Table S1. Folds of genes expression change in HUVEC after treatment with 10ug/mL S100A8

| Probe  | RefSeq     | Gene description                                           | fold-4hr | fold-24hr |
|--------|------------|------------------------------------------------------------|----------|-----------|
| A_23_P120883 | NM_002133 | heme oxygenase (decycling) 1                               | 1.686    | 1.881     |
| A_24_P418517 | AL353580 | nucleososmin pseudogene                                    | 1.746    | 1.746     |
| A_24_P59239  |           |                                                            | 1.751    | 1.723     |
| A_24_P170186 |           |                                                            | 1.724    | 1.744     |
| A_24_P178154 |           |                                                            | 1.716    | 1.678     |
| A_24_P58759  | AC008628  | similar to chaperonin containing Tcp1, subunit 5 (epsilon) | 1.651    | 1.670     |
| A_24_P33429  | AADB02001452 | similar to nucleososmin 1                                 | 1.635    | 1.690     |
| A_24_P621434 |           |                                                            | 1.605    | 1.709     |
| A_24_P58337  |           |                                                            | 1.687    | 1.678     |
| A_24_P814872 |           |                                                            | 1.635    | 1.635     |
| A_24_P350160 | NM_198262 | arginine-serine-rich coiled-coil 2                        | 1.690    | 1.543     |
| A_24_P306921 | AADB02017686 | similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1 | 1.629 | 1.591 |
| A_24_P332862 | NM_175910 | zinc finger protein 493                                   | 1.642    | 1.561     |
| A_24_P202497 | NM_020648 | twisted gastrulation homolog 1 (Drosophila)               | 1.565    | 1.548     |
| A_24_P209378 | NM_016220 | zinc finger protein 107                                   | 1.553    | 1.519     |
| A_24_P281801 |           |                                                            | 1.533    | 1.526     |
| A_24_P32849  | NM_001011725 | heterogeneous nuclear ribonucleoprotein A1-like 2       | 1.764    |           |
| A_32_P165477 | NM_014331 | solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 |           | 1.755     |
| A_32_P24376  | NM_033184 | keratin associated protein 2-1; keratin associated protein 2-4; keratin associated protein 2-3; similar to keratin associated protein 2-4; keratin associated protein 2-2 | 1.742 |           |
| A_32_P87013  | NM_000584 | interleukin 8                                             | 1.738    |           |
| A_23_P253622 | XM_001719592 | similar to KIAA1641; similar to ankyrin repeat domain 26; ankyrin repeat domain 36B | 1.725 |           |
| A_23_P428287 | NM_001080383 | gap junction protein, gamma 1, 45kDa                   | 1.724    |           |
| A_24_P187094 |           |                                                            | 1.723    |           |
| A_24_P307075 | AC097709  | similar to heterogeneous nuclear ribonucleoprotein A1     | 1.708    |           |
| A_23_P142272 | NM_019088 | Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae) | 1.706 |           |
| A_24_P717305 |           |                                                            | 1.699    |           |
| A_32_P24382  | NM_033184 | keratin associated protein 2-1; keratin associated protein 2-4; keratin associated protein 2-3; similar to keratin associated protein 2-4; keratin associated protein 2-2 | 1.683 |           |
| Accession   | Gene ID         | Description                                                                                       | Score |
|------------|----------------|--------------------------------------------------------------------------------------------------|-------|
| A_24_P273284 | NM_005737      | ADP-ribosylation factor-like 4C                                                               | 1.660 |
| A_23_P317620 | NM_152298      | nuclear autoantigenic sperm protein (histone-binding)                                             | 1.644 |
| A_32_P28365 | NM_003184      | TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa                | 1.625 |
| A_24_P16892 | BX537549       | hypothetical LOC645784                                                                         | 1.612 |
| A_32_P12647 | NM_002342      | lymphotoxin beta receptor (TNFR superfamily, member 3)                                          | 1.611 |
| A_24_P58187 | XM_062025      | similar to heterogeneous nuclear ribonucleoprotein A1-like                                      | 1.608 |
| A_24_P521662 |            |                                                                                                 | 1.604 |
| A_24_P229807 |            |                                                                                                 | 1.604 |
| A_24_P256764 | NM_005964      | myosin, heavy chain 10, non-muscle                                                              | 1.587 |
| A_23_P501634 | NM_078476      | butyrophilin, subfamily 2, member A1                                                             | 1.585 |
| A_24_P42316 | NM_018429      | B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB                | 1.585 |
| A_23_P4014 | NM_017575      | Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)                                  | 1.583 |
| A_32_P56525 | NM_014719      | family with sequence similarity 115, member A; family with sequence similarity 115, member B (pseudogene) | 1.580 |
| A_24_P541482 |            |                                                                                                 | 1.579 |
| A_32_P83326 | AC139495       | hypothetical LOC100272216                                                                      | 1.578 |
| A_24_P150486 | NM_004863      | serine palmitoyltransferase, long chain base subunit 2                                           | 1.577 |
| A_32_P207054 | NM_013986      | similar to Ewing sarcoma breakpoint region 1; Ewing sarcoma breakpoint region 1                  | 1.576 |
| A_24_P247536 | NM_152789      | family with sequence similarity 133, member B pseudogene; similar to FAM133B protein; family with sequence similarity 133, member B | 1.569 |
| A_24_P409904 | AK130705       | hypothetical LOC100272216                                                                      | 1.568 |
| A_32_P181513 | XM_001719792   | zinc finger protein 730                                                                         | 1.565 |
| A_23_P103996 | NM_002061      | glutamate-cysteine ligase, modifier subunit                                                     | 1.561 |
| A_23_P161698 | NM_002422      | matrix metallopeptidase 3 (stromelysin 1, progelatinase)                                        | 1.557 |
| A_23_P50834 | NM_182515      | zinc finger protein 714                                                                         | 1.553 |
| A_24_P41662 |            |                                                                                                 | 1.552 |
| A_32_P221958 | NM_001077685   | ArfGAP with GTPase domain, ankyrin repeat and PH domain 7                                        | 1.552 |
| A_24_P324405 | XM_001720760   | ankyrin repeat domain 11; hypothetical                                                          | 1.545 |
| Accession  | Description                                                                 | Value 1  | Value 2  |
|------------|------------------------------------------------------------------------------|----------|----------|
| A_24_P288993 | NM_001168331 hypothetical gene supported by AF044957; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa | 1.541    |          |
| A_32_P82409   |                                                                               | 1.537    |          |
| A_24_P131785  | NM_003704 chromosome 4 open reading frame 8                                  | 1.535    | 1.531    |
| A_24_P41530   |                                                                               | 1.528    |          |
| A_23_P44643   | NM_001137664 anaphase promoting complex subunit 7                            | 1.526    |          |
| A_32_P148345  | NM_004039 annexin A2 pseudogene 3; annexin A2; annexin A2 pseudogene 1       | 1.524    |          |
| A_24_P891276  | CH236948 hypothetical LOC442292                                              | 1.518    |          |
| A_24_P384059  | AL450226 heterogeneous nuclear ribonucleoprotein A1 pseudogene               | 1.517    |          |
| A_32_P116556  | NM_001127464 zinc finger protein 469                                          | 1.515    |          |
| A_24_P101601  |                                                                               | 1.512    |          |
| A_24_P418536  | AL359915 ribosomal protein L6 pseudogene 2                                   | 1.511    |          |
| A_24_P187355  |                                                                               | 1.510    |          |
| A_24_P33525   |                                                                               | 1.510    |          |
| A_32_P209735  | BI907421 glucuronidase, beta-like 2; glucuronidase, beta pseudogene          | 1.510    |          |
| A_24_P290188  |                                                                               | 1.509    |          |
| A_23_P206822  | NM_015171 exportin 6                                                          | 1.509    |          |
| A_23_P416395  | NM_003714 stanniocalcin 2                                                     | 1.507    |          |
| A_24_P204238  | XR_078725 similar to Huntingtin interacting protein K                         | 1.507    |          |
| A_24_P312189  | NM_019606 methylphosphate capping enzyme                                       | 1.501    |          |
| A_24_P889720  | NM_021009 ubiquitin C                                                         | 0.636    | 0.657    |
| A_24_P681218  |                                                                               | 0.642    | 0.610    |
| A_23_P60933   | NM_005950 metallothionein 1G                                                  | 0.589    | 0.654    |
| A_23_P90143   | NM_012423 ribosomal protein L13a pseudogene 7; ribosomal protein L13a pseudogene 5; ribosomal protein L13a pseudogene 16; ribosomal protein L13a; ribosomal protein L13a pseudogene 18 | 0.610    | 0.624    |
| A_24_P151544  | NM_199187 keratin 18; keratin 18 pseudogene 26; keratin 18 pseudogene 19     | 0.589    | 0.620    |
| A_24_P142223  | NM_033251 ribosomal protein L13 pseudogene 12; ribosomal protein L13         | 0.585    | 0.624    |
| A_23_P217609  | NM_001032393 ribosomal protein L36a pseudogene 51; ribosomal protein L36a pseudogene 37; ribosomal protein L36a pseudogene 49; heterogeneous nuclear ribonucleoprotein H2 | 0.549    | 0.653    |
| Accession   | Description                                                                 | First | Last  |
|-------------|------------------------------------------------------------------------------|-------|-------|
| A_24_P315986| ribosomal protein L36a                                                       | 0.551 | 0.613 |
| A_23_P166459| lectin, galactoside-binding, soluble, 1                                      | 0.526 | 0.637 |
| A_23_P46182 | ribosomal protein S8; ribosomal protein S8 pseudogene 8; ribosomal protein S8 pseudogene 10 | 0.515 | 0.646 |
| A_32_P208178| ribosomal protein S3A pseudogene 5; ribosomal protein S3a pseudogene 47; ribosomal protein S3a pseudogene 49; ribosomal protein S3A; hypothetical LOC100131699; hypothetical LOC100130107 | 0.509 | 0.650 |
| A_23_P252413| metallothionein 2A                                                           | 0.530 | 0.624 |
| A_32_P11931 | ribosomal protein L26 pseudogene 33; ribosomal protein L26; ribosomal protein L26 pseudogene 16; ribosomal protein L26 pseudogene 19; ribosomal protein L26 pseudogene 6 | 0.524 | 0.627 |
| A_24_P681301| ubiquitin C                                                                  | 0.553 | 0.581 |
| A_32_P857658| ribosomal protein, large, P1                                                 | 0.515 | 0.616 |
| A_24_P754803| ribosomal protein L10; ribosomal protein L10 pseudogene 15; ribosomal protein L10 pseudogene 6; ribosomal protein L10 pseudogene 16; ribosomal protein L10 pseudogene 9 | 0.565 | 0.558 |
| A_23_P120660| ribosomal protein S21                                                         | 0.495 | 0.626 |
| A_23_P423419| chromosome 15 open reading frame 21                                          | 0.528 | 0.552 |
| A_32_P137939| actin, beta                                                                  | 0.508 | 0.565 |
| A_23_P147888| ribosomal protein, large, P2 pseudogene 3; ribosomal protein, large, P2      | 0.478 | 0.589 |
| A_32_P190488| ribosomal protein L26 pseudogene 32                                          | 0.461 | 0.605 |
| A_24_P142228| ribosomal protein L13 pseudogene 12; ribosomal protein L13                   | 0.521 | 0.524 |
| A_32_P175198| actin, gamma 1                                                               | 0.484 | 0.545 |
| A_24_P135902| ribosomal protein S2 pseudogene 8; ribosomal protein S2 pseudogene 11; ribosomal protein S2 pseudogene 5; ribosomal protein S2 pseudogene 12; ribosomal protein S2 pseudogene 51; ribosomal protein S2 pseudogene 17; ribosomal protein S2 pseudogene 55; ribosomal protein S2 pseudogene 20; ribosomal protein S2 | 0.437 | 0.571 |
| Accession     | Name                                      | Score1 | Score2 |
|--------------|-------------------------------------------|--------|--------|
| A_32_P184796 | NM_053275 ribosomal protein, large, P0 pseudogene 2; ribosomal protein, large, P0 pseudogene 3; ribosomal protein, large, P0 pseudogene 6; ribosomal protein, large, P0 | 0.507  | 0.499  |
| A_24_P922631 | NM_001102609 hypothetical protein LOC133874 | 0.461  | 0.515  |
| A_23_P201711 | NM_014624 S100 calcium binding protein A6  | 0.418  | 0.552  |
| A_24_P148235 | NM_001030 ribosomal protein S27 pseudogene 29; ribosomal protein S27 pseudogene 9; ribosomal protein S27 pseudogene 23; ribosomal protein S27 pseudogene 13; ribosomal protein S27; ribosomal protein S27 pseudogene 21; ribosomal protein S27 pseudogene 7; ribosomal protein S27 pseudogene 6; ribosomal protein S27 pseudogene 19 | 0.438  | 0.524  |
| A_24_P179339 |                                           | 0.499  | 0.450  |
| A_24_P113109 | NM_018955 ubiquitin B                      | 0.484  | 0.460  |
| A_23_P331028 | NM_015335 mediator complex subunit 13-like | 0.446  | 0.490  |
| A_23_P106708 | NM_002952 ribosomal protein S2 pseudogene 8; ribosomal protein S2 pseudogene 11; ribosomal protein S2 pseudogene 5; ribosomal protein S2 pseudogene 12; ribosomal protein S2 pseudogene 51; ribosomal protein S2 pseudogene 17; ribosomal protein S2 pseudogene 55; ribosomal protein S2 pseudogene 20; ribosomal protein S2 | 0.418  | 0.513  |
| A_23_P106844 | NM_005953 metallothionein 2A               | 0.421  | 0.492  |
| A_24_P361896 | NM_005953 metallothionein 2A               | 0.417  | 0.470  |
| A_24_P179336 |                                           | 0.454  | 0.426  |
| A_23_P37445  | NM_213725 ribosomal protein, large, P1     | 0.401  | 0.470  |
| A_23_P135084 | NM_000972 ribosomal protein L7a pseudogene 70; ribosomal protein L7a pseudogene 30; ribosomal protein L7a pseudogene 66; ribosomal protein L7a pseudogene 27; ribosomal protein L7a pseudogene 11; ribosomal protein L7a pseudogene 62 | 0.405  | 0.421  |
| A_24_P323805 |                                           |        |        |
| A_23_P214046 | NM_033644 F-box and WD repeat domain containing 11 | 0.665  |       |
| A_32_P49728  | XM_002342218 hypothetical protein LOC339803 | 0.664  |       |
| A_24_P188071 | NM_032704 tubulin, alpha 1c                | 0.662  |       |
| Accession | EntrezGene ID | Description                                                                 | Score |
|-----------|---------------|------------------------------------------------------------------------------|-------|
| A_32_P342064 | NM_002032 | ferritin, heavy polypeptide 1; ferritin, heavy polypeptide-like 16; similar to ferritin, heavy polypeptide 1; ferritin, heavy polypeptide-like 3 pseudogene | 0.659 |
| A_23_P368205 | NM_001135637 | phosphatidylinositol-4-phosphate 5-kinase, type I, alpha | 0.658 |
| A_24_P366989 | | | 0.658 |
| A_24_P582241 | | | 0.657 |
| A_32_P94798 | NM_004039 | annexin A2 pseudogene 3; annexin A2; annexin A2 pseudogene 1 | 0.657 |
| A_23_P97283 | NM_198406 | progestin and adipoQ receptor family member VI | 0.655 |
| A_32_P112380 | NM_178518 | transmembrane protein 102 | 0.655 |
| A_23_P38167 | NM_022036 | G protein-coupled receptor, family C, group 5, member C | 0.654 |
| A_32_P53670 | | | 0.653 |
| A_23_P59179 | NM_021976 | retinoid X receptor, beta | 0.653 |
| A_23_P141389 | NM_000988 | ribosomal protein L27 | 0.652 |
| A_23_P77779 | NM_000981 | ribosomal protein L19; ribosomal protein L19 pseudogene 12 | 0.652 |
| A_32_P231391 | | | 0.650 |
| A_32_P41487 | XM_001725257 | hypothetical LOC729505; similar to hCG2040565; high-mobility group nucleosomal binding domain 2; similar to high-mobility group nucleosomal binding domain 2 | 0.649 |
| A_24_P144025 | NM_001024 | ribosomal protein S21 | 0.648 |
| A_23_P208991 | NM_002579 | paralemmin | 0.648 |
| A_23_P65307 | NM_032229 | SLIT and NTRK-like family, member 6 | 0.648 |
| A_23_P400181 | NR_026052 | hypothetical LOC65996 | 0.647 |
| A_24_P134074 | NM_001022 | ribosomal protein S19 pseudogene 3; ribosomal protein S19 | 0.647 |
| A_24_P14485 | NM_017495 | RNA binding motif protein 38 | 0.646 |
| A_23_P208358 | NM_001136134 | ribosomal protein L28 | 0.645 |
| A_23_P68240 | XM_002348280 | hypothetical protein LOC150763; similar to hCG1732629; similar to glycerol-3-phosphate acyltransferase, mitochondrial | 0.645 |
| A_23_P79323 | NM_003936 | cyclin-dependent kinase 5, regulatory subunit 2 (p39) | 0.644 |
| A_24_P258235 | NM_001004739 | olfactory receptor, family 5, subfamily L, member 2 | 0.643 |
| A_32_P24794 | | | 0.642 |
| A_23_P218675 | NM_006103 | WAP four-disulfide core domain 2 | 0.641 |
| Gene Name | Accession | Description                                                                 | Confidence |
|-----------|-----------|-----------------------------------------------------------------------------|------------|
| ribosomal protein S15 pseudogene 6 | AC008446 | ribosomal protein S15 pseudogene 6 | 0.641 |
| Ets2 repressor factor | NM_006494 | Ets2 repressor factor | 0.640 |
| calcium regulated heat stable protein 1, 24kDa | NM_001042476 | calcium regulated heat stable protein 1, 24kDa | 0.637 |
| eukaryotic translation elongation factor 1 alpha-like 7; eukaryotic translation elongation factor 1 alpha-like 3; similar to eukaryotic translation elongation factor 1 alpha 1; eukaryotic translation elongation factor 1 alpha 1 | NM_001402 | eukaryotic translation elongation factor 1 alpha-like 7; eukaryotic translation elongation factor 1 alpha-like 3; similar to eukaryotic translation elongation factor 1 alpha 1; eukaryotic translation elongation factor 1 alpha 1 | 0.636 |
| ribosomal protein S11 pseudogene 5; ribosomal protein S11 | NM_001015 | ribosomal protein S11 pseudogene 5; ribosomal protein S11 | 0.634 |
| ribosomal protein L14 | NM_003973 | ribosomal protein L14 | 0.632 |
| ribosomal protein L26 pseudogene 33; ribosomal protein L26; ribosomal protein L26 pseudogene 16; ribosomal protein L26 pseudogene 19; ribosomal protein L26 pseudogene 6 | NM_000987 | ribosomal protein L26 pseudogene 33; ribosomal protein L26; ribosomal protein L26 pseudogene 16; ribosomal protein L26 pseudogene 19; ribosomal protein L26 pseudogene 6 | 0.632 |
| ribosomal protein S7; ribosomal protein S7 pseudogene 11; ribosomal protein S7 pseudogene 4; ribosomal protein S7 pseudogene 10 | NM_001011 | ribosomal protein S7; ribosomal protein S7 pseudogene 11; ribosomal protein S7 pseudogene 4; ribosomal protein S7 pseudogene 10 | 0.629 |
| glutathione transferase zeta 1 | NM_145870 | glutathione transferase zeta 1 | 0.626 |
| ribosomal protein S17 | NM_001021 | ribosomal protein S17 | 0.620 |
| transmembrane emp24 protein transport domain containing 9 | NM_017510 | transmembrane emp24 protein transport domain containing 9 | 0.616 |
| GNAS complex locus | NM_016592 | GNAS complex locus | 0.614 |
| chromosome 19 open reading frame 22 | NM_138774 | chromosome 19 open reading frame 22 | 0.613 |
| FtsJ methyltransferase domain containing 2 | NM_015050 | FtsJ methyltransferase domain containing 2 | 0.612 |
| nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin) pseudogene 21; hypothetical LOC100131044; similar to nucleophosmin 1; nucleophosmin (nucleolar phosphoprotein B23, numatrin) | XM_496355 | nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin) pseudogene 21; hypothetical LOC100131044; similar to nucleophosmin 1; nucleophosmin (nucleolar phosphoprotein B23, numatrin) | 0.609 |
| RAB1B, member RAS oncogene family | NM_030981 | RAB1B, member RAS oncogene family | 0.606 |
| FK506 binding protein 1C | CH471143 | FK506 binding protein 1C | 0.605 |
| ribosomal protein S17 | NM_001021 | ribosomal protein S17 | 0.605 |
| E74-like factor 3 (ets domain transcription factor, epithelial-specific) | NM_004433 | E74-like factor 3 (ets domain transcription factor, epithelial-specific) | 0.603 |
| Accession       | Gene Symbol       | Description                                                                 | Score |
|-----------------|-------------------|-----------------------------------------------------------------------------|-------|
| A_24_P213783    | NM_001099693      | ribosomal protein L31 pseudogene 49; ribosomal protein L31 pseudogene 17; ribosomal protein L31 | 0.599 |
| A_24_P160001    | NM_000801         | FK506 binding protein 1A, 12kDa                                             | 0.599 |
| A_23_P325093    | NM_178026         | gamma-glutamyltransferase 7                                                 | 0.597 |
| A_23_P157405    | XM_946272         | coiled-coil-helix-coiled-coil-helix domain containing 2; similar to coiled-coil-helix-coiled-coil-helix domain containing 2 | 0.595 |
| A_24_P418239    | NM_001025071      | ribosomal protein S14                                                       | 0.595 |
| A_23_P33045     | NM_000987         | ribosomal protein L26 pseudogene 33; ribosomal protein L26 pseudogene 16; ribosomal protein L26 pseudogene 19; ribosomal protein L26 pseudogene 6 | 0.591 |
| A_23_P38167     |                  |                                                                               | 0.591 |
| A_23_P141405    | NM_198175         | non-metastatic cells 1, protein (NM23A) expressed in; NME1-NME2 readthrough transcript; non-metastatic cells 2, protein (NM23B) expressed in | 0.588 |
| A_23_P30464     | NM_030567         | proline rich 7 (synaptic)                                                   | 0.583 |
| A_23_P24763     | NM_001017         | ribosomal protein S13 pseudogene 8; ribosomal protein S13 pseudogene 2       | 0.580 |
| A_23_P104318    | NM_019058         | DNA-damage-inducible transcript 4                                           | 0.579 |
| A_23_P128067    | NM_021104         | ribosomal protein L41                                                       | 0.575 |
| A_24_P388252    | NM_000945         | protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform       | 0.567 |
| A_23_P6433      | NM_005368         | myoglobin                                                                    | 0.567 |
| A_23_P251593    | NM_007104         | ribosomal protein L10a pseudogene 6; ribosomal protein L10a; ribosomal protein L10a pseudogene 9 | 0.564 |
| A_23_P29747     | NM_000984         | ribosomal protein L23a pseudogene 63; ribosomal protein L23a pseudogene 75; ribosomal protein L23a pseudogene 37; ribosomal protein L23a pseudogene 65; ribosomal protein L23a pseudogene 43; ribosomal protein L23a pseudogene 44; ribosomal protein L23a | 0.559 |
| A_23_P502274    | NM_002751         | mitogen-activated protein kinase 11                                          | 0.557 |
| A_23_P208925    | NM_003025         | SH3-domain GRB2-like 1                                                      | 0.556 |
| A_23_P142475    | NM_001031         | ribosomal protein S28 pseudogene 6; ribosomal protein S28 pseudogene 9       | 0.546 |
| Agilent Probe ID | Accession Number | Gene Name and Description | Change Fold |
|------------------|------------------|---------------------------|-------------|
| A_23_P81492      | NM_001025071     | ribosomal protein S14     | 0.536       |
| A_32_P220307     | NM_0010000       | ribosomal protein L39 pseudogene 10; ribosomal protein L39 pseudogene 20; ribosomal protein L39 pseudogene 27; ribosomal protein L39; ribosomal protein L39 pseudogene 13; ribosomal protein L39 pseudogene 32 | 0.536       |
| A_32_P187327     | NM_006088        | tubulin, beta 2C          | 0.530       |
| A_23_P252322     | NM_001001977     | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2; ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit | 0.512       |
| A_32_P75141      |                  |                           | 0.498       |
| A_23_P33759      | NM_004753        | dehydrogenase/reductase (SDR family) member 3 | 0.496       |
| A_23_P52298      | NM_006993        | nucleophosmin/nucleoplasmin, 3 | 0.477       |

Note: ^Agilent probe ID in 4X44 microarray.

^b The probes/genes are basically listed in the order of change folds in either group.
|                     | Up-regulated genes |                     | down-regulated genes |                     |
|---------------------|--------------------|---------------------|----------------------|--------------------|
|                     | only at 4hr        | At both 4hr and 24hr| Only at 24hr         | only at 4hr        | At both 4hr and 24hr| Only at 24hr         |
| probes              | 37                 | 16                  | 20                   | 54                 | 38                   | 22                   |
| Defined genes       | 29                 | 10                  | 13                   | 44                 | 27                   | 20                   |
Table S3. Altered pathways upon S100A8 treatment*

|                                      | Count | (%)  | P value    | Fold enrichment |
|--------------------------------------|-------|------|------------|-----------------|
| **Up-regulated at 4hr or 24hr**     |       |      |            |                 |
| none                                 |       |      |            |                 |
| **Downregulated at 4hr (total 2)**  |       |      |            |                 |
| Ribosome                             | 29    | 42.0 | 9.47E-41   | 37.7            |
| Pathogenic Escherichia coli infection| 4     | 5.8  | 0.01       | 7.93            |
| **Downregulated at 24hr (total 4)** |       |      |            |                 |
| Ribosome                             | 14    | 28.6 | 3.66E-17   | 30.31           |
| Pathogenic Escherichia coli infection| 4     | 8.2  | 0.003      | 13.22           |
| Vibrio cholerae infection            | 3     | 6.1  | 0.033      | 10.09           |
| Dilated cardiomyopathy              | 3     | 6.1  | 0.080      | 6.14            |
Table S4. Representatives of altered GOs upon S100A8 treatment

| Count | (%) | P value | Fold enrichment |
|-------|-----|---------|-----------------|
| **Up-regulation at 4hr (total 13)** | | | |
| regulation of transcription | 9 | 22.5 | 2.23 |
| in utero embryonic development | 3 | 7.5 | 10.98 |
| blood vessel morphogenesis | 3 | 7.5 | 9.16 |
| positive regulation of signal transduction | 3 | 7.5 | 6.55 |
| secretion | 3 | 7.5 | 6.44 |
| skeletal system development | 3 | 7.5 | 6.06 |
| cardiac muscle tissue development | 2 | 5.0 | 22.6 |
| positive regulation of cell communication | 3 | 7.5 | 5.87 |
| **Up-regulation at 24hr (total 1)** | | | |
| response to oxidative stress | 3 | 12.5 | 19.04 |
| **Downregulation at 4hr (total 55)** | | | |
| translational elongation | 32 | 46.4 | 71.43 |
| ribosome biogenesis | 11 | 15.9 | 20.33 |
| rRNA processing | 8 | 11.6 | 19.61 |
| ncRNA processing | 8 | 11.6 | 9.65 |
| negative regulation of protein modification process | 4 | 5.8 | 7.58 |
| erythrocyte homeostasis | 3 | 4.3 | 13.80 |
| negative regulation of RNA splicing | 2 | 2.9 | 90.19 |
| long-term strengthening of neuromuscular junction | 2 | 2.9 | 90.19 |
| regulation of apoptosis | 9 | 13.0 | 2.52 |
| response to caffeine | 2 | 2.9 | 56.37 |
| cytokine-mediated signaling pathway | 3 | 4.3 | 9.66 |
| response to purine | 2 | 2.9 | 45.09 |
| negative regulation of cellular protein metabolic process | 4 | 5.8 | 5.01 |
| homeostatic process | 8 | 11.6 | 2.40 |
| positive regulation of binding | 3 | 4.3 | 8.67 |
| axonogenesis | 4 | 5.8 | 4.67 |
| positive regulation of protein ubiquitination | 3 | 4.3 | 8.05 |
| release of sequestered calcium ion into cytosol | 2 | 2.9 | 32.21 |
| Term                                                                 | Count | Score  | FDR    | p-value |
|----------------------------------------------------------------------|-------|--------|--------|---------|
| Homeostasis of number of cells                                       | 3     | 4.3    | 0.071  | 6.76    |
| Nucleoside diphosphate metabolic process                             | 2     | 2.9    | 0.072  | 26.53   |
| Cellular di-, tri-valent inorganic cation homeostasis                 | 4     | 5.8    | 0.077  | 3.97    |
| Cell morphogenesis involved in differentiation                        | 4     | 5.8    | 0.090  | 3.70    |
| **Downregulation at 24hr (total 32)**                                |       |        |        |         |
| Translational elongation                                             | 17    | 34.7   | 2.36E-24| 54.21   |
| Axonogenesis                                                         | 5     | 10.2   | 0.003  | 8.34    |
| Cell morphogenesis involved in neuron differentiation                 | 5     | 10.2   | 0.004  | 7.71    |
| Cell morphogenesis involved in differentiation                        | 5     | 10.2   | 0.006  | 6.60    |
| Cellular component morphogenesis                                      | 6     | 12.2   | 0.007  | 4.87    |
| Cell motion                                                          | 6     | 12.2   | 0.014  | 4.07    |
| Long-term strengthening of neuromuscular junction                     | 2     | 4.1    | 0.015  | 128.84  |
| Cell morphogenesis                                                   | 5     | 10.2   | 0.022  | 4.52    |
| Muscle cell differentiation                                           | 3     | 6.1    | 0.052  | 7.99    |
| Ribosome biogenesis                                                  | 3     | 6.1    | 0.053  | 7.92    |
| ER-associated protein catabolic process                              | 2     | 4.1    | 0.070  | 26.84   |
| **Induction of apoptosis**                                            | 4     | 8.2    | 0.072  | 4.03    |

For clarity and simplicity, only representative (i.e. the one with least P value) in each group of similar GO terms were given. For example, “blood vessel development” and “vasculature development” are similar to “blood vessel morphogenesis” and thus omitted from this list. Similarly, “regulation of apoptosis”, “regulation of programmed cell death”, “induction of programmed cell death” and “regulation of cell death” overlaps “induction of apoptosis” thus omitted in this table. For the whole lists of GO, please refer to supplementary Table x.
Table S5. Expression levels of S100A family members in S100A8-treated HUVEC compared with control cells

| Probe    | Gene  | 4hr Signal (mean) | 4hr Ratio | 24hr Signal (mean) | 24hr Ratio |
|----------|-------|-------------------|-----------|--------------------|------------|
|          |       | Control           | S100A8    | Mean    | Stdev  | Control   | S100A8    | Mean    | Stdev  |
| A_23_P137984 | S100A10 | 62774.1          | 64817.9  | 1.035  | 0.046  | 61219.6    | 69547.2  | 1.139  | 0.063  |
| A_23_P126593 | S100A11 | 20579.4          | 24018.0  | 1.168  | 0.083  | 21724.7    | 24256.9  | 1.117  | 0.112  |
| A_23_P145863 | S100A11 | 22441.6          | 23169.6  | 1.031  | 0.086  | 23787.3    | 23388.7  | 0.983  | 0.072  |
| A_23_P372874 | S100A13 | 44426.6          | 45256.3  | 1.021  | 0.080  | 42314.6    | 47599.2  | 1.126  | 0.050  |
| A_23_P147918 | S100A14 | 30449.6          | 30527.1  | 1.002  | 0.022  | 28849.5    | 28965.2  | 1.004  | 0.021  |
| A_23_P201706 | S100A2  | 12544.5          | 10876.3  | 0.868  | 0.052  | 7201.4     | 5968.9   | 0.832  | 0.054  |
| A_23_P104073 | S100A3  | 4291.4           | 3752.1   | 0.875  | 0.020  | 3466.9     | 3153.7   | 0.909  | 0.033  |
| A_23_P94800  | S100A4  | 347.1            | 295.2    | 0.852  | 0.067  | 291.6      | 257.2    | 0.883  | 0.065  |
| A_23_P201711 | S100A6  | 92629.2          | 38507.6  | 0.418  | 0.043  | 106115.7   | 58853.7  | 0.552  | 0.036  |
| A_24_P222835 | S100PBP | 973.3            | 1028.6   | 1.058  | 0.048  | 1008.1     | 1070.9   | 1.065  | 0.115  |
| A_23_P338952 | S100PBP | 1783.4           | 1719.3   | 0.966  | 0.076  | 1754.5     | 1780.0   | 1.014  | 0.082  |
| A_23_P200425 | S100PBP | 2362.1           | 2174.5   | 0.920  | 0.030  | 2374.2     | 2248.8   | 0.946  | 0.92  |

*a* Shown were mean of three arrays in each group. *b* Mean and standard deviation of ratios in three arrays were give.
Table S6. Comparison of cell cycle-related gene expression in Viemann studies (with 200µg/mL S100A8/A9) (1, 2) to that of current study (with 10µg/mL S100A8 only)

| Genes up-regulated over 1.7 folds at 6 hr by S100A8/A9 | Our data at 4 hr | Genes down-regulated over 1.7 folds at 6 hr by S100A8/A9 | Our data at 4 hr |
|--------------------------------------------------------|-----------------|----------------------------------------------------------|-----------------|
| Bak (Bcl-2—antagonist/killer 1) BAK1                   | 1.320           | ERCC5 (excision repair protein complementation group 5)   | 0.994           |
| Bax (Bcl-2—associated X protein)                       | 0.886, 0.790, 0.737 | NEK3 (never in mitosis gene A—related kinase 3)           | 1.129, 1.036, 1.027 |
| TP53 (Transcription factor p53)                        | 0.943           | MAD2L1 (MAD2 (mitotic arrest deficient 2)—like 1)         | 0.975           |
|                                                        |                 | CDC2 (Cell division cycle 2 (G1 to S and G2 to M))       | 1.018           |
|                                                        |                 | API5 (Apoptosis inhibitor 5)                              | 1.033, 0.903    |
|                                                        |                 | NEK4 (NIMA-related kinase 4)                              |                 |
|                                                        |                 | STAG2 (Stromal antigen 2)                                 | 1.028, 1.105    |
|                                                        |                 | CFLAR (c-FLIP (CASP8 and FADD-like apoptosis regulator)    | 0.968, 1.104    |
|                                                        |                 | CGRRF1 (Cell growth regulator with ring finger domain 1)  | 1.135, 1.019    |
|                                                        |                 | BBP (Beta-amyloid binding protein)                        |                 |
|                                                        |                 | PMS1 (Postmeiotic segregation increased 1)                 | 1.050           |
|                                                        |                 | CAST (Calpastatin)                                         | 1.143, 0.987    |
|                                                        |                 | RB1 (Retinoblastoma 1)                                    | 1.060, 1.032    |
### Table S7. Summary of references concerning S100A8/A9 in tumors form patients or tumor cells lines

| Tumor                                    | Methods  | Main findings                                                                 | Ref. |
|------------------------------------------|----------|-------------------------------------------------------------------------------|------|
| squamous cervical cancer (SCC)           | 2DE-MS,  | S100A9 protein was highly up-regulated in SCC samples (by 2D-MS), found in all of 20 SCC tissues and 4 of 20 matched normal cervical tissues (by WB). Positive staining in all SSC samples but focal and weak staining in part of normal cervical tissues. | (3)  |
| gastric cancer                           | MS       | S100A8, A9 and α defensin 1, 2 were over-expressed in tumor biopsies compared with normal tissues. | (4)  |
| invasive ductal carcinoma of the breast  | IHC      | S100A8 is S100A9-dependently expressed. Co-expression of both proteins was associated with poor tumor differentiation, vessel invasion, node metastasis, and advanced stage. Co-expression of the proteins was also observed in MCF-7 cells. | (5)  |
| advanced stage ovarian cancer            | 2DE-MS,  | S100A8 was significantly up-regulated in pathological tissues and interstitial fluid. Weak S100A8 expression in epithelium but not stroma of normal ovarian tissues. | (6)  |
| colorectal cancer (CRC) samples          | 2DE-MS,  | S100A8 and S100A9 were over-expressed in both CRC tumor samples and serum. IHC showed that S100A8/A9 were mainly in tumor infiltrating immune cells rather than in tumor cells. | (7)  |
| human breast tumor cell line and patients samples | MS, MA, IHC (tissue array) | S100A9 was over expressed in basallike compared to luminal-like cell lines, and much more frequently expressed in basallike tumors versus luminal-like tumors. Higher expression of S100A9 was associated with lower metastasis-free and overall survival rates. | (8)  |
| non-muscle-invasive bladder cancer (NMIBC) | RT-qPCR  | S100A8 may contribute to the generation of certain aspects of the aggressive phenotype rather than simply promoting cell proliferation in NMIBC. | (9)  |
| muscle invasive bladder cancer (MIBC)    | MA, RT-qPCR | Together with *IL1B* and *EGFR*, *S100A8 and S100A9 form a four-gene* indicator of tumor progression. | (10) |
| human prostate cancers                   | IHC, ISH, ELISA | S100A8, S100A9, and their potential receptor RAGE were up-regulated in prostatic intraepithelial neoplasia and preferentially in high-grade adenocarcinomas, whereas benign tissue was negative or showed weak expression of the proteins. There was a high degree of overlap of S100A8 and S100A9 expression patterns and of S100A8 or S100A9 and RAGE, respectively. | (11) |
| bladder cancer                           | HPLC,    | S100A8 was over-expression more often in tumor with bladder                   | (12) |
| Experiment Type | Methodology | Result Summary |
|-----------------|-------------|---------------|
| 2DE-MS, IHC     |             | Enhanced expression of S100A8, S100A9, and RAGE is an early event in prostate tumorigenesis and may contribute to development and progression or extension of prostate carcinomas. Furthermore, S100A9 in serum may serve as useful marker to discriminate between prostate cancer and BPH. |
| pancreatic adenocarcinoma | 2DE-MS | Abnormal expression of S100A8 and A9 are correlated with poor prognosis. |
| Human cancers over-express S100A2, A3, A5, A7, A8, A9, A14, A15, A16 and S100P, and underexpress S100A1, A4 and S100B. S100A1, A3, A8, A9, A14, A15 and A16 showed similar change patterns in bladder cancers from mouse, rat and human. |
| chemical-induced mouse and rat bladder cancers, human bladder cancers | Array, RT-qPCR | A8 and A9 were expressed in 12% and 28% of breast cancers, respectively. S100A11 exclusively expressed in nuclear in normal tissues but translocated to cytoplasmic and nuclear in all common cancers. |
| 21 common tumor types | Tissue array | Down-regulation of TNFSF7, S100A4, S100A7, S100A8, and S100A9 (calcium binding protein family) were associated with transformation and progression of breast cancer cells. Exogenous expressions of S100A8 and S100A9 inhibit growth in benign and noninvasive carcinoma cells, suggesting their negative role in cell proliferation. |
| untransformed and isogenic human breast cancer cell lines including a normal, benign, noninvasive and invasive carcinoma. | MA, RT-PCR, WB | S100A8 and S100A9 distinguish between normal cells (high expression) and tumor cells (expression undetectable) with a sensitivity of 100% and specificity of 91% and can distinguish inflammatory/hyperproliferative lesions (intermediate expression) from tumor cells with a sensitivity of up to 91% and specificity of up to 90%. |
| oral brush of normal, premalignant, and tumor cells | ProteinChip Arrays, IHC | S100A1, A2, A4, A8, A9, A10, A11, A12, A14, S100B, and S100P genes were significantly down-regulated in ESCC while S100A7 markedly up-regulated. |
| human esophageal squamous cell carcinoma (ESCC) versus normal esophageal | RT-PCR | |

**Negative relationship of S100A8/A9 expression with tumor**

| Tumor Type | Methodology | Result Summary |
|------------|-------------|---------------|
| untransformed and isogenic human breast cancer cell lines including a normal, benign, noninvasive and invasive carcinoma. | MA, RT-PCR, WB | Down-regulation of TNFSF7, S100A4, S100A7, S100A8, and S100A9 (calcium binding protein family) were associated with transformation and progression of breast cancer cells. Exogenous expressions of S100A8 and S100A9 inhibit growth in benign and noninvasive carcinoma cells, suggesting their negative role in cell proliferation. |
| oral brush of normal, premalignant, and tumor cells | ProteinChip Arrays, IHC | S100A8 and S100A9 distinguish between normal cells (high expression) and tumor cells (expression undetectable) with a sensitivity of 100% and specificity of 91% and can distinguish inflammatory/hyperproliferative lesions (intermediate expression) from tumor cells with a sensitivity of up to 91% and specificity of up to 90%. |
| human esophageal squamous cell carcinoma (ESCC) versus normal esophageal | RT-PCR | S100A1, A2, A4, A8, A9, A10, A11, A12, A14, S100B, and S100P genes were significantly down-regulated in ESCC while S100A7 markedly up-regulated. |
mucosa.

a. 2DE-MS, two dimension gel electrophoresis followed by mass spectrum of interested protein spors. WB, western blotting. IHC, immunohistochemistry. RT-PCR, reverse transcription-PCR. RT-qPCR, RT-quantitative PCR. MA, microarray. ISH, in situ hybridization. HPLC, high performance liquid chromatography. b. Some of the statements were directly copied from original references while others edited from references.
**Figure S1.** Downregulated genes that belong to the Ribosome pathways. Red stars indicate the genes that were downregulated at both 4 hr and 24 hr, blue ovals indicate the genes that were downregulated only at 4 hr. No genes were downregulated at 24 hr only without change at 4 hr.
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