9
regulator of G-protein signaling 16	0.012879	-0.89
oxytocin receptor	0.001894	-0.88
serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor 1) type 1	0.009561	-0.87
regulator of G-protein signaling 2	0.000458	-0.86
bone morphogenetic protein 4	0.000566	-0.83
matrix Gla protein	0.007638	-0.83
matrix Gla protein	0.00508	-0.81
polo-like kinase 2	0.022276	-0.81
dysferlin	0.000458	-0.81
myoglobin	0.000991	-0.81
ADAM metallopeptidase with thrombospondin type 1 motif, 4	0.010658	-0.8
prepronociceptin	0.018663	-0.78
GRB2 associated, regulator of MAPK1	0.001251	-0.78
regulator of G-protein signaling 1	0.001057	-0.77
PAX8 antisense RNA 1	0.000327	-0.76
nestin	0.002003	-0.74
growth differentiation factor 15	0.024916	-0.73
LON peptidase N-terminal domain and ring finger 2	0.001564	-0.73
S100 calcium binding protein A16	0.006025	-0.71
HOP homeobox	0.019833	-0.71
early growth response 2	0.001084	-0.71
MAP3K7 C-terminal like	0.030269	-0.71
collagen, type XI, alpha 2	0.000327	-0.71
interleukin 2 receptor, gamma	0.000778	-0.71
protein tyrosine phosphatase type IVA, member 3	0.00443	-0.7
NA	0.000428	-0.69
lysyl oxidase-like 4	0.003741	-0.69
collagen, type IV, alpha 2	0.000327	-0.67
killer cell lectin-like receptor subfamily C, member 1	0.032994	-0.66
tripartite motif containing 2	0.002462	-0.66
nestin	0.004969	-0.66
neuronal regeneration related protein	0.0175	-0.66

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2	F-box protein 38	0.011748	-0.65
3	MX dynamin-like GTPase 1	0.006199	-0.65
4	MAM domain containing glycosylphosphatidylinositol anchor 1	0.005376	-0.65
5	nerve growth factor receptor	0.013643	-0.65
6	platelet-derived growth factor alpha polypeptide	0.023664	-0.64
7	inhibin, beta A	0.002735	-0.63
8	transmembrane protein 132A	0.003289	-0.63
9	epoxide hydrolase 4	0.003919	-0.63
10	gliomedin	0.000566	-0.63
11	thrombospondin 2	0.02416	-0.63
12	sortilin-related VPS10 domain containing receptor 2	0.01241	-0.62
13	dual specificity phosphatase 5	0.000779	-0.62
14	homer scaffolding protein 2	0.011137	-0.62
15	transmembrane and tetratricopeptide repeat containing 1	0.00062	-0.62
16	tubulin, alpha 3c	0.000991	-0.61
17	cyclin D1	0.045088	-0.61
18	coagulation factor II (thrombin) receptor	0.013784	-0.61
19	human immunodeficiency virus type I enhancer binding protein 3	0.024916	-0.61
20	chromosome 8 open reading frame 60	0.013787	-0.61
21	bridging integrator 1	0.014392	-0.6
22	oxysterol binding protein-like 3	0.000779	-0.6
23	epithelial membrane protein 1	0.002344	-0.6
24	cholesterol 25-hydroxylase	0.005299	-0.6
25	caveolin 1, caveolae protein, 22kDa	0.027121	-0.6
26	EFR3 homolog B	0.010339	-0.6
27	NA	0.000612	-0.59
28	protein tyrosine phosphatase type IVA, member 3	0.007406	-0.59
29	four jointed box 1	0.011677	-0.59
30	transmembrane 4 L six family member 19	0.009045	-0.59
31	glypican 4	0.006129	-0.59
32	KN motif and ankyrin repeat domains 1	0.005739	-0.59
33	guanine nucleotide binding protein (G protein), alpha inhibiting activit	0.015315	-0.58
34	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrob	0.037646	-0.58
35	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0.008431	-0.58
36	fatty acid 2-hydroxylase	0.001969	-0.58
37	polypeptide N-acetylgalactosaminyltransferase 16	0.00508	-0.58
38	CD3g molecule, gamma (CD3-TCR complex)	0.023483	-0.58
39	distal-less homeobox 3	0.003289	-0.58
40	NA	0.005094	0.58
41	chemokine (C-X-C motif) receptor 4	0.018274	0.58
42	adenosine A3 receptor	0.01318	0.58
43	galactose mutarotase (aldose 1-epimerase)	0.029912	0.58
44	chemokine (C-X-C motif) receptor 5	0.029738	0.58
45	G protein-coupled receptor 82	0.008297	0.58
46	major histocompatibility complex, class II, DM beta	0.003443	0.58
47	NA	0.010339	0.59
48	NA	0.035202	0.59
49	NA	0.015731	0.6
50	peripheral myelin protein 22	0.010658	0.6
51	nuclear protein, transcriptional regulator, 1	0.023847	0.6

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2	formyl peptide receptor 1	0.028907	0.61
3	scavenger receptor cysteine rich family, 4 domains	0.000566	0.62
4	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testicular)	0.010282	0.62
5	NA	0.001268	0.62
6	MER proto-oncogene, tyrosine kinase	0.009573	0.62
7	Ras association (RalGDS/AF-6) domain family member 2	0.011132	0.63
8	orosomucoid 1	0.003468	0.63
9	protein kinase, cAMP-dependent, regulatory, type II, beta	0.002003	0.63
10	B-cell CLL/lymphoma 11A (zinc finger protein)	0.000612	0.64
11	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0.006212	0.64
12	microphthalmia-associated transcription factor	0.005984	0.64
13	membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase	0.002003	0.65
14	ral guanine nucleotide dissociation stimulator-like 1	0.020855	0.65
15	microphthalmia-associated transcription factor	0.009186	0.66
16	ras homolog family member H	0.000859	0.66
17	leukocyte specific transcript 1	0.023805	0.66
18	NA	0.002432	0.67
19	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.006212	0.67
20	CD163 molecule	0.005438	0.68
21	galactose mutarotase (aldose 1-epimerase)	0.041464	0.68
22	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity)	0.033505	0.68
23	B-cell linker	0.003664	0.68
24	family with sequence similarity 13, member A	0.024916	0.68
25	NA	0.001043	0.69
26	V-set and immunoglobulin domain containing 4	0.004567	0.69
27	ribonuclease, RNase A family, k6	0.00089	0.69
28	thromboxane A synthase 1 (platelet)	0.03093	0.69
29	Fc fragment of IgG, low affinity IIb, receptor (CD32)	0.041464	0.7
30	fibronectin 1	0.022664	0.7
31	orosomucoid 2	0.000188	0.71
32	transmembrane protein 119	0.026773	0.71
33	G protein-coupled receptor 183	0.000566	0.72
34	chromosome 1 open reading frame 162	0.01397	0.72
35	G protein-coupled receptor 35	0.003298	0.72
36	nuclear factor, erythroid 2	0.00508	0.73
37	allograft inflammatory factor 1	0.000764	0.73
38	S100 calcium binding protein B	0.002344	0.75
39	NA	0.000508	0.76
40	collagen, type XXIII, alpha 1	0.010339	0.76
41	glutamate-cysteine ligase, catalytic subunit	0.01397	0.77
42	collectin sub-family member 12	0.009186	0.77
43	IGF-like family receptor 1	0.001969	0.78
44	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	0.015002	0.78
45	haptoglobin	0.007672	0.79
46	arachidonate 5-lipoxygenase	0.002344	0.82
47	complement component 1, q subcomponent, A chain	0.035079	0.82
48	solute carrier family 7 (anionic amino acid transporter light chain, xc-)	0.002344	0.82
49	polycystic kidney disease 2-like 1	0.002344	0.84
50	nucleotide-binding oligomerization domain containing 2	0.001268	0.84
51	macrophage expressed 1	0.003443	0.85

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2	cytochrome P450, family 27, subfamily A, polypeptide 1	0.002179	0.86
3	NA	0.002735	0.88
4	phospholipase A2, group VII (platelet-activating factor acetylhydrolase	0.032337	0.88
5	lectin, galactoside-binding, soluble, 2	0.00508	0.92
6	erythrocyte membrane protein band 4.1-like 3	0.011637	0.94
7	leucine-rich repeat LGI family, member 2	0.005061	0.99
8	Src-like-adaptor	0.003811	1
9	NME/NM23 family member 8	0.001043	1.02
10	ADAM-like, decysin 1	0.002102	1.15
11	CD14 molecule	0.001894	1.16
12	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	0.000256	1.18
13	S100 calcium binding protein A9	0.000428	1.18
14	metallothionein 1X	0.00508	1.29
15	cytochrome P450, family 1, subfamily B, polypeptide 1	0.001268	1.36
16	cytochrome P450, family 1, subfamily B, polypeptide 1	0.002344	1.37
17	phosphotyrosine interaction domain containing 1	0.000991	1.46
18	S100 calcium binding protein A12	0.000188	1.56
19	metallothionein 1M	0.000205	1.86
20	S100 calcium binding protein A12	0.000188	1.97
21	metallothionein 1G	0.032743	2.3
22	S100 calcium binding protein A8	0.000023	2.59
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Exposure: 24h Zinc oxide nanoparticles (20 nm

Probe ID	TargetID	GeneSymbol
A_19_P00320067	NR_026874	LOC100130417
A_23_P119778	NM_020342	SLC39A10
A_33_P3333232	ENST00000621947	CCDC162P
A_23_P36882	NM_006183	NTS
A_24_P49199	NM_181789	GLDN
A_23_P360754	NM_005099	ADAMTS4
A_33_P3258046	NM_170685	TAC4
A_23_P167096	NM_005429	VEGFC
A_23_P52761	NM_002423	MMP7
A_23_P92730	NM_006308	HSPB3
A_23_P218442	NM_002483	CEACAM6
A_33_P3380457	NM_022049	GPR88
A_23_P54144	NM_001202	BMP4
A_23_P204286	NM_000900	MGP
A_23_P150316	NM_002426	MMP12
A_33_P3402474	NM_001031722	ATAT1
A_23_P257003	NM_006200	PCSK5
A_23_P344421	NM_019055	ROBO4
A_33_P3371989	NM_205833	IGSF1
A_23_P379789	NM_013305	ST8SIA5
A_22_P00000184	lnc-ABHD16B-1:1	lnc-ABHD16B-1
A_22_P00009165	NR_046696	IPO9-AS1
A_23_P134085	NM_173515	CNKSR3
A_21_P0014129	NR_047568	LINC00578
A_23_P202448	NM_199168	CXCL12
A_33_P3316878	NM_024536	CHPF
A_23_P207564	NM_001291470	CCL4L2
A_23_P259692	NM_058179	PSAT1
A_22_P00010760	ENST00000563424	
A_33_P3396527	NM_006467	POLR3G
A_21_P0001923	ENST00000450667	
A_23_P319583	NM_014747	RIMS3
A_23_P40657	NM_014291	GCAT
A_22_P00006819	NR_038852	LINC00929
A_23_P34142	NM_016303	WBP5
A_22_P00014843	ENST00000550684	
A_24_P238131	NM_015551	SUSD5
A_33_P3216869	NM_004378	CRABP1
A_33_P3342628	NM_021170	HES4
A_23_P101992	NM_006770	MARCO
A_33_P3265301	NM_152219	GJD3
A_21_P0014368	ENST00000596510	PLA2G4C
A_33_P3326483	NM_004378	CRABP1
A_23_P86470	NM_003956	CH25H
A_33_P3590259	NM_004887	CXCL14
A_23_P64372	NM_001062	TCN1
A_33_P3291454	NM_198515	CCDC172

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2	A_23_P365738	NM_015193	ARC
3	A_32_P171061	NM_005170	ASCL2
4	A_23_P23815	NM_021194	SLC30A1
5	A_24_P156748	NM_001004434	SLC30A2
6	A_23_P420942	XM_005255956	MT1E
7	A_23_P215913	NM_001831	CLU
8	A_23_P422831	NM_004816	FAM189A2
9	A_21_P0009476	lnc-KATNAL2-4:1	lnc-KATNAL2-4
10	A_32_P135336	NR_002556	LOC388242
11	A_33_P3367301	NM_152219	GJD3
12	A_23_P106844	NM_005953	MT2A
13	A_23_P114903	NM_002155	HSPA6
14	A_23_P54840	NM_005946	MT1A
15	A_22_P00010235	NM_005947	MT1B
16	A_23_P37983	NM_005947	MT1B
17	A_23_P427703	NR_001447	MT1L
18	A_33_P3231156	ENST00000567054	
19	A_33_P3315314	NM_001276687	MT1HL1
20	A_23_P206724	NM_175617	MT1E
21	A_21_P0000671	NM_175617	MT1E
22	A_33_P3368313	NM_005951	MT1H
23	A_23_P15174	NM_005949	MT1F
24	A_33_P3236868	NM_005952	MT1X
25	A_23_P66241	NM_176870	MT1M
26	A_33_P3233645	NM_001301267	MT1G
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n)

description	adj. p value	log 2 FC
uncharacterized LOC100130417	0.036166	-0.47
solute carrier family 39 (zinc transporter), member 10	0.000027	-1.44
NA	0.002041	-0.93
neurotensin	0.039818	-0.9
gliomedin	0.000001	-0.83
ADAM metalloproteinase with thrombospondin type 1 motif, 4	0.017826	-0.79
tachykinin 4 (hemokinin)	0.036018	-0.77
vascular endothelial growth factor C	0.002958	-0.76
matrix metalloproteinase 7	0	-0.72
heat shock 27kDa protein 3	0.000007	-0.71
carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific)	0.000004	-0.69
G protein-coupled receptor 88	0.043316	-0.69
bone morphogenetic protein 4	0.005141	-0.67
matrix Gla protein	0.044598	-0.65
matrix metalloproteinase 12	0.003182	-0.63
alpha tubulin acetyltransferase 1	0.002041	-0.63
proprotein convertase subtilisin/kexin type 5	0.03064	-0.62
roundabout guidance receptor 4	0.003925	-0.62
immunoglobulin superfamily, member 1	0.000389	-0.6
ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 5	0.000051	-0.59
NA	0.002633	0.59
NA	0.000391	0.6
CNKSR family member 3	0.000523	0.6
NA	0.000003	0.61
chemokine (C-X-C motif) ligand 12	0.000003	0.61
chondroitin polymerizing factor	0.000702	0.61
chemokine (C-C motif) ligand 4	0.033006	0.63
phosphoserine aminotransferase 1	0.017993	0.64
NA	0.002877	0.65
polymerase (RNA) III (DNA directed) polypeptide G (32kD)	0.00001	0.65
NA	0.044598	0.66
regulating synaptic membrane exocytosis 3	0.000702	0.67
glycine C-acetyltransferase	0.000145	0.68
NA	0.000003	0.69
WW domain binding protein 5	0.00001	0.7
NA	0.002877	0.71
sushi domain containing 5	0.000004	0.71
cellular retinoic acid binding protein 1	0	0.71
hes family bHLH transcription factor 4	0.002782	0.73
macrophage receptor with collagenous structure	0.000002	0.74
gap junction protein, delta 3, 31.9kDa	0.000063	0.75
NA	0.001652	0.78
cellular retinoic acid binding protein 1	0	0.78
cholesterol 25-hydroxylase	0.000086	0.81
chemokine (C-X-C motif) ligand 14	0.000025	0.91
transcobalamin I (vitamin B12 binding protein, R binder family)	0	1
coiled-coil domain containing 172	0.000574	1.01

1			
2	activity-regulated cytoskeleton-associated protein	0.039746	1.06
3	achaete-scute family bHLH transcription factor 2	0	1.09
4	solute carrier family 30 (zinc transporter), member 1	0	1.18
5	solute carrier family 30 (zinc transporter), member 2	0	1.35
6	metallothionein 1E	0	1.37
7	clusterin	0	1.4
8	family with sequence similarity 189, member A2	0	1.43
9	NA	0	1.5
10	SAGA complex associated factor 29 pseudogene	0	1.52
11	gap junction protein, delta 3, 31.9kDa	0	1.8
12	metallothionein 2A	0.03736	2.25
13	heat shock 70kDa protein 6 (HSP70B)	0.003204	2.35
14	metallothionein 1A	0	3.04
15	NA	0	3.36
16	metallothionein 1B	0	3.43
17	metallothionein 1L (gene/pseudogene)	0	3.47
18	NA	0.000025	3.5
19	metallothionein 1H	0	3.54
20	metallothionein 1E	0	3.81
21	NA	0	3.87
22	metallothionein 1H	0	3.98
23	metallothionein 1F	0	4.05
24	metallothionein 1X	0	4.38
25	metallothionein 1M	0	4.88
26	metallothionein 1G	0	5.69
27			
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Exposure: 24h Zinc oxide particles (300 nm)

Probe ID	TargetID	GeneSymbol
A_23_P119778	NM_020342	SLC39A10
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A_33_P3361636	NM_001190839	MGP
A_23_P204286	NM_000900	MGP
A_23_P36882	NM_006183	NTS
A_33_P3333232	ENST00000621947	CCDC162P
A_22_P00008494	NR_002798	NAPSB
A_33_P3380457	NM_022049	GPR88
A_23_P253321	NM_006228	PNOC
A_23_P1691	NM_002421	MMP1
A_33_P3287472	NM_001007533	PPP1R27
A_23_P360754	NM_005099	ADAMTS4
A_23_P140384	NM_001911	CTSG
A_23_P218442	NM_002483	CEACAM6
A_23_P56559	NM_001142270	DHRS9
A_23_P254863	NM_153361	NIM1K
A_23_P36120	NM_022349	MS4A6A
A_23_P54144	NM_001202	BMP4
A_22_P00008493	NR_002798	NAPSB
A_23_P150316	NM_002426	MMP12
A_33_P3229918	NM_001243168	PTCRA
A_33_P3371989	NM_205833	IGSF1
A_24_P363408	NM_012259	HEY2
A_23_P142345	NM_002777	PRTN3
A_23_P344421	NM_019055	ROBO4
A_23_P408285	NM_153026	PRICKLE1
A_33_P3258046	NM_170685	TAC4
A_23_P212608	NM_022131	CLSTN2
A_23_P24616	NM_170601	SIAE
A_23_P257003	NM_006200	PCSK5
A_23_P402765	NM_198060	NRAP
A_24_P49199	NM_181789	GLDN
A_23_P110851	NM_198253	TERT
A_23_P130961	NM_001972	ELANE
A_23_P167096	NM_005429	VEGFC
A_23_P256107	NM_006665	HPSE
A_32_P86739	NM_001010911	CASC10
A_22_P00004867	ENST00000523769	
A_23_P151046	NM_002259	KLRC1
A_23_P301521	NM_020848	KIAA1462
A_33_P3229953	NM_001958	EEF1A2
A_22_P00004214	ENST00000458420	CLSTN2
A_23_P379789	NM_013305	ST8SIA5
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A_24_P406754	NM_032211	LOXL4
A_33_P3209960	NM_153819	RASGRP2
A_21_P0014223	XR_113143	

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3	A_23_P212354	NM_001123041	CCR2
4	A_23_P22444	NM_002621	CFP
5	A_24_P391586	NM_178507	OAF
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7	A_23_P52761	NM_002423	MMP7
8	A_24_P766716	NM_001142343	CMKLR1
9	A_33_P3293446	NM_020848	KIAA1462
10	A_33_P3236020	NM_138379	TIMD4
11	A_21_P0009034	NR_126340	LOC100996338
12	A_22_P00019635	lnc-CIB3-1:1	lnc-CIB3-1
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15	A_23_P121926	NM_005410	SEPP1
16	A_23_P426021	NM_015187	SEL1L3
17	A_23_P64058	NM_153819	RASGRP2
18	A_23_P138541	NM_003739	AKR1C3
19	A_23_P161507	NM_004923	MTL5
20	A_23_P330561	NM_174918	MCEMP1
21	A_24_P190472	NM_003064	SLPI
22	A_32_P76853	NM_001282484	GOLGA8R
23	A_19_P00320067	NR_026874	LOC100130417
24	A_22_P00007941	NR_125986	LOC101929592
25	A_23_P121716	NM_005139	ANXA3
26	A_23_P48596	NM_198232	RNASE1
27	A_23_P67569	NM_024888	LPPR3
28	A_23_P203376	NM_152852	MS4A6A
29	A_24_P133905	NM_005064	CCL23
30	A_33_P3209962	NM_153819	RASGRP2
31	A_33_P3413741	NM_000916	OXTR
32	A_23_P8981	NM_000349	STAR
33	A_24_P299318	NM_182705	FAM101B
34	A_33_P3216442	NM_080680	COL11A2
35	A_33_P3403053	lnc-GUSB-5:1	lnc-GUSB-5
36	A_22_P00023104	lnc-RREB1-1:1	lnc-RREB1-1
37	A_23_P125303	NM_001555	IGSF1
38	A_23_P23194	NM_032409	PINK1
39	A_23_P257971	NM_001353	AKR1C1
40	A_33_P3282390	NM_000841	GRM4
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42	A_23_P42322	NM_080680	COL11A2
43	A_24_P379820	NM_030926	ITM2C
44	A_23_P2543	NM_015267	CUX2
45	A_23_P96501	NM_001003811	TEX11
46	A_33_P3267799	NM_001278426	LILRB4
47	A_33_P3390868	NM_133477	SYNPO2
48	A_33_P3391796	NM_005450	NOG
49	A_23_P102000	NM_001008540	CXCR4
50	A_23_P19517	NM_002224	ITPR3
51	A_23_P86470	NM_003956	CH25H

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3	A_23_P42718	NM_004289	NFE2L3
4	A_23_P52207	NM_012342	BAMBI
5	A_33_P3414912	NM_001200056	NPL
6	A_33_P3593774	NM_001303429	PIK3R3
7	A_33_P3781228	NR_125739	CEBPB-AS1
8	A_22_P00011370	ENST00000328963	P2RX7
9	A_23_P371266	NM_015569	DNM3
10	A_23_P55706	NM_006509	RELB
11	A_21_P0004750	lnc-SUPT3H-1:5	lnc-SUPT3H-1
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14	A_32_P71788	NM_002014	FKBP4
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18	A_23_P44724	NM_001321	CSRP2
19	A_32_P32254	NM_001848	COL6A1
20	A_23_P121657	NM_005114	HS3ST1
21	A_23_P95640	NM_001007544	C1orf186
22	A_33_P3216869	NM_004378	CRABP1
23	A_23_P148990	NM_031935	HMCN1
24	A_23_P93032	NM_032367	ZBED3
25	A_23_P41942	NM_006467	POLR3G
26	A_23_P134176	NM_001024465	SOD2
27	A_23_P144916	NM_005110	GFPT2
28	A_23_P253536	NM_000908	NPR3
29	A_23_P82651	NM_002523	NPTX2
30	A_24_P257416	NM_002089	CXCL2
31	A_23_P417918	NM_006211	PENK
32	A_23_P50081	NM_014214	IMPA2
33	A_19_P00809119	NR_015410	CASC15
34	A_21_P0005747	ENST00000523572	
35	A_23_P321501	NM_182908	DHRS2
36	A_24_P303097	NM_031953	SNX25
37	A_23_P4592	NM_001245	SIGLEC6
38	A_33_P3226212	NM_001270408	JAM2
39	A_33_P3259393	NM_178232	HAPLN3
40	A_21_P0003297	lnc-SLC12A8-1:1	lnc-SLC12A8-1
41	A_21_P0014129	NR_047568	LINC00578
42	A_22_P00009165	NR_046696	IPO9-AS1
43	A_23_P110531	NM_013409	FST
44	A_23_P121064	NM_002852	PTX3
45	A_23_P131846	NM_005985	SNAI1
46	A_22_P00006819	NR_038852	LINC00929
47	A_33_P3249534	NM_005382	NEFM
48	A_33_P3390172	NM_001145271	ADAMDEC1
49	A_33_P3326483	NM_004378	CRABP1
50	A_21_P0000504	NR_023344	RNU6ATAC
51	A_23_P128372	NM_002014	FKBP4

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2	A_33_P3235053	NM_033452	TRIM47
3	A_22_P00000184	Inc-ABHD16B-1:1	Inc-ABHD16B-1
4	A_23_P15146	NM_001012631	IL32
5	A_23_P215634	NM_001013398	IGFBP3
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7	A_22_P00014843	ENST00000550684	
8	A_23_P4536	NM_012307	EPB41L3
9	A_33_P3262012	THC2603411	
10	A_21_P0001923	ENST00000450667	
11	A_23_P215048	NM_014702	KIAA0408
12	A_23_P358597	NM_022361	POPDC3
13	A_23_P319583	NM_014747	RIMS3
14	A_33_P3316878	NM_024536	CHPF
15	A_33_P3405424	NM_152899	IL4I1
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17	A_24_P262127	NM_004165	RRAD
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22	A_23_P202448	NM_199168	CXCL12
23	A_23_P134085	NM_173515	CNKSR3
24	A_23_P429998	NM_006732	FOSB
25	A_23_P58676	NM_001204375	NPR3
26	A_33_P3265301	NM_152219	GJD3
27	A_21_P0014368	ENST00000596510	PLA2G4C
28	A_23_P393620	NM_006528	TFPI2
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30	A_23_P207564	NM_001291470	CCL4L2
31	A_24_P238131	NM_015551	SUSD5
32	A_24_P355944	NM_004093	EFNB2
33	A_33_P3396527	NM_006467	POLR3G
34	A_23_P40657	NM_014291	GCAT
35	A_33_P3354607	NM_001291470	CCL4L2
36	A_23_P34142	NM_016303	WBP5
37	A_33_P3422802	NM_025218	ULBP1
38	A_22_P00023255	ENST00000438158	
39	A_23_P101992	NM_006770	MARCO
40	A_21_P0014512	AK097695	
41	A_33_P3269636	NM_001166034	SBSN
42	A_32_P171061	NM_005170	ASCL2
43	A_33_P3291454	NM_198515	CCDC172
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46	A_23_P23815	NM_021194	SLC30A1
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50	A_23_P64372	NM_001062	TCN1
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53	A_32_P74409	NM_001145033	C11orf96

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A_32_P135336	NR_002556	LOC388242
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A_23_P114903	NM_002155	HSPA6
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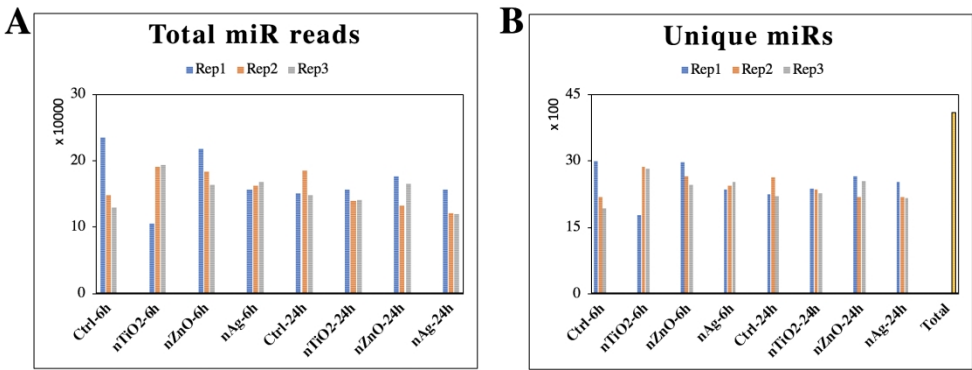
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5	description	adj. p value	log 2 FC
6	solute carrier family 39 (zinc transporter), member 10	0	-1.92
7	protein phosphatase 1, regulatory subunit 27	0	-1.3
8	matrix Gla protein	0.000006	-1.27
9	matrix Gla protein	0.000004	-1.22
10	neurotensin	0.000505	-1.21
11	NA	0.000015	-1.17
12	NA	0	-1.09
13	G protein-coupled receptor 88	0.000078	-1.07
14	prepronociceptin	0.000285	-1.05
15	matrix metalloproteinase 1	0.024905	-1.04
16	protein phosphatase 1, regulatory subunit 27	0.000006	-1.02
17	ADAM metalloproteinase with thrombospondin type 1 motif, 4	0.000476	-0.98
18	cathepsin G	0.000013	-0.96
19	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific)	0	-0.93
20	dehydrogenase/reductase (SDR family) member 9	0.000021	-0.93
21	NIM1 serine/threonine protein kinase	0.000135	-0.91
22	membrane-spanning 4-domains, subfamily A, member 6A	0	-0.91
23	bone morphogenetic protein 4	0.000043	-0.87
24	NA	0.000007	-0.86
25	matrix metalloproteinase 12	0.000007	-0.86
26	pre T-cell antigen receptor alpha	0.000015	-0.85
27	immunoglobulin superfamily, member 1	0	-0.85
28	hes-related family bHLH transcription factor with YRPW motif 2	0.009415	-0.84
29	proteinase 3	0.000024	-0.83
30	roundabout guidance receptor 4	0.000018	-0.83
31	prickle homolog 1	0.000009	-0.82
32	tachykinin 4 (hemokinin)	0.007265	-0.82
33	calsynenin 2	0.000803	-0.81
34	sialic acid acetyltransferase	0.001131	-0.8
35	proprotein convertase subtilisin/kexin type 5	0.000598	-0.8
36	nebulin-related anchoring protein	0.009562	-0.8
37	gliomedin	0.000002	-0.78
38	telomerase reverse transcriptase	0.000029	-0.77
39	elastase, neutrophil expressed	0.000035	-0.76
40	vascular endothelial growth factor C	0.000897	-0.76
41	heparanase	0.000001	-0.76
42	cancer susceptibility candidate 10	0.000006	-0.76
43	NA	0.000001	-0.75
44	killer cell lectin-like receptor subfamily C, member 1	0.005743	-0.75
45	KIAA1462	0.000132	-0.75
46	eukaryotic translation elongation factor 1 alpha 2	0.000011	-0.75
47	NA	0.000195	-0.74
48	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	0	-0.74
49	uncharacterized protein FLJ30901	0	-0.73
50	lysyl oxidase-like 4	0.00073	-0.72
51	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	0.000004	-0.72
52	NA	0.000011	-0.71

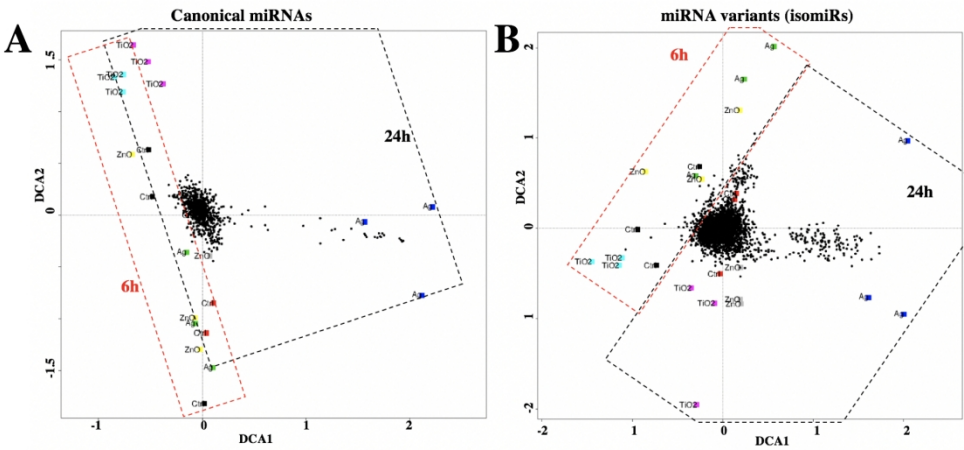
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2	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrob	0.002975	-0.71
3	chemokine (C-C motif) receptor 2	0.000893	-0.71
4	complement factor properdin	0.003849	-0.71
5	out at first homolog	0.000011	-0.7
6	synaptotagmin XVII	0.003077	-0.69
7	matrix metalloproteinase 7	0	-0.69
8	chemerin chemokine-like receptor 1	0.000144	-0.69
9	KIAA1462	0.000006	-0.69
10	T-cell immunoglobulin and mucin domain containing 4	0.000309	-0.67
11	NA	0.000022	-0.66
12	NA	0.000052	-0.66
13	long intergenic non-protein coding RNA 1140	0.002089	-0.66
14	alpha tubulin acetyltransferase 1	0.000285	-0.66
15	selenoprotein P, plasma, 1	0.000362	-0.65
16	sel-1 suppressor of lin-12-like 3 (C. elegans)	0.000011	-0.65
17	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	0.000742	-0.65
18	aldo-keto reductase family 1, member C3	0.000742	-0.64
19	metallothionein-like 5, testis-specific (tesmin)	0.000898	-0.64
20	mast cell-expressed membrane protein 1	0.000022	-0.64
21	secretory leukocyte peptidase inhibitor	0.000729	-0.64
22	golgin A8 family, member T	0.003343	-0.64
23	uncharacterized LOC100130417	0.000404	-0.63
24	NA	0.000075	-0.63
25	annexin A3	0.000349	-0.63
26	ribonuclease, RNase A family, 1 (pancreatic)	0.002904	-0.63
27	lipid phosphate phosphatase-related protein type 3	0.001869	-0.63
28	membrane-spanning 4-domains, subfamily A, member 6A	0.002594	-0.62
29	chemokine (C-C motif) ligand 23	0.011006	-0.62
30	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	0.000024	-0.62
31	oxytocin receptor	0.023396	-0.62
32	steroidogenic acute regulatory protein	0.000579	-0.61
33	family with sequence similarity 101, member B	0	-0.61
34	collagen, type XI, alpha 2	0.000259	-0.61
35	uncharacterized LOC441242	0.00015	-0.61
36	NA	0.000728	-0.6
37	immunoglobulin superfamily, member 1	0.004496	-0.6
38	PTEN induced putative kinase 1	0.001009	-0.6
39	aldo-keto reductase family 1, member C1	0.001702	-0.6
40	glutamate receptor, metabotropic 4	0.000114	-0.6
41	NA	0.000161	-0.59
42	collagen, type XI, alpha 2	0.000135	-0.59
43	integral membrane protein 2C	0.004108	-0.59
44	cut-like homeobox 2	0.000565	-0.58
45	testis expressed 11	0.000059	-0.58
46	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITI	0.000106	-0.58
47	synaptopodin 2	0.004924	-0.58
48	noggin	0.000075	-0.58
49	chemokine (C-X-C motif) receptor 4	0.010878	0.58
50	inositol 1,4,5-trisphosphate receptor, type 3	0.000103	0.58
51	cholesterol 25-hydroxylase	0.003533	0.58

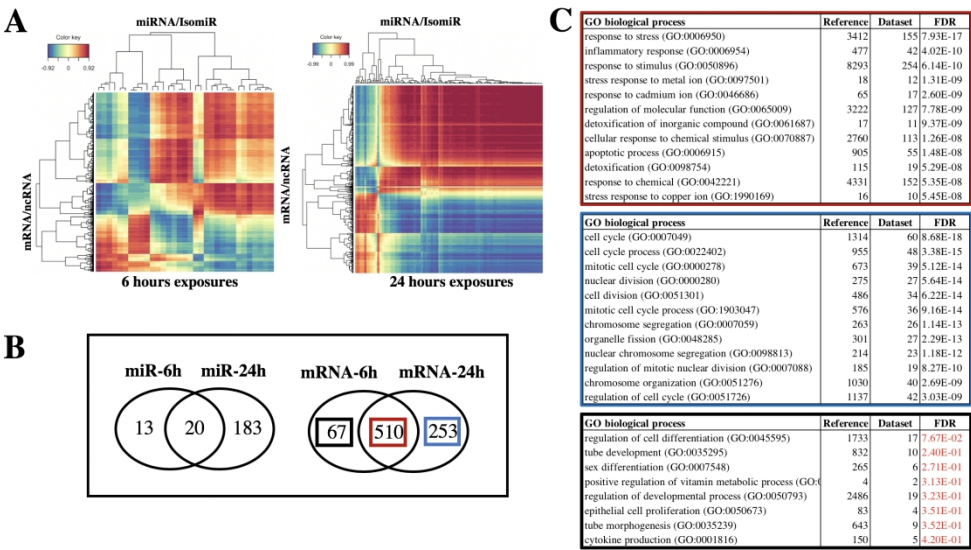
1			
2	phosphoserine aminotransferase 1	0.013164	0.59
3	nuclear factor, erythroid 2-like 3	0.000049	0.59
4	BMP and activin membrane-bound inhibitor	0.001702	0.59
5	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	0.000285	0.59
6	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	0.000135	0.59
7	NA	0.001043	0.59
8	NA	0.000033	0.6
9	dynamamin 3	0.006084	0.6
10	v-rel avian reticuloendotheliosis viral oncogene homolog B	0.000887	0.6
11	NA	0.027628	0.61
12	NA	0	0.61
13	mannosidase, endo-alpha-like	0.000285	0.61
14	FK506 binding protein 4, 59kDa	0.000742	0.61
15	solute carrier family 7 (anionic amino acid transporter light chain, xc-)	0.017565	0.61
16	sorting nexin 25	0.000004	0.62
17	chemokine (C-C motif) receptor 7	0.000559	0.62
18	cysteine and glycine-rich protein 2	0.000018	0.62
19	collagen, type VI, alpha 1	0.011006	0.62
20	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0.000215	0.63
21	chromosome 1 open reading frame 186	0	0.63
22	cellular retinoic acid binding protein 1	0.000001	0.63
23	hemocentin 1	0.002148	0.64
24	zinc finger, BED-type containing 3	0.000861	0.64
25	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	0.000236	0.65
26	superoxide dismutase 2, mitochondrial	0.000311	0.66
27	glutamine-fructose-6-phosphate transaminase 2	0.000001	0.66
28	natriuretic peptide receptor 3	0.00081	0.66
29	neuronal pentraxin II	0.000067	0.66
30	chemokine (C-X-C motif) ligand 2	0.007265	0.66
31	proenkephalin	0.000197	0.67
32	inositol(myo)-1(or 4)-monophosphatase 2	0.000075	0.67
33	cancer susceptibility candidate 15 (non-protein coding)	0.012153	0.68
34	NA	0.000451	0.68
35	dehydrogenase/reductase (SDR family) member 2	0.000226	0.68
36	sorting nexin 25	0.000007	0.68
37	sialic acid binding Ig-like lectin 6	0.000195	0.69
38	junctional adhesion molecule 2	0	0.69
39	hyaluronan and proteoglycan link protein 3	0.000002	0.69
40	NA	0.000021	0.71
41	NA	0	0.71
42	NA	0.000006	0.72
43	folliculin	0.000077	0.72
44	pentraxin 3, long	0.001404	0.72
45	snail family zinc finger 1	0	0.72
46	NA	0	0.74
47	neurofilament, medium polypeptide	0	0.74
48	ADAM-like, decysin 1	0.047487	0.75
49	cellular retinoic acid binding protein 1	0	0.76
50	NA	0	0.77
51	FK506 binding protein 4, 59kDa	0.000012	0.77

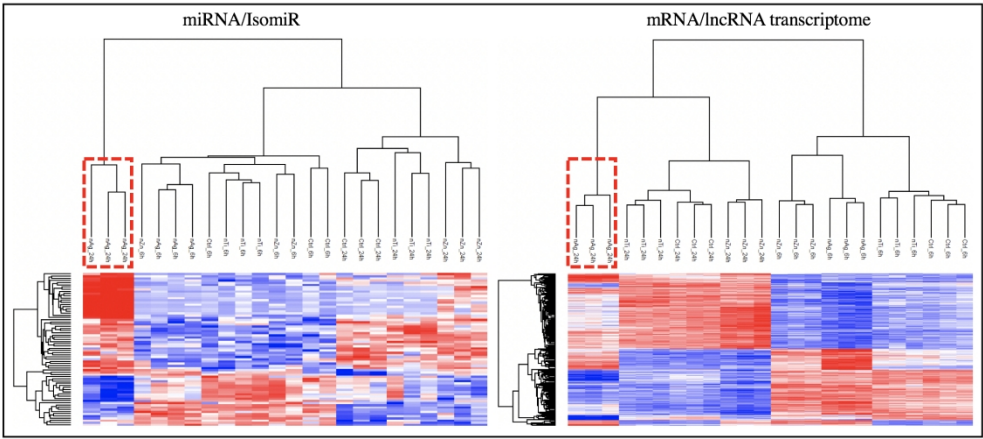
tripartite motif containing 47	0.000001	0.77
NA	0.000009	0.78
interleukin 32	0.007698	0.78
insulin-like growth factor binding protein 3	0.00638	0.78
NA	0.000217	0.79
erythrocyte membrane protein band 4.1-like 3	0.026679	0.79
NA	0.000004	0.79
NA	0.002489	0.8
KIAA0408	0.000046	0.81
popeye domain containing 3	0.000122	0.81
regulating synaptic membrane exocytosis 3	0.000008	0.82
chondroitin polymerizing factor	0.000001	0.83
interleukin 4 induced 1	0.000001	0.83
chemokine (C-X-C motif) ligand 2	0.000047	0.85
Ras-related associated with diabetes	0.000121	0.85
placenta-specific 9	0.016934	0.85
chemokine (C-C motif) ligand 19	0	0.88
regulating synaptic membrane exocytosis 3	0.000001	0.88
chemokine (C-X-C motif) ligand 12	0	0.89
CNKSR family member 3	0	0.9
FBJ murine osteosarcoma viral oncogene homolog B	0	0.9
natriuretic peptide receptor 3	0	0.91
gap junction protein, delta 3, 31.9kDa	0	0.93
NA	0.000024	0.94
tissue factor pathway inhibitor 2	0.000024	0.94
growth arrest and DNA-damage-inducible, beta	0	0.94
chemokine (C-C motif) ligand 4	0.00005	0.97
sushi domain containing 5	0	0.97
ephrin-B2	0	0.97
polymerase (RNA) III (DNA directed) polypeptide G (32kD)	0	0.97
glycine C-acetyltransferase	0	0.99
chemokine (C-C motif) ligand 4	0.000001	0.99
WW domain binding protein 5	0	1
UL16 binding protein 1	0	1
NA	0	1.02
macrophage receptor with collagenous structure	0	1.07
NA	0	1.15
suprabasin	0	1.16
achaete-scute family bHLH transcription factor 2	0	1.18
coiled-coil domain containing 172	0.000007	1.22
Epstein-Barr virus induced 3	0	1.24
chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	0	1.25
solute carrier family 30 (zinc transporter), member 1	0	1.28
chemokine (C-X-C motif) ligand 8	0.000034	1.28
metallothionein 1E	0	1.31
heat shock 70kDa protein 1B	0	1.36
transcobalamin I (vitamin B12 binding protein, R binder family)	0	1.38
heat shock 70kDa protein 1A	0	1.4
RAS, dexamethasone-induced 1	0	1.4
chromosome 11 open reading frame 96	0	1.47

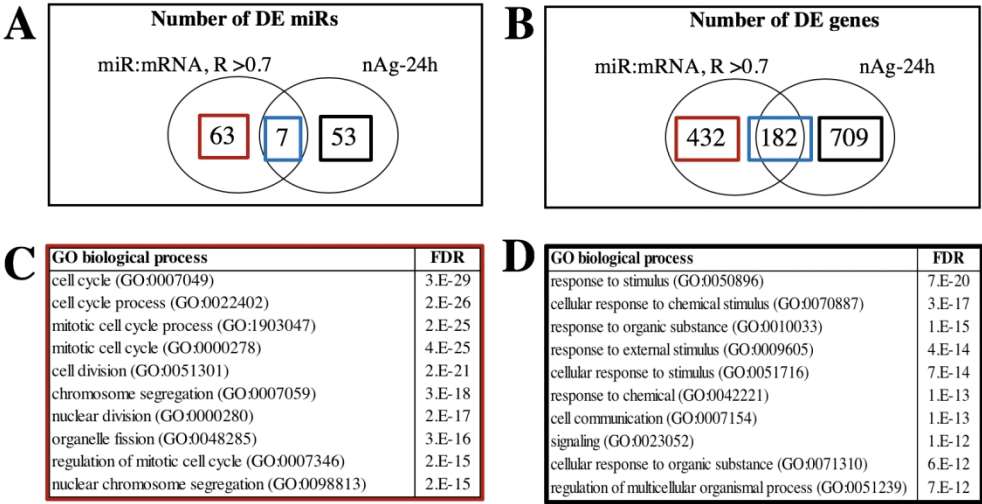
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2	chemokine (C-C motif) ligand 3	0	1.47
3	chemokine (C-C motif) ligand 3-like 3	0	1.55
4	solute carrier family 30 (zinc transporter), member 2	0	1.59
5	chemokine (C-C motif) ligand 3-like 3	0.000029	1.61
6	family with sequence similarity 189, member A2	0	1.63
7	NA	0	1.77
8	chemokine (C-X-C motif) ligand 14	0	1.85
9	hes family bHLH transcription factor 4	0	1.88
10	SAGA complex associated factor 29 pseudogene	0	1.96
11	gap junction protein, delta 3, 31.9kDa	0	2.03
12	heat shock 70kDa protein 6 (HSP70B)	0.000003	2.33
13	activity-regulated cytoskeleton-associated protein	0	2.53
14	clusterin	0	2.57
15	metallothionein 1A	0	2.99
16	NA	0	3.35
17	metallothionein 1L (gene/pseudogene)	0	3.42
18	metallothionein 1B	0	3.43
19	metallothionein 1H	0	3.63
20	NA	0.000003	3.71
21	metallothionein 1E	0	3.82
22	NA	0	3.92
23	metallothionein 1F	0	4.2
24	metallothionein 1H	0	4.26
25	heat shock 70kDa protein 6 (HSP70B)	0	4.62
26	metallothionein 1X	0	4.65
27	metallothionein 1M	0	5.05
28	metallothionein 1G	0	5.96
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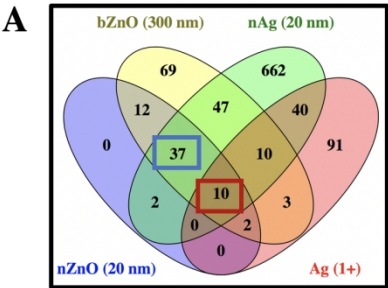












B

GO biological process	FDR
stress response to metal ion (GO:0097501)	5.09E-14
zinc ion homeostasis (GO:0055069)	6.21E-14
cellular zinc ion homeostasis (GO:0006882)	6.27E-14
detoxification of inorganic compound (GO:0061687)	6.78E-14
stress response to copper ion (GO:1990169)	4.67E-12
detoxification of copper ion (GO:0010273)	5.60E-12
cellular response to zinc ion (GO:0071294)	4.26E-11
response to zinc ion (GO:0010043)	6.08E-11
cellular transition metal ion homeostasis (GO:0046916)	1.11E-10
cellular response to copper ion (GO:0071280)	1.16E-10

GO biological process	FDR
stress response to metal ion (GO:0097501)	4.09E-04
detoxification of inorganic compound (GO:0061687)	5.45E-04
stress response to copper ion (GO:1990169)	5.96E-04
cellular response to zinc ion (GO:0071294)	7.19E-04
cellular response to copper ion (GO:0071280)	1.12E-03
detoxification of copper ion (GO:0010273)	1.19E-03
cellular zinc ion homeostasis (GO:0006882)	1.25E-03
zinc ion homeostasis (GO:0055069)	1.40E-03
cellular response to cadmium ion (GO:0071276)	1.45E-03
response to copper ion (GO:0046688)	2.11E-03

