

## Supplement tables

**Table1S. Fold Change between Baseline vs Mc Donald's meal in Inflammasome genes.**

| <b>Gene Description</b>  | <b>Symbol</b> | <b>Gene Bank (NM)</b> | <b>Fold Change between Baseline and McD<br/>(a) <math>p &lt; 0,05</math><br/>(b) <math>p &gt; 0,05</math></b> |
|--|---------------|-----------------------|---|
| Absent in melanoma 2   | AIM2          | 004833                | -1,03 (b)   |
| B-cell ccl/lymphoma 2  | BCL2          | 000633                | -1,00 (b)   |
| Bcl2 like 1  | BCL2L1        | 138578                | -1,58 (b)   |
| Baculoviral iap repeat containig 2   | BIRC2         | 001166                | -1,04 (b)   |
| Baculoviral iap repeat containig 3   | BIRC3         | 001165                | 1,30 (b)  |
| Caspase recruitment domain family memer 18                                     | CARD18        | 021571                | 1,36 (b)  |
| Caspase recruitment domain family memer 6                                      | CARD6         | 032587                | 1,16 (b)  |
| Caspase 1 apoptosis related cysteine peptidase (interleukin 1 beta convertase) | CASP1         | 033292                | -1,22 (b)   |
| Caspase 1 apoptosis related cysteine peptidase                                 | CASP5         | 004347                | -1,45 (b)   |
| Caspase 1 apoptosis related cysteine peptidase                                 | CASP8         | 001228                | 1,30 (b)  |
| Chemokyna (c-c motive) ligand 2  | CCL2          | 002982                | -1,72 (b)   |
| Chemokyna (c-c motive) ligand 7  | CCL7          | 006273                | 1,36 (b)  |
| Cd 40 ligand   | CD40LG        | 000074                | 1,66 (b)  |
| Casp8 and fad dlike apoptosis regulator  | CFLAR         | 003879                | -1,56 (b)   |
| Conserved helix loop helix ubiquitose kinase                                   | CKUK          | 001278                | -1,50 (b)   |
| Class ii maior histocompatibility complex trans activator                      | CIITA         | 000246                | -1,16 (b)   |
| Cathepsin b  | CTSB          | 001908                | 1,13 (b)  |
| Chemokine (cxc motif) ligand 1 (melanome growth stimolating activity alpha)    | CXCL1         | 001511                | 1,07 (b)  |
| Chemokine (cxc motif) ligand 2   | CXCL2         | 002089                | 1,07 (b)  |
| Fas (tnfrsf6) asociated via death domain                                       | FAD D         | 003824                | -1,13 (b)   |
| Heat shock protein 90 kda alpha (citosolyc) class a member 1                   | HSP90AA1      | 001017963             | -1,71(b)  |
| Interferon beta 1 fibrobalst   | IFNB1         | 002176                | -1,08 (b)   |
| Interferon gamma   | IFNG          | 000919                | -1,03 (b)   |
| Inibitor of kappa light  | IKKB          | 001556                | -1,32 (b)   |

|  |        |        |           |
|--|--------|--------|-----------|
| polypeptide gene<br>Enhancer in b-cell kinase<br>beta  |        |        |           |
| Inhibitor of kappa light<br>polypeptide gene<br>Enhancer in b-cell kinase<br>gamma                                   | IKBKG  | 003639 | -1,09 (b) |
| Interleukine 12a (natural<br>killer cell stimulatory<br>factor 1 cytotoxic<br>lymphocyte<br>maturation factor 1 p35) | IL12A  | 000882 | 1,18 (b)  |
| Interleukine 12b (natural<br>killer cell stimulatory<br>Factor 2 cytotoxic<br>lymphocyte<br>maturation factor 2 p40) | IL 12B | 002187 | 1,36 (b)  |
| Interleukine 18 (interferon<br>gamma inducing factor)  | IL18   | 001562 | -1,09 (b) |
| Interleukine 1 beta  | IL1B   | 000576 | 1,35 (b)  |
| Interleukine 33  | IL33   | 033439 | 1,36 (b)  |
| Interleukine 6 (interferon<br>beta 2)  | IL 6   | 000600 | -2,91 (a) |
| Interferon regulatory<br>factor 2  | IRF2   | 002199 | 1,26 (b)  |
| Mitogen activated protein<br>kinase kinase kinase 7  | MAP3K7 | 003188 | -1,17 (b) |
| Mitogen activated protein<br>kinase 1  | MAPK1  | 002745 | -1,48 (b) |
| Mitogen activated protein<br>kinase 11   | MAPK11 | 002751 | -1,09 (b) |
| Mitogen activated protein<br>kinase 12   | MAPK12 | 002969 | 1,62 (b)  |
| Mitogen activated protein<br>kinase 13   | MAPK13 | 002754 | -1,43 (b) |
| Mitogen activated protein<br>kinase 3  | MAPK3  | 002746 | -1,24 (b) |
| Mitogen activated protein<br>kinase 8  | MAPK8  | 002750 | -1,16 (b) |
| Mitogen activated protein<br>kinase 9  | MAPK9  | 002752 | 1,39 (b)  |
| Myeloid differentiation<br>primary response gene<br>(88)   | MYD88  | 002468 | -1,11 (b) |
| Nuclear factor of kappa<br>light polypeptides<br>Gene enhancer in b-cells 1  | NFKB1  | 003998 | 1,29 (b)  |
| Nuclear factor of kappa light<br>polypeptides<br>Gene enhancer in b-cells<br>inhibitor alpha                         | NFKBIA | 020529 | -1,35 (b) |
| Nuclear factor of kappa<br>light polypeptides<br>Gene enhancer in b-cells<br>inhibitor beta                          | NFKBIB | 002503 | -1,53(b)  |
| Nrl family card domain   | NLRC4  | 021209 | -1,32 (b) |

|   |         |           |           |
|---|---------|-----------|-----------|
| containing 4  |         |           |           |
| Nrl family card domain containing 5   | NLRC5   | 032206    | -1,77 (b) |
| Nrl family pyrin domain containing 1  | NLRP1   | 033004    | -1,32 (b) |
| Nrl family pyrin domain containing 12   | NLRP12  | 033297    | 2,10 (a)  |
| Nrl family pyrin domain containing 3  | NLRP3   | 183395    | 1,10(b)   |
| Nrl family pyrin domain containing 4  | NLRP4   | 134444    | 1,36 (b)  |
| Nrl family pyrin domain containing 5  | NLRP5   | 153447    | 1,36 (b)  |
| Nrl family pyrin domain containing 6  | NLRP6   | 138329    | -1,52 (b) |
| Nrl family x 1  | NLRX1   | 024618    | -1,43 (b) |
| Nucleotide binding oligomerization Domain containing 1                                  | NOD1    | 006092    | -1,45 (b) |
| Nucleotide binding oligomerization Domain containing 2                                  | NOD2    | 022162    | 1,05 (b)  |
| Purinergic receptor p2x ligand gated ion channel 7                                      | P2RX7   | 002562    | -1,06 (b) |
| Pannexin 1  | PANX1   | 015368    | -1,65 (b) |
| Phosphoprotein enriched in astrocytes 15  | PEA15   | 003768    | 1,08 (b)  |
| Prolin serin threonine phosphatase Interacting protein 1                                | PSTPIP1 | 003978    | 1,06 (b)  |
| Prostaglandin endoperoxidase synthase 2 (prostaglandin g/h synthase and cyclooxygenase) | PTGS2   | 000963    | -1,65 (b) |
| Pyd and card domain containing  | PYCARD  | 013258    | 2,19 (a)  |
| Pyd (pyrin domain) conteing 1   | PYCD1   | 152901    | 1,36 (b)  |
| Receptor interacting serin threonine kinase 2   | RIPK2   | 003821    | -1,30 (b) |
| Sgt1 suppressor of g2 allele of skp 1 (s. <i>Cerevisiae</i> )                           | SUGT1   | 006704    | -1,01 (b) |
| Tgf beta activated kinase 1/map 3k7 binding protein 1                                   | TAB1    | 006116    | -1,60 (b) |
| Tgf beta activated kinase 1/map 3k7 binding protein 2                                   | TAB2    | 015093    | -1,11 (b) |
| Tool interleukine 1 receptor (tir) domain containing adaptor protein)                   | TIRAP   | 001039661 | 1,03 (b)  |
| Tumor necrosis factor   | TNF     | 000594    | 1,74 (b)  |
| Tumor necrosis factor   | TNFSF11 | 003701    | 1,73 (b)  |

|  |         |        |           |
|--|---------|--------|-----------|
| (ligand) superfamily member 11                       |         |        |           |
| Tumor necrosis factor (ligand) superfamily member 14 | TNFSF14 | 003807 | 1,18 (b)  |
| Tumor necrosis factor (ligand) superfamily member 4  | TNFS4   | 003326 | -1,20 (b) |
| Tnf receptor associated factor 6                     | TRAF 6  | 004620 | -1,27 (b) |
| Tioredoxine intercatating protein                    | TXNPI   | 006472 | -1,87 (b) |

**Table 2S. Fold Change between Baseline vs Mc Donald's meal with not pruned vineyard red wine in Inflammasome genes.**

| <b>Gene Description</b>  | <b>Symbol</b> | <b>Gene Bank (NM)</b> | <b>Fold Change between Baseline and McDRW<br/>(a) <math>p &lt; 0,05</math><br/>(b) <math>p &gt; 0,05</math></b> |
|--|---------------|-----------------------|---|
| Absent in melanoma 2   | AIM2          | 004833                | -1,18 (b)   |
| B-cell ccl/lymphoma 2  | BCL2          | 000633                | -1,14 (b)   |
| Bcl2 like 1  | BCL2L1        | 138578                | -2,47 (a)   |
| Baculoviral iap repeat containig 2   | BIRC2         | 001166                | -1,28 (b)   |
| Baculoviral iap repeat containig 3   | BIRC3         | 001165                | -2,11 (a)   |
| Caspase recruitment domain family memer 18                                     | CARD18        | 021571                | 1,33 (b)  |
| Caspase recruitment domain family memer 6                                      | CARD6         | 032587                | 2,08 (a)  |
| Caspase 1 apoptosis related cysteine peptidase (interleukin 1 beta convertase) | CASP1         | 033292                | -1,25 (b)   |
| Caspase 1 apoptosis related cysteine peptidase                                 | CASP5         | 004347                | -1,36 (b)   |
| Caspase 1 apoptosis related cysteine peptidase                                 | CASP8         | 001228                | -1,33 (b)   |
| Chemokyna (c-c motive) ligand 2  | CCL2          | 002982                | -1,05(b)  |
| Chemokyna (c-c motive) ligand 7  | CCL7          | 006273                | 2,49 (a)  |
| Cd 40 ligand   | CD40LG        | 000074                | 2,72 (a)  |
| Casp8 and fad dlike apoptosis regulator  | CFLAR         | 003879                | -1,34 (b)   |
| Conserved helix loop helix ubiquitose kinase                                   | CKUK          | 001278                | -1,95 (b)   |
| Class ii maior histocompatibility complex trans activator                      | CIITA         | 000246                | -2,09 (a)   |
| Cathepsin b  | CTSB          | 001908                | 1,25 (b)  |
| Chemokine (cxc motif) ligand 1 (melanome growth stimolating activity alpha)    | CXCL1         | 001511                | 2,34 (a)  |
| Chemokine (cxc motif) ligand 2   | CXCL2         | 002089                | 1,31 (b)  |
| Fas (tnfrsf6) asociated via death domain                                       | FAD D         | 003824                | 1,02 (b)  |
| Heat shock protein 90 kda alpha (citosolyc) class a member 1                   | HSP90AA1      | 001017963             | -1,94 (b)   |
| Interferon beta 1 fibrobalst   | IFNB1         | 002176                | -1,58 (b)   |
| Interferon gamma   | IFNG          | 000919                | -1,40 (b)   |
| Inibitor of kappa light polypeptide gene                                       | IKBKB         | 001556                | -1,48 (b)   |

|  |        |        |           |
|--|--------|--------|-----------|
| Enhancer in b-cell kinase beta   |        |        |           |
| Inhibitor of kappa light polypeptide gene enhancer in b-cell kinase gamma                                | IKBKG  | 003639 | -1,23 (b) |
| Interleukine 12a (natural killer cell stimulatory factor 1 cytotoxic lymphocyte maturation factor 1 p35) | IL12A  | 000882 | 2,52 (a)  |
| Interleukine 12b (natural killer cell stimulatory factor 2 cytotoxic lymphocyte maturation factor 2 p40) | IL 12B | 002187 | 1,33 (b)  |
| Interleukine 18 (interferon gamma inducing factor)   | IL18   | 001562 | -1,08 (b) |
| Interleukine 1 beta  | IL1B   | 000576 | 1,58 (b)  |
| Interleukine 33  | IL33   | 033439 | 1,33 (b)  |
| Interleukine 6 (interferon beta 2)   | IL 6   | 000600 | -2,98 (a) |
| Interferon regulatory factor 2   | IRF2   | 002199 | 1,14 (b)  |
| Mitogen activated protein kinase kinase kinase 7   | MAP3K7 | 003188 | 1,09 (b)  |
| Mitogen activated protein kinase 1   | MAPK1  | 002745 | -1,29 (b) |
| Mitogen activated protein kinase 11  | MAPK11 | 002751 | -1,11 (b) |
| Mitogen activated protein kinase 12  | MAPK12 | 002969 | -1,18 (b) |
| Mitogen activated protein kinase 13  | MAPK13 | 002754 | -1,07 (b) |
| Mitogen activated protein kinase 3   | MAPK3  | 002746 | -1,51 (b) |
| Mitogen activated protein kinase 8   | MAPK8  | 002750 | 1,05 (b)  |
| Mitogen activated protein kinase 9   | MAPK9  | 002752 | 1,65 (b)  |
| Myeloid differentiation primary response gene (88)   | MYD88  | 002468 | -1,02 (b) |
| Nuclear factor of kappa light polypeptides Gene enhancer in b-cells 1                                    | NFKB1  | 003998 | 1,36 (b)  |
| Nuclear factor of kappa light polypeptides Gene enhancer in b-cells inhibitor alpha                      | NFKBIA | 020529 | -1,04 (b) |
| Nuclear factor of kappa light polypeptides Gene enhancer in b-cells inhibitor beta                       | NFKBIB | 002503 | -1,30 (b) |
| Nrl family card domain   | NLRC4  | 021209 | 1,61 (b)  |

|   |         |           |           |
|---|---------|-----------|-----------|
| containing 4  |         |           |           |
| Nrl family card domain containing 5   | NLRC5   | 032206    | -1,70 (b) |
| Nrl family pyrin domain containing 1  | NLRP1   | 033004    | -1,53 (b) |
| Nrl family pyrin domain containing 12   | NLRP12  | 033297    | 1,53 (b)  |
| Nrl family pyrin domain containing 3  | NLRP3   | 183395    | 1,45 (b)  |
| Nrl family pyrin domain containing 4  | NLRP4   | 134444    | 1,33 (b)  |
| Nrl family pyrin domain containing 5  | NLRP5   | 153447    | 1,33 (b)  |
| Nrl family pyrin domain containing 6  | NLRP6   | 138329    | -1,48 (b) |
| Nrl family x 1  | NLRX1   | 024618    | -1,75 (b) |
| Nucleotide binding oligomerization Domain containing 1                                  | NOD1    | 006092    | -1,20 (b) |
| Nucleotide binding oligomerization Domain containing 2                                  | NOD2    | 022162    | -1,36 (b) |
| Purinergic receptor p2x ligand gated ion channel 7                                      | P2RX7   | 002562    | 1,65 (b)  |
| Pannexin 1  | PANX1   | 015368    | 1,09 (b)  |
| Phosphoprotein enriched in astrocytes 15  | PEA15   | 003768    | -1,16 (b) |
| Prolin serin threonine phosphatase Interacting protein 1                                | PSTPIP1 | 003978    | 1,52 (b)  |
| Prostaglandin endoperoxidase synthase 2 (prostaglandin g/h synthase and cyclooxygenase) | PTGS2   | 000963    | -1,08 (b) |
| Pyd and card domain containing  | PYCARD  | 013258    | 2,32 (a)  |
| Pyd (pyrin domain) conteing 1   | PYCD1   | 152901    | 1,33 (b)  |
| Receptor interacting serin threonine kinase 2   | RIPK2   | 003821    | 1,11 (b)  |
| Sgt1 suppressor of g2 allele of skp 1 (s. <i>Cerevisiae</i> )                           | SUGT1   | 006704    | 1,27 (b)  |
| Tgf beta activated kinase 1/map 3k7 binding protein 1                                   | TAB1    | 006116    | -1,15 (b) |
| Tgf beta activated kinase 1/map 3k7 binding protein 2                                   | TAB2    | 015093    | 1,33 (b)  |
| Tool interleukine 1 receptor (tir) domain containing adaptor protein)                   | TIRAP   | 001039661 | -1,39 (b) |
| Tumor necrosis factor   | TNF     | 000594    | 1,83 (b)  |

|  |         |        |           |
|--|---------|--------|-----------|
| Tumor necrosis factor (ligand) superfamily member 11 | TNFSF11 | 003701 | 1,19 (b)  |
| Tumor necrosis factor (ligand) superfamily member 14 | TNFSF14 | 003807 | 1,32 (b)  |
| Tumor necrosis factor (ligand) superfamily member 4  | TNFS4   | 003326 | -1,80 (b) |
| Tnf receptor associated factor 6                     | TRAF 6  | 004620 | -1,03 (b) |
| Tioredoxine intercatating protein                    | TXNPI   | 006472 | -1,03 (b) |



**Table 3S. Fold Change between Mc Donald's meal vs Mc Donald's meal with not pruned vineyard red wine in Inflammasome genes.**

| <b>Gene Description</b>  | <b>Symbol</b> | <b>Gene Bank (NM)</b> | <b>Fold Change between McD and McDRW<br/>(a) <math>p &lt; 0,05</math><br/>(b) <math>p &gt; 0,05</math></b> |
|--|---------------|-----------------------|--|
| Absent in melanoma 2   | AIM2          | 004833                | -1,14 (b)  |
| B-cell ccl/lymphoma 2  | BCL2          | 000633                | -1,14 (b)  |
| Bcl2 like 1  | BCL2L1        | 138578                | -1,56 (b)  |
| Baculoviral iap repeat containig 2   | BIRC2         | 001166                | -1,23 (b)  |
| Baculoviral iap repeat containig 3   | BIRC3         | 001165                | -2,74 (a)  |
| Caspase recruitment domain family memer 18                                     | CARD18        | 021571                | -1,02 (b)  |
| Caspase recruitment domain family memer 6                                      | CARD6         | 032587                | 1,80 (b)   |
| Caspase 1 apoptosis related cysteine peptidase (interleukin 1 beta convertase) | CASP1         | 033292                | -1,03 (b)  |
| Caspase 1 apoptosis related cysteine peptidase                                 | CASP5         | 004347                | -1,77 (b)  |
| Caspase 1 apoptosis related cysteine peptidase                                 | CASP8         | 001228                | 1,30 (b)   |
| Chemokyna (c-c motive) ligand 2  | CCL2          | 002982                | -2,98 (a)  |
| Chemokyna (c-c motive) ligand 7  | CCL7          | 006273                | 1,82 (b)   |
| Cd 40 ligand   | CD40LG        | 000074                | 1,64 (b)   |
| Casp8 and fad dlake apoptosis regulator  | CFLAR         | 003879                | 1,16 (b)   |
| Conserved helix loop helix ubiquitous kinase                                   | CKUK          | 001278                | -1,30 (b)  |
| Class ii maior histocompatibility complex trans activator                      | CIITA         | 000246                | -1,81 (b)  |
| Cathepsin b  | CTSB          | 001908                | 1,11 (b)   |
| Chemokine (cxc motif) ligand 1 (melanome growth stimolating activity alpha)    | CXCL1         | 001511                | 2,18 (a)   |
| Chemokine (cxc motif) ligand 2   | CXCL2         | 002089                | 1,23 (b)   |
| Fas (tnfrsf6) asociated via death domain                                       | FAD D         | 003824                | 1,15 (b)   |
| Heat shock protein 90 kda alpha (citosolyc) class a member 1                   | HSP90AA1      | 001017963             | -1,14 (b)  |
| Interferon beta 1 fibrobalst   | IFNB1         | 002176                | -1,46 (b)  |
| Interferon gamma   | IFNG          | 000919                | -1,36 (b)  |
| Inibitor of kappa light  | IKBKB         | 001556                | -1,12 (b)  |

|  |        |        |           |
|--|--------|--------|-----------|
| polypeptide gene<br>Enhancer in b-cell kinase<br>beta  |        |        |           |
| Inhibitor of kappa light<br>polypeptide gene<br>Enhancer in b-cell kinase<br>gamma                                   | IKBKG  | 003639 | -1,13 (b) |
| Interleukine 12a (natural<br>killer cell stimulatory<br>factor 1 cytotoxic<br>lymphocyte<br>maturation factor 1 p35) | IL12A  | 000882 | 2,14 (a)  |
| Interleukine 12b (natural<br>killer cell stimulatory<br>Factor 2 cytotoxic<br>lymphocyte<br>maturation factor 2 p40) | IL 12B | 002187 | -1,02 (b) |
| Interleukine 18 (interferon<br>gamma inducing factor)  | IL18   | 001562 | 1,00 (b)  |
| Interleukine 1 beta  | IL1B   | 000576 | 1,17 (b)  |
| Interleukine 33  | IL33   | 033439 | -1,02 (b) |
| Interleukine 6 (interferon<br>beta 2)  | IL 6   | 000600 | -1,02 (b) |
| Interferon regulatory<br>factor 2  | IRF2   | 002199 | -1,11 (b) |
| Mitogen activated protein<br>kinase kinase kinase 7  | MAP3K7 | 003188 | 1,27 (b)  |
| Mitogen activated protein<br>kinase 1  | MAPK1  | 002745 | 1,15 (b)  |
| Mitogen activated protein<br>kinase 11   | MAPK11 | 002751 | -1,02 (b) |
| Mitogen activated protein<br>kinase 12   | MAPK12 | 002969 | -1,91 (b) |
| Mitogen activated protein<br>kinase 13   | MAPK13 | 002754 | 1,33 (b)  |
| Mitogen activated protein<br>kinase 3  | MAPK3  | 002746 | -1,22 (b) |
| Mitogen activated protein<br>kinase 8  | MAPK8  | 002750 | 1,22 (b)  |
| Mitogen activated protein<br>kinase 9  | MAPK9  | 002752 | 1,19 (b)  |
| Myeloid differentiation<br>primary response gene<br>(88)   | MYD88  | 002468 | 1,13 (b)  |
| Nuclear factor of kappa<br>light polypeptides<br>Gene enhancer in b-cells 1  | NFKB1  | 003998 | 1,05 (b)  |
| Nuclear factor of kappa light<br>polypeptides<br>Gene enhancer in b-cells<br>inhibitor alpha                         | NFKBIA | 020529 | 1,30 (b)  |
| Nuclear factor of kappa<br>light polypeptides<br>Gene enhancer in b-cells<br>inhibitor beta                          | NFKBIB | 002503 | 1,18 (b)  |
| Nrl family card domain   | NLRC4  | 021209 | 2,12 (a)  |

|   |         |           |           |
|---|---------|-----------|-----------|
| containing 4  |         |           |           |
| Nrl family card domain containing 5   | NLRC5   | 032206    | 1,04 (b)  |
| Nrl family pyrin domain containing 1  | NLRP1   | 033004    | -1,16 (b) |
| Nrl family pyrin domain containing 12   | NLRP12  | 033297    | -1,37 (b) |
| Nrl family pyrin domain containing 3  | NLRP3   | 183395    | 1,32 (b)  |
| Nrl family pyrin domain containing 4  | NLRP4   | 134444    | -1,02 (b) |
| Nrl family pyrin domain containing 5  | NLRP5   | 153447    | -1,02 (b) |
| Nrl family pyrin domain containing 6  | NLRP6   | 138329    | 1,03 (b)  |
| Nrl family x 1  | NLRX1   | 024618    | -1,23 (b) |
| Nucleotide binding oligomerization Domain containing 1                                  | NOD1    | 006092    | 1,20 (b)  |
| Nucleotide binding oligomerization Domain containing 2                                  | NOD2    | 022162    | -1,43 (b) |
| Purinergic receptor p2x ligand gated ion channel 7                                      | P2RX7   | 002562    | 1,75 (b)  |
| Pannexin 1  | PANX1   | 015368    | 1,80 (b)  |
| Phosphoprotein enriched in astrocytes 15  | PEA15   | 003768    | -1,25 (b) |
| Prolin serin threonine phosphatase Interacting protein 1                                | PSTPIP1 | 003978    | 1,43 (b)  |
| Prostaglandin endoperoxidase synthase 2 (prostaglandin g/h synthase and cyclooxygenase) | PTGS2   | 000963    | 1,52 (b)  |
| Pyd and card domain containing  | PYCARD  | 013258    | 1,06 (b)  |
| Pyd (pyrin domain) conteing 1   | PYCD1   | 152901    | -1,02 (b) |
| Receptor interacting serin threonine kinase 2   | RIPK2   | 003821    | 1,45 (b)  |
| Sgt1 suppressor of g2 allele of skp 1 (s. <i>Cerevisiae</i> )                           | SUGT1   | 006704    | 1,28 (b)  |
| Tgf beta activated kinase 1/map 3k7 binding protein 1                                   | TAB1    | 006116    | 1,39 (b)  |
| Tgf beta activated kinase 1/map 3k7 binding protein 2                                   | TAB2    | 015093    | 1,48 (b)  |
| Tool interleukine 1 receptor (tir) domain containing adaptor protein)                   | TIRAP   | 001039661 | -1,43 (b) |
| Tumor necrosis factor   | TNF     | 000594    | 1,05 (b)  |
| Tumor necrosis factor   | TNFSF11 | 003701    | -1,45 (b) |

|  |         |        |           |
|--|---------|--------|-----------|
| (ligand) superfamily member 11                       |         |        |           |
| Tumor necrosis factor (ligand) superfamily member 14 | TNFSF14 | 003807 | 1,12 (b)  |
| Tumor necrosis factor (ligand) superfamily member 4  | TNFS4   | 003326 | -1,50 (b) |
| Tnf receptor associated factor 6                     | TRAF 6  | 004620 | 1,24 (b)  |
| Tioredoxine intercatating protein                    | TXNPI   | 006472 | 1,81 (b)  |

**Table 1S. Fold Change between Baseline vs Mc Donald's meal in Oxidative Stress genes**

| Gene Description   | Symbol | Gene Bank (NM) | Fold Change between Baseline and McD<br>(a) $p < 0,05$<br>(b) $p > 0,05$ |
|--|--------|----------------|--|
| Albumin  | ALB    | 000477         | -2,43 (a)  |
| Arachidonate 12 lipoxygenase                                   | ALO12  | 000697         | 1,51 (b)   |
| Aldheyde oxidase 1   | AOX1   | 001159         | -2,43 (a)  |
| Apolipoprotein - e   | APOE   | 000041         | -2,43 (a)  |
| Atx1 antioxidant protein 1 omolog (yeast)                      | ATOX1  | 004045         | -1,16 (b)  |
| BCL2_ADENOVIRUS e1b19kda ITERACRTING PROTEIN 3                 | BNIP3  | 004052         | 1,21 (b)   |
| Catalase   | CAT    | 001752         | 1,48 (b)   |
| Copper chaperone for superoxide dismutase                      | CCL5   | 002985         | -2,60 (a)  |
| Cytocrome b-245 beta polypeptide                               | CYBB   | 000397         | 1,04 (b)   |
| Cytoglobin   | CYGB   | 134268         | -1,21 (b)  |
| 24 dehydrocholesterol reductase                                | DHCR24 | 014762         | -1,59 (b)  |
| Dual oxidase 1   | DUOX1  | 175940         | 1,88 (b)   |
| Dual specificity phosphatase 1                                 | DUSP1  | 004417         | 1,42 (b)   |
| Epoxide hydrolase 2 citoplasmic                                | EPHX2  | 001979         | 1,53 (b)   |
| Eosinophyl peroxidase  | EPX    | 000502         | 1,79 (b)   |
| Forkhead box m1  | FOXM1  | 021953         | -1,22 (b)  |
| Ferritin heavy polypeptide 1                                   | FTH1   | 002032         | -1,75 (b)  |
| Glutammate cisteine ligase, catalytic subunit                  | GCL2   | 001498         | -1,30 (b)  |
| Glutammate cisteine ligase, modifier subunit                   | GCLM   | 002061         | -1,01 (b)  |
| Glutathione peroxidase 1                                       | GPX1   | 000581         | 1,09 (b)   |
| Glutathione peroxidase 1 (gastrointestinal)                    | GPX2   | 002083         | 1,23 (b)   |
| Glutathione peroxidase (plasma)                                | GPX3   | 002084         | 1,59 (b)   |
| Glutathione peroxidase (phospholipid hydroperoxidase)          | GPX4   | 002085         | 1,36 (b)   |
| Glutathione peroxidase 5 (epididymal androgen-related protein) | GPX5   | 001509         | -2,43 (a)  |
| Glutathione peroxidase (olfactory)                             | GPX 6  | 182701         | -2,43 (a)  |
| Glutathione peroxidase 7                                       | GPX7   | 015696         | -1,64 (b)  |
| Glutathione synthetase   | GSS    | 000178         | -1,27 (b)  |
| Glutathione s-transpherase pi 1                                | GSTP1  | 000852         | -1,35 (b)  |
| Glutathione traspherase zeta 1                                 | GSTZ1  | 001513         | -1,12 (b)  |
| General transcription factor ii i                              | GTF2I  | 001518         | 1,11 (b)   |
| Eme oxigenase (decycling) 1                                    | HMOX1  | 002133         | -1,26 (b)  |
| Heat shock 70 kda protein 1a                                   | HSPA1A | 005345         | 1,42 (b)   |
| Keratin  | KRT1   | 006121         | 1,15 (b)   |
| Lactoperoxidase  | LPO    | 006151         | -2,43 (a)  |
| Myoglobin  | MB     | 005368         | -2,43 (a)  |

|  |         |        |           |
|--|---------|--------|-----------|
| Mannose-binding electin (protein c) 2 soluble  | MBL2    | 000242 | -2,19 (a) |
| Microsomal glutathione s-transferase 3   | MGST3   | 004528 | -1,26 (b) |
| Mieloperoxidase  | MPO     | 000250 | -1,09 (b) |
| Mpv17 mytochondrial inner membrane protein   | MPV17   | 002437 | -1,15 (b) |
| Methionine sulfoxide reductase a   | MSRA    | 012331 | -1,42 (b) |
| Metallo thionein 3   | MT3     | 005954 | -2,43 (a) |
| Neutrophyl cytosolic factor 1  | NCF1    | 000265 | 1,31 (b)  |
| Neutrophyl cytosolic factor 2  | NCF2    | 000433 | -1,26 (b) |
| Nitric oxide synthase 2 inducible  | NOS2    | 000625 | 1,21 (b)  |
| Nadph oxidase 4  | NOX4    | 016931 | -2,36 (a) |
| Nadph oxidase ef-hand calcium binding domani 5                                       | NOX5    | 024505 | -2,43 (a) |
| Nadph dehydrogenase quinone 1  | NQO1    | 000903 | -1,29 (b) |
| Nudix (nucleoside dyphosphosphate linked moiety x)type motif 1                       | NUDT1   | 002452 | 1,42 (b)  |
| Oxidation resistance 1   | OXR1    | 181354 | 1,20 (b)  |
| Oxidative stress responsive 1  | OXSRI   | 005109 | -1,70 (b) |
| Pdz end lim domain 1   | PDLIM1  | 020992 | -1,35 (b) |
| Polynuclotide kinase 3' phosphatase  | PNKB    | 007254 | 1,20 (b)  |
| Peroxiredoxin 1  | PRDX1   | 002574 | -1,26 (b) |
| Peroxiredoxin 2  | PRDX2   | 005809 | -1,20 (b) |
| Peroxiredoxin 3  | PRDX3   | 006793 | 1,09 (b)  |
| Peroxiredoxin 4  | PRDX4   | 006406 | -1,78 (b) |
| Peroxiredoxin 5  | PRDX5   | 181652 | -1,63 (b) |
| Peroxiredoxin 6  | PRDX6   | 004905 | -1,09 (b) |
| Phosphatidylinositol 3,4,5 triphosphate dependent rac exchange factor 1              | PREX1   | 020820 | 1,04 (b)  |
| Prion protein  | PRNP    | 183079 | 1,22 (b)  |
| Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase | PTGS1   | 000962 | 1,10 (b)  |
| Prostaglandin-endoperoxide synthase 2 (prostaglandin g/h synthase and cyclooxygenase | PTGS2   | 000963 | 1,33 (b)  |
| Peroxidasin omolog (drosophyla)  | PXDN    | 012293 | 1,03 (b)  |
| Ring finger protein 7  | RNF7    | 014245 | 1,28 (b)  |
| Scavenger receptro class a member 3  | SCARA 3 | 182826 | -2,43 (a) |
| Seleno protein s   | SELS    | 203472 | -1,09 (b) |
| Seleno protein p, plasma,1   | SEPP1   | 005410 | 1,01 (b)  |
| Sulfactant protein d   | SFTPD   | 003019 | -1,83 (b) |
| Sirtuin 2  | SIRT 2  | 012237 | -1,07 (b) |
| Superoxide dismustase 1 soluble  | SOD 1   | 000454 | -2,22 (a) |
| Superoxide dismustase 2  | SOD 2   | 000636 | -1,03 (b) |

|  |        |        |           |
|--|--------|--------|-----------|
| mitochondrial  |        |        |           |
| Superoxide dismutase 3<br>extracellular                | SOD 3  | 003102 | -2,43 (a) |
| Sequestosome 1   | SQSTM1 | 003900 | 1,07 (b)  |
| Sulfiredoxine 1  | SRXN1  | 080725 | 1,56 (b)  |
| Serina/treonina kinase 25                              | STK25  | 006374 | 1,44 (b)  |
| Thyroid peroxidase                                     | TPO    | 000547 | -2,00 (a) |
| Titin  | TTN    | 003319 | 1,05 (b)  |
| Thioredoxine   | TXN    | 003329 | -2,43 (a) |
| Thioredoxine reductase 1                               | TXNRD1 | 003330 | -1,02 (b) |
| Thioredoxine reductase 2                               | TXNRD2 | 006440 | -1,01(b)  |
| Uncoupling protein 2<br>(mitochondrial proton carrier) | UCP2   | 003355 | -2,22 (a) |

**Table 2S. Fold Change between Baseline vs Mc Donald's meal with not pruned vineyard Red Wine, in Oxidative Stress genes.**

| Gene Description   | Symbol | Gene Bank (NM) | Fold Change between Baseline and McDRW<br>(a) $p < 0,05$<br>(b) $p > 0,05$ |
|--|--------|----------------|--|
| Albumin  | ALB    | 000477         | -1,40 (b)  |
| Arachidonate 12 lipoxygenase                                   | ALO12  | 000697         | 1,04 (b)   |
| Aldheyde oxidase 1   | AOX1   | 001159         | -1,40 (b)  |
| Apolipoprotein - e   | APOE   | 000041         | -1,40 (b)  |
| Atx1 antioxidant protein 1 omolog (yeast)                      | ATOX1  | 004045         | 1,14 (b)   |
| BCL2_ADENOVIRUS e1b19kda ITERACRTING PROTEIN 3                 | BNIP3  | 004052         | 1,07(b)  |
| Catalase   | CAT    | 001752         | 1,05(b)  |
| Copper chaperone for superoxide dismutase                      | CCL5   | 002985         | -1,25 (b)  |
| Cytocrome b-245 beta polypeptide                               | CYBB   | 000397         | -1,29 (b)  |
| Cytoglobin   | CYGB   | 134268         | -1,08 (b)  |
| 24 dehydrocholesterol reductase                                | DHCR24 | 014762         | -1,51 (b)  |
| Dual oxidase 1   | DUOX1  | 175940         | 1,17 (b)   |
| Dual specificity phosphatase 1                                 | DUSP1  | 004417         | 1,05 (b)   |
| Epoxide hydrolase 2 citoplasmic                                | EPHX2  | 001979         | 1,02 (b)   |
| Eosinophyl peroxidase  | EPX    | 000502         | 1,99 (b)   |
| Forkhead box m1  | FOXM1  | 021953         | -2,10  |
| Ferritin heavy polypeptide 1                                   | FTH1   | 002032         | 1,41 (b)   |
| Glutammate cisteine ligase, catalytic subunit                  | GCL2   | 001498         | -1,41 (b)  |
| Glutammate cisteine ligase, modifier subunit                   | GCLM   | 002061         | 1,25 (b)   |
| Glutathione peroxidase 1                                       | GPX1   | 000581         | 1,37 (b)   |
| Glutathione peroxidase 1 (gastrointestinal)                    | GPX2   | 002083         | 1,32 (b)   |
| Glutathione peroxidase (plasma)                                | GPX3   | 002084         | -1,15 (b)  |
| Glutathione peroxidase (phospholipid hydroperoxidase)          | GPX4   | 002085         | 1,32 (b)   |
| Glutathione peroxidase 5 (epididymal androgen-related protein) | GPX5   | 001509         | -1,40 (b)  |
| Glutathione peroxidase (olfactory)                             | GPX 6  | 182701         | -1,40 (b)  |
| Glutathione peroxidase 7                                       | GPX7   | 015696         | 1,04 (b)   |
| Glutathione synthetase   | GSS    | 000178         | 1,46 (b)   |
| Glutathione s-transpherase pi 1                                | GSTP1  | 000852         | 1,55 (b)   |
| Glutathione traspherase zeta 1                                 | GSTZ1  | 001513         | 1,33 (b)   |
| GENERAL TRANSCRIPTION FACTOR II i                              | GTF2I  | 001518         | 1,29 (b)   |
| Eme oxigenase (decycling) 1                                    | HMOX1  | 002133         | 1,04 (b)   |
| Heat shock 70 kda protein 1a                                   | HSPA1A | 005345         | 1,56 (b)   |



|   |         |        |           |
|---|---------|--------|-----------|
| Keratin   | KRT1    | 006121 | -1,01 (b) |
| Lactoperoxidase   | LPO     | 006151 | -1,40 (b) |
| Myoglobin   | MB      | 005368 | -1,40 (b) |
| Mannose-binding electin<br>(protein c) 2 soluble  | MBL2    | 000242 | -1,81 (b) |
| Microsomal glutathione s-<br>transferase 3  | MGST3   | 004528 | 1,27 (b)  |
| Mieloperoxidase   | MPO     | 000250 | 1,31 (b)  |
| Mpv17 mitochondrial inner<br>membrane protein   | MPV17   | 002437 | 1,22 (b)  |
| Methionine sulfoxide reductase<br>a   | MSRA    | 012331 | 1,34 (b)  |
| Metallo thionein 3  | MT3     | 005954 | -1,40 (b) |
| Neutrophyl cytosolic factor 1   | NCF1    | 000265 | 1,24 (b)  |
| Neutrophyl cytosolic factor 2   | NCF2    | 000433 | 1,30 (b)  |
| Nitric oxide synthase 2<br>inducible  | NOS2    | 000625 | -1,25 (b) |
| Nadph oxidase 4   | NOX4    | 016931 | -1,40 (b) |
| Nadph oxidase ef-hand calcium<br>binding domani 5   | NOX5    | 024505 | -1,40 (b) |
| Nadph dehydrogenase quinone 1   | NQO1    | 000903 | -1,09 (b) |
| Nudix (nucleoside<br>dyphosphosphate linked moiety<br>x)type motif 1                          | NUDT1   | 002452 | 1,24 (b)  |
| Oxidation resistance 1  | OXR1    | 181354 | -1,55 (b) |
| Oxidative stress responsive 1   | OXSRI   | 005109 | 1,10 (b)  |
| Pdz end lim domain 1  | PDLIM1  | 020992 | 1,42 (b)  |
| Polynuclotide kinase 3'<br>phosphatase  | PNKB    | 007254 | 1,10 (b)  |
| Peroxiredoxin 1   | PRDX1   | 002574 | 1,02 (b)  |
| Peroxiredoxin 2   | PRDX2   | 005809 | 1,01 (b)  |
| Peroxiredoxin 3   | PRDX3   | 006793 | -1,01 (b) |
| Peroxiredoxin 4   | PRDX4   | 006406 | 1,00 (b)  |
| Peroxiredoxin 5   | PRDX5   | 181652 | 1,10 (b)  |
| Peroxiredoxin 6   | PRDX6   | 004905 | -1,03 (b) |
| Phosphatidylinositol 3,4,5<br>triphosphate dependent rac<br>exchange factor 1                 | PREX1   | 020820 | -1,17 (b) |
| Prion protein   | PRNP    | 183079 | 1,09 (b)  |
| Prostaglandin-endoperoxide<br>synthase 1 (prostaglandin g/h<br>synthase<br>and cyclooxygenase | PTGS1   | 000962 | 1,09 (b)  |
| Prostaglandin-endoperoxide<br>synthase 2 (prostaglandin g/h<br>synthase<br>and cyclooxygenase | PTGS2   | 000963 | 1,02 (b)  |
| Peroxidasin omolog<br>(drosophyla)  | PXDNI   | 012293 | -1,40 (b) |
| Ring finger protein 7   | RNF7    | 014245 | 1,42 (b)  |
| Scavenger receptro class a member<br>3  | SCARA 3 | 182826 | -1,40 (b) |
| Seleno protein s  | SELS    | 203472 | 1,10 (b)  |
| Seleno protein p, plasma, 1   | SEPP1   | 005410 | -1,58 (b) |
| Sulfactant protein d  | SFTPD   | 003019 | -1,59 (b) |

|   |        |        |           |
|---|--------|--------|-----------|
| Sirtuin 2   | SIRT 2 | 012237 | 1,29 (b)  |
| Superoxide dismutase 1 soluble                      | SOD 1  | 000454 | -1,31 (b) |
| Superoxide dismutase 2 mitochondrial                | SOD 2  | 000636 | 1,17 (b)  |
| Superoxide dismutase 3 extracellular                | SOD 3  | 003102 | -1,40 (b) |
| Sequestosome 1                                      | SQSTM1 | 003900 | 1,25 (b)  |
| Sulfiredoxine 1                                     | SRXN1  | 080725 | -1,01 (b) |
| Serina/treonina kinase 25                           | STK25  | 006374 | 1,26 (b)  |
| Thyroid peroxidase                                  | TPO    | 000547 | -1,27 (b) |
| Titin   | TTN    | 003319 | -1,20 (b) |
| Thioredoxine  | TXN    | 003329 | -2,23 (a) |
| Thioredoxine reductase 1                            | TXNRD1 | 003330 | 1,17 (b)  |
| Thioredoxine reductase 2                            | TXNRD2 | 006440 | -1,39 (b) |
| Uncoupling protein 2 (mitochondrial proton carrier) | UCP2   | 003355 | 1,28 (b)  |

**Table 3S. Fold Change between Mc Donald's meal vs Mc Donald's meal with not pruned vineyard red wine, in Oxidative Stress genes.**

| Gene Description   | Symbol | Gene Bank (NM) | Fold Change between McD and McDRW<br>(a) $p < 0,05$<br>(b) $p > 0,05$ |
|--|--------|----------------|---|
| Albumin  | ALB    | 000477         | 1,73 (b)  |
| Arachidonate 12 lipoxygenase                                   | ALO12  | 000697         | -1,45 (b)   |
| Aldheyde oxidase 1   | AOX1   | 001159         | 1,73 (b)  |
| Apolipoprotein - e   | APOE   | 000041         | 1,73 (b)  |
| Atx1 antioxidant protein 1 omolog (yeast)                      | ATOX1  | 004045         | 1,32 (b)  |
| BCL2_ADENOVIRUS e1b19kda ITERACRTING PROTEIN 3                 | BNIP3  | 004052         | -1,13 (b)   |
| Catalase   | CAT    | 001752         | -1,40 (b)   |
| Copper chaperone for superoxide dismutase                      | CCL5   | 002985         | 2,08 (a)  |
| Cytocrome b-245 beta polypeptide                               | CYBB   | 000397         | -1,34 (b)   |
| Cytoglobin   | CYGB   | 134268         | 1,13 (b)  |
| 24 dehydrocholesterol reductase                                | DHCR24 | 014762         | 1,05 (b)  |
| Dual oxidase 1   | DUOX1  | 175940         | -1,60 (b)   |
| Dual specificity phosphatase 1                                 | DUSP1  | 004417         | -1,35 (b)   |
| Epoxide hydrolase 2 citoplasmic                                | EPHX2  | 001979         | -1,49 (b)   |
| Eosinophyl peroxidase  | EPX    | 000502         | 1,11 (b)  |
| Forkhead box m1  | FOXO1  | 021953         | -1,72 (b)   |
| Ferritin heavy polypeptide 1                                   | FTH1   | 002032         | 2,46 (a)  |
| Glutammate cisteine ligase, catalytic subunit                  | GCL2   | 001498         | -1,09 (b)   |
| Glutammate cisteine ligase, modifier subunit                   | GCLM   | 002061         | 1,26 (b)  |
| Glutathione peroxidase 1                                       | GPX1   | 000581         | 1,26 (b)  |
| Glutathione peroxidase 1 (gastrointestinal)                    | GPX2   | 002083         | 1,07 (b)  |
| Glutathione peroxidase (plasma)                                | GPX3   | 002084         | -1,83 (b)   |
| Glutathione peroxidase (phospholipid hydroperoxidase)          | GPX4   | 002085         | -1,03 (b)   |
| Glutathione peroxidase 5 (epididymal androgen-related protein) | GPX5   | 001509         | 1,73 (b)  |
| Glutathione peroxidase (olfactory)                             | GPX 6  | 182701         | 1,73 (b)  |
| Glutathione peroxidase 7                                       | GPX7   | 015696         | 1,72 (b)  |
| Glutathione synthetase   | GSS    | 000178         | 1,85 (b)  |
| Glutathione s-transferase pi 1                                 | GSTP1  | 000852         | 2,08 (a)  |
| Glutathione transferase zeta 1                                 | GSTZ1  | 001513         | 1,48 (b)  |
| GENERAL TRANSCRIPTION FACTOR II i                              | GTF2I  | 001518         | 1,16 (b)  |
| HEME oxygenase (decycling) 1                                   | HMOX1  | 002133         | 1,30 (b)  |
| Heat shock 70 kda protein 1a                                   | HSPA1A | 005345         | 1,10 (b)  |
| Keratin  | KRT1   | 006121         | -1,16 (b)   |

|   |         |        |           |
|---|---------|--------|-----------|
| Lactoperoxidase   | LPO     | 006151 | 1,73 (b)  |
| Myoglobin   | MB      | 005368 | 1,73 (a)  |
| Mannose-binding electin<br>(protein c) 2 soluble  | MBL2    | 000242 | 1,21 (b)  |
| Microsomal glutathione s-<br>transferase 3  | MGST3   | 004528 | 1,59 (b)  |
| Mieloperoxidase   | MPO     | 000250 | 1,43 (b)  |
| Mpv17 mitochondrial inner<br>membrane protein   | MPV17   | 002437 | 1,40 (b)  |
| Methionine sulfoxide reductase<br>a   | MSRA    | 012331 | 1,91 (b)  |
| Metallo thionein 3  | MT3     | 005954 | 1,73 (b)  |
| Neutrophyl cytosolic factor 1   | NCF1    | 000265 | -1,06 (b) |
| Neutrophyl cytosolic factor 2   | NCF2    | 000433 | 1,64 (b)  |
| Nitric oxide synthase 2<br>inducible  | NOS2    | 000625 | -1,51 (b) |
| Nadph oxidase 4   | NOX4    | 016931 | 1,68 (b)  |
| Nadph oxidase ef-hand calcium<br>binding domani 5   | NOX5    | 024505 | 1,73 (b)  |
| Nadph dehydrogenase quinone 1   | NQO1    | 000903 | 1,19 (b)  |
| Nudix (nucleoside<br>dyphosphosphate linked moiety<br>x)type motif 1                          | NUDT1   | 002452 | -1,14 (b) |
| Oxidation resistance 1  | OXR1    | 181354 | -1,85 (b) |
| Oxidative stress responsive 1   | OXSRI   | 005109 | 1,88 (b)  |
| Pdz end lim domain 1  | PDLIM1  | 020992 | 1,91 (b)  |
| Polynuclotide kinase 3'<br>phosphatase  | PNKB    | 007254 | -1,09 (b) |
| Peroxiredoxin 1   | PRDX1   | 002574 | 1,28 (b)  |
| Peroxiredoxin 2   | PRDX2   | 005809 | 1,21 (b)  |
| Peroxiredoxin 3   | PRDX3   | 006793 | -1,10 (b) |
| Peroxiredoxin 4   | PRDX4   | 006406 | 1,78 (b)  |
| Peroxiredoxin 5   | PRDX5   | 181652 | 1,80 (b)  |
| Peroxiredoxin 6   | PRDX6   | 004905 | 1,05 (b)  |
| Phosphatidylinositol 3,4,5<br>triphosphate dependent rac<br>exchange factor 1                 | PREX1   | 020820 | -1,22 (b) |
| Prion protein   | PRNP    | 183079 | -1,12 (b) |
| Prostaglandin-endoperoxide<br>synthase 1 (prostaglandin g/h<br>synthase<br>and cyclooxygenase | PTGS1   | 000962 | -1,01 (b) |
| Prostaglandin-endoperoxide<br>synthase 2 (prostaglandin g/h<br>synthase<br>and cyclooxygenase | PTGS2   | 000963 | -1,30 (b) |
| Peroxidasin omolog<br>(drosophyla)  | PXDN    | 012293 | -1,44 (b) |
| Ring finger protein 7   | RNF7    | 014245 | 1,11 (b)  |
| Scavenger receptro class a<br>member 3  | SCARA 3 | 182826 | 1,73 (b)  |
| Seleno protein s  | SELS    | 203472 | 1,20 (b)  |
| Seleno protein p, plasma,1  | SEPP1   | 005410 | -1,59 (b) |
| Sulfactant protein d  | SFTPD   | 003019 | 1,15 (b)  |
| Sirtuin 2   | SIRT 2  | 012237 | 1,39 (b)  |

|   |        |        |           |
|---|--------|--------|-----------|
| Superoxide dismutase 1 soluble                      | SOD 1  | 000454 | 1,69 (b)  |
| Superoxide dismutase 2 mitochondrial                | SOD 2  | 000636 | 1,20 (b)  |
| Superoxide dismutase 3 extracellular                | SOD 3  | 003102 | 1,73 (b)  |
| Sequestosome 1                                      | SQSTM1 | 003900 | 1,17 (b)  |
| Sulfiredoxine 1                                     | SRXN1  | 080725 | -1,57 (b) |
| Serina/treonina kinase 25                           | STK25  | 006374 | -1,14 (b) |
| Thyroid peroxidase                                  | TPO    | 000547 | 1,57 (b)  |
| Titin   | TTN    | 003319 | -1,26 (b) |
| Thioredoxine  | TXN    | 003329 | 1,09 (b)  |
| Thioredoxine reductase 1                            | TXNRD1 | 003330 | 1,19 (b)  |
| Thioredoxine reductase 2                            | TXNRD2 | 006440 | -1,38 (b) |
| Uncoupling protein 2 (mitochondrial proton carrier) | UCP2   | 003355 | 2,83 (a)  |

**Table 1S. Fold Change between Baseline and Mc Donald's meal, in Human Drug Metabolism**

| <b>Gene Description</b>   | <b>Symbol</b> | <b>Gene Bank (NM)</b> | <b>Fold Change between Baseline and McD<br/>(a) <math>p &lt; 0,05</math><br/>(b) <math>p &gt; 0,05</math></b> |
|---|---------------|-----------------------|---|
| Atp binding cassette sub family c (cfr/mrp) member 1            | ABCC1         | 004996                | 1,54 (b)  |
| Amiloride binding protein 1 (amine oxidase (copper containing)) | ABP1          | 001091                | -1,30 (b)   |
| Alcohol dehydrogenase 1 c (classe 1) gamma polypeptide          | ADH1C         | 000669                | -1,61 (b)   |
| Alcohol dehydrogenase 4 classe 2 pi polypeptide                 | ADH4          | 000670                | 2,15 (a)  |
| Alcohol dehydrogenase 5 classe 3 ch i polypeptide               | ADH5          | 000671                | -1,44 (b)   |
| Alcohol dehydrogenase 6 (classe 5)                              | ADH6          | 000672                | 1,12 (b)  |
| Aryl hydrocarbon receptro                                       | AHR           | 001621                | -1,33 (b)   |
| Aminolevulinate dehydratase                                     | ALA D         | 000031                | -1,60 (b)   |
| Aldhyde dehydrogenase 1 family member a1                        | ALDH1A1       | 000689                | -2,28 (a)   |
| Arachidonate 15-lipoxygenase                                    | ALOX15        | 001140                | 2,02 (a)  |
| Arachidonate 5-lipoxygenase                                     | ALOX5         | 000698                | -2,02 (a)   |
| Apolipoprotein - e  | APOE          | 000041                | 2,23 (a)  |
| Aryl hydrocarbon receptor nuclear translocator                  | ARNT          | 001668                | -1,00 (b)   |
| Arsa arsenite transporter atp binding omolog 1 (bacterial)      | ANSA1         | 004317                | 1,25 (b)  |
| Biliverdin reductase a  | DLDR A        | 000712                | 1,10 (b)  |
| Biliverdin reductase b (flavinreductase nadph)                  | DLDR B        | 000713                | -1,32 (b)   |
| Carboxylesterase 2  | CES 2         | 198061                | -1,70 (b)   |
| Carboxylesterase 1 pseudogene 1                                 | CES1P1        | 003276                | 1,73 (b)  |
| Carbohydrate (keratan sulphate gal-6) sulphotransferase 1       | CHST1         | 003654                | -1,70 (b)   |
| Cytocrome p450 family 11 subfamily b polypeptide 2              | CYP11B2       | 000498                | -1,70 (b)   |
| Cytocrome p450 family 17 subfamily a polypeptide1               | CYP17A1       | 000102                | -1,70 (b)   |
| Cytocrome p450 family 19 subfamily a polypeptide 1              | CYP19A1       | 000103                | -1,70 (b)   |
| Cytocrome p450 family 1 subfamily a polypeptide 1               | CYP1A1        | 000499                | -1,70 (b)   |
| Cytocrome p450 family 2 subfamily b polypeptide 6               | CYP2B6        | 000767                | -1,70 (b)   |
| Cytocrome p450 family 2 subfamily c polypeptide 8               | CYP2C8        | 000770                | -1,70 (b)   |
| Cytocrome p450 family 2 subfamily c polypeptide 9               | CYP2C9        | 000771                | -1,70 (b)   |
| Cytocrome p450 family 2 subfamily d polypeptide 6               | CYP2D6        | 000106                | 1,30 (b)  |
| Cytocrome p450 family 2   | CYP2E1        | 000773                | 1,34 (b)  |

|  |          |         |           |
|--|----------|---------|-----------|
| subfamily e polypeptide 1  |          |         |           |
| Cytocrome p450 family 2<br>subfamily f polypeptide 1                 | CYP2F1   | 000774  | -1,70 (b) |
| Cytocrome p450 family 2<br>subfamily j polypeptide 2                 | CY2J2    | 000775  | 1,11 (b)  |
| Cytocrome b5 reductase 3   | CYB5R3   | 007326  | -1,65 (b) |
| Epoxide hydrolase 1<br>microsomal (xenobiotic)                       | EPHX1    | 000120  | -1,37 (b) |
| Fat acide hydrolase  | FAAH     | 001441  | 1,09 (b)  |
| Fructose 1,6 biphosphatase 1   | FBP1     | 000507  | -1,62 (b) |
| Glutamate decarboxylase 1<br>(brain 67 kda)                          | GAD1     | 000817  | -1,70 (b) |
| Glucokinase (exokinase)<br>regulator                                 | GCKR     | 001486  | 1,36 (b)  |
| Gamma glutamil tranferase 1  | GGT1     | 005265  | 1,14 (b)  |
| Glucose 6 phosphate isomerase  | GPI      | 000175  | -1,56 (b) |
| Glutathione peroxidase 1<br>(gastrointestinal)                       | GPX2     | 000581  | 1,42 (b)  |
| Glutathione peroxidase (plasma)                                      | GPX3     | 002083  | -1,48 (b) |
| Glutathione peroxidase 5<br>(epididymal androgen-related<br>protein) | GPX5     | 002085  | -1,70 (b) |
| Glutathione s-transferase alpha<br>4                                 | GSTA4    | 001512  | 1,51 (b)  |
| Glutathione s-transferase mu 3<br>(brain)                            | GSTM3    | 000849  | -1,64 (b) |
| Glutathione s-transferase mu 5                                       | GSTM5    | 000851  | -1,03 (b) |
| Glutathione s-transferase p 1  | GSTP1    | 000852  | -1,20 (b) |
| Glutathione s-transferase t 1  | GSTT1    | 000853  | 1,48 (b)  |
| Glutathione s-transferase z 1  | GSTZ1    | 001513  | 1,19 (b)  |
| Hydroxisteroid (17 beta)<br>dehydrogenase 2                          | HSD17 B2 | 002153  | -2,26 (a) |
| Hydroxisteroid (17 beta)<br>dehydrogenase 3                          | HSD17 B3 | 000197  | 1,58 (b)  |
| Lactoperoxidase  | LPO      | 006151  | 1,73 (b)  |
| Myristoidated alanine rich<br>protein kinase c substrate             | MARCKS   | 002356  | 1,49 (b)  |
| Microsomal glutathione s-<br>transferase 1                           | MGST1    | 0203000 | -1,03 (b) |
| Microsomal glutathione s-<br>transferase 2                           | MGST2    | 002413  | -1,39 (b) |
| Microsomal glutathione s-<br>transferase 3                           | MGST3    | 004528  | -1,08 (b) |
| Myeloperoxidase  | MPO      | 000250  | -1,86 (b) |
| Metallotioneine 2a   | MT2A     | 005953  | -2,28 (a) |
| Metallotioneine 3  | MT3      | 005954  | 1,53 (b)  |
| Methileneraydropholate<br>reductase (nadph)                          | MTHFR    | 005957  | 1,23 (b)  |
| N-acetiltransferase 1 (arilamina n-<br>acetiltrasnferase)            | NAT1     | 000662  | -1,61 (b) |
| N-acetiltransferase 2 (arilamina<br>n-acetiltrasnferase)             | NAT2     | 000015  | -1,62 (b) |
| Nitric oxide synthase 3<br>(endotelial cell)                         | NOS3     | 000603  | -1,93 (b) |
| Nadph dehydrogenase quinone 1  | NQO1     | 000903  | -1,07 (b) |

|  |           |        |           |
|--|-----------|--------|-----------|
| Piruvate kinase liver and rbc  | PKLR      | 000298 | -1,35 (b) |
| Piruvate kinase (muscle)   | PKM2      | 002654 | 1,04 (b)  |
| Paraoxonase 1  | PON1      | 000446 | -1,70 (b) |
| Paraoxonase 2  | PON2      | 000305 | 1,27 (b)  |
| Paraoxonase 3  | PON3      | 000940 | 1,65 (b)  |
| Swi-snf related matrix associated actin dependent regulator of cromatin subfamily a-like 1         | SMARCAL 1 | 014140 | 1,13 (b)  |
| Stannin  | SNN       | 003498 | 1,29 (b)  |
| Steroid 5 alpha reductase alpha polipeptide 1 (3-oxo-5-alpha-steroid delta 4-dehydrogenase alpha1) | SRD5A1    | 001047 | 1,02 (b)  |
| Steroid 5 alpha reductase alpha polipeptide 2 (3-oxo-5-alpha-steroid delta 4-dehydrogenase alpha2) | SRD5A2    | 000348 | -1,70 (b) |



**Table 2S. Fold Change between Baseline vs Mc Donald's meal with Not pruned vineyard red wine, in Oxidative Stress genes.**

| <b>Gene Description</b>   | <b>Symbol</b> | <b>Gene Bank (NM)</b> | <b>Fold Change between Baseline and McDRW<br/>(a) <math>p &lt; 0,05</math><br/>(b) <math>p &gt; 0,05</math></b> |
|---|---------------|-----------------------|---|
| Atp binding cassette sub family c (cftr/mrp) member 1           | ABCC1         | 004996                | 1,43 (b)  |
| Amiloride binding protein 1 (amine oxidase (copper containing)) | ABP1          | 001091                | -1,97 (b)   |
| Alcohol dehydrogenase 1 c (classe 1) gamma polypeptide          | ADH1C         | 000669                | -1,26 (b)   |
| Alcohol dehydrogenase 4 classe 2 pi polypeptide                 | ADH4          | 000670                | -1,16 (b)   |
| Alcohol dehydrogenase 5 classe 3 ch i polypeptide               | ADH5          | 000671                | -1,50 (b)   |
| Alcohol dehydrogenase 6 (classe 5)                              | ADH6          | 000672                | -1,41 (b)   |
| Aryl hydrocarbon receptro                                       | AHR           | 001621                | 2,03 (a)  |
| Aminolevulinate dehydratase                                     | ALA D         | 000031                | 1,08 (b)  |
| Aldhyde dehydrogenase 1 family member a1                        | ALDH1A1       | 000689                | 1,00 (b)  |
| Arachidonate 15-lipoxygenase                                    | ALOX15        | 001140                | 1,18 (b)  |
| Arachidonate 5-lipoxygenase                                     | ALOX5         | 000698                | 1,31 (b)  |
| Apolipoprotein - e  | APOE          | 000041                | -1,26 (b)   |
| Aril hydrocarbon receptor nuclear translocator                  | ARNT          | 001668                | -1,42 (b)   |
| Arsa arsenite transporter atp binding omolog 1 (bacterial)      | ANSA1         | 004317                | 1,41 (b)  |
| Biliverdin reductase a  | DLDR A        | 000712                | 1,49 (b)  |
| Biliverdin reductase b (flavinreductase nadph)                  | DLDR B        | 000713                | -1,03 (b)   |
| Carboxylesterase 2  | CES 2         | 198061                | -1,26 (b)   |
| Carboxilesterase 1 pseudogene 1                                 | CES1P1        | 003276                | -1,08 (b)   |
| Carbohydrate (keratan sulphate gal-6) sulphotransferase 1       | CHST1         | 003654                | -1,26 (b)   |
| Cytocrome p450 family 11 subfamily b polypeptide 2              | CYP11B2       | 000498                | -1,26 (b)   |
| Cytocrome p450 family 17 subfamily a polypeptide1               | CYP17A1       | 000102                | -1,26 (b)   |
| Cytocrome p450 family 19 subfamily a polypeptide 1              | CYP19A1       | 000103                | -1,26 (b)   |
| Cytocrome p450 family 1 subfamily a polypeptide 1               | CYP1A1        | 000499                | -1,26 (b)   |
| Cytocrome p450 family 2 subfamily b polypeptide 6               | CYP2B6        | 000767                | -1,26 (b)   |
| Cytocrome p450 family 2 subfamily c polypeptide 8               | CYP2C8        | 000770                | -1,26 (b)   |
| Cytocrome p450 family 2 subfamily c polypeptide 9               | CYP2C9        | 000771                | -1,26 (b)   |

|  |          |         |           |
|--|----------|---------|-----------|
| Cytocrome p450 family 2 subfamily d polypeptide 6              | CYP2D6   | 000106  | 1,07 (b)  |
| Cytocrome p450 family 2 subfamily e polypeptide 1              | CYP2E1   | 000773  | 1,12 (b)  |
| Cytocrome p450 family 2 subfamily f polypeptide 1              | CYP2F1   | 000774  | -1,26 (b) |
| Cytocrome p450 family 2 subfamily j polypeptide 2              | CY2J2    | 000775  | 1,95 (b)  |
| Cytocrome b5 reductase 3                                       | CYB5R3   | 007326  | 1,13 (b)  |
| Epoxide hydrolase 1 microsomal (xenobiotic)                    | EPHX1    | 000120  | -1,25 (b) |
| Fat acide hydrolase  | FAAH     | 001441  | -1,18 (b) |
| Fructose 1,6 bisphosphatase 1                                  | FBP1     | 000507  | 1,20 (b)  |
| Glutamate decarboxylase 1 (brain 67 kda)                       | GAD1     | 000817  | -1,26 (b) |
| Glucokinase (exokinase) regulator                              | GCKR     | 001486  | -1,26 (b) |
| Gamma glutamil tranferase 1                                    | GGT1     | 005265  | 1,04 (b)  |
| Glucose 6 phosphate isomerase                                  | GPI      | 000175  | -1,07 (b) |
| Glutathione peroxidase 1 (gastrointestinal)                    | GPX2     | 000581  | 1,12 (b)  |
| Glutathione peroxidase (plasma)                                | GPX3     | 002083  | 1,59 (b)  |
| Glutathione peroxidase 5 (epididymal androgen-related protein) | GPX5     | 002085  | -1,26 (b) |
| Glutathione s-transferase alpha 4                              | GSTA4    | 001512  | -1,15 (b) |
| Glutathione s-transferase mu 3 (brain)                         | GSTM3    | 000849  | 1,40 (b)  |
| Glutathione s-transferase mu 5                                 | GSTM5    | 000851  | -1,26 (b) |
| Glutathione s-transferase p 1                                  | GSTP1    | 000852  | 1,03 (b)  |
| Glutathione s-transferase t 1                                  | GSTT1    | 000853  | 1,77 (b)  |
| Glutathione s-transferase z 1                                  | GSTZ1    | 001513  | 1,25 (b)  |
| Hydroxisteroid (17 beta) dehydrogenase 2                       | HSD17 B2 | 002153  | -1,83 (b) |
| Hydroxisteroid (17 beta) dehydrogenase 3                       | HSD17 B3 | 000197  | -1,49 (b) |
| Lactoperoxidase  | LPO      | 006151  | -1,49 (b) |
| Myristoidated alanine rich protein kinase c substrate          | MARCKS   | 002356  | 1,66 (b)  |
| Microsomal glutathione s-tranferase 1                          | MGST1    | 0203000 | 1,42 (b)  |
| Microsomal glutathione s-tranferase 2                          | MGST2    | 002413  | 1,11 (b)  |
| Microsomal glutathione s-tranferase 3                          | MGST3    | 004528  | 1,02 (b)  |
| Myeloperoxidase  | MPO      | 000250  | -1,26 (b) |
| Metallotioneine 2a   | MT2A     | 005953  | 1,18 (b)  |
| Metallotioneine 3  | MT3      | 005954  | 2,06 (a)  |
| Methileneteraydropholate reductase (nadph)                     | MTHFR    | 005957  | 1,65 (b)  |
| N-acetiltransferase 1 (arilamina n-acetiltrasnferase)          | NAT1     | 000662  | 1,76 (b)  |
| N-acetiltransferase 2 (arilamina n-acetiltrasnferase)          | NAT2     | 000015  | -1,26 (b) |

|  |           |        |           |
|--|-----------|--------|-----------|
| Nitric oxide synthase 3<br>(endotelial cell)   | NOS3      | 000603 | 1,30 (b)  |
| Nadph dehydrogenase quinone 1  | NQO1      | 000903 | 1,14 (b)  |
| Piruvate kinase liver and rbc  | PKLR      | 000298 | -1,26 (b) |
| Piruvate kinase (muscle)   | PKM2      | 002654 | -1,61 (b) |
| Paraoxonase 1  | PON1      | 000446 | -1,26 (b) |
| Paraoxonase 2  | PON2      | 000305 | -1,45 (b) |
| Paraoxonase 3  | PON3      | 000940 | -1,26 (b) |
| Swi-snf related matrix<br>associated actin dependent<br>regulator of cromatin<br>subfamily a-like 1          | SMARCAL 1 | 014140 | 1,08 (b)  |
| Stannin  | SNN       | 003498 | 1,09 (b)  |
| Steroid 5 alpha reductase alpha<br>polipeptide 1<br>(3-oxo-5-alpha-steroid delta 4-<br>dehydrogenase alpha1) | SRD5A1    | 001047 | 1,22 (b)  |
| Steroid 5 alpha reductase alpha<br>polipeptide 2<br>(3-oxo-5-alpha-steroid delta 4-<br>dehydrogenase alpha2) | SRD5A2    | 000348 | -1,26 (b) |

**Table 3S. Fold Change between Mc Donald's meal vs Mc Donald's meal with not pruned vineyard red wine, in Human Drug Metabolism genes.**

| <b>Gene Description</b>   | <b>Symbol</b> | <b>Gene Bank (NM)</b> | <b>Fold Change between McD and McDRW<br/>(a) <math>p &lt; 0,05</math><br/>(b) <math>p &gt; 0,05</math></b> |
|---|---------------|-----------------------|--|
| Atp binding cassette sub family c (cftr/mrp) member 1           | ABCC1         | 004996                | -1,08 (b)  |
| Amiloride binding protein 1 (amine oxidase (copper containing)) | ABP1          | 001091                | -1,52 (b)  |
| Alcohol dehydrogenase 1 c (classe 1) gamma polypeptide          | ADH1C         | 000669                | 1,28 (b)   |
| Alcohol dehydrogenase 4 classe 2 pi polypeptide                 | ADH4          | 000670                | -2,48 (a)  |
| Alcohol dehydrogenase 5 classe 3 ch i polypeptide               | ADH5          | 000671                | -1,04 (b)  |
| Alcohol dehydrogenase 6 (classe 5)                              | ADH6          | 000672                | -1,58 (b)  |
| Aryl hydrocarbon receptro                                       | AHR           | 001621                | 2,71 (a)   |
| Aminolevulinate dehydratase                                     | ALA D         | 000031                | 1,73 (b)   |
| Aldhyde dehydrogenase 1 family member a1                        | ALDH1A1       | 000689                | 2,28 (a)   |
| Arachidonate 15-lipoxygenase                                    | ALOX15        | 001140                | -1,71 (b)  |
| Arachidonate 5-lipoxygenase                                     | ALOX5         | 000698                | 2,65   |
| Apolipoprotein - e  | APOE          | 000041                | -2,79  |
| Aryl hydrocarbon receptor nuclear translocator                  | ARNT          | 001668                | -1,42 (b)  |
| Arsa arsenite transporter atp binding omolog 1 (bacterial)      | ANSA1         | 004317                | 1,12 (b)   |
| Biliverdin reductase a  | DLDR A        | 000712                | 1,35 (b)   |
| Biliverdin reductase b (flavinreductase nadph)                  | DLDR B        | 000713                | 1,27 (b)   |
| Carboxylesterase 2  | CES 2         | 198061                | 1,35 (b)   |
| Carboxilesterase 1 pseudogene 1                                 | CES1P1        | 003276                | -1,87 (b)  |
| Carbohydrate (keratan sulphate gal-6) sulphotransferase 1       | CHST1         | 003654                | 1,35 (b)   |
| Cytocrome p450 family 11 subfamily b polypeptide 2              | CYP11B2       | 000498                | 1,35 (b)   |
| Cytocrome p450 family 17 subfamily a polypeptide1               | CYP17A1       | 000102                | 1,35 (b)   |
| Cytocrome p450 family 19 subfamily a polypeptide 1              | CYP19A1       | 000103                | 1,35 (b)   |
| Cytocrome p450 family 1 subfamily a polypeptide 1               | CYP1A1        | 000499                | 1,35 (b)   |
| Cytocrome p450 family 2 subfamily b polypeptide 6               | CYP2B6        | 000767                | 1,35 (b)   |
| Cytocrome p450 family 2 subfamily c polypeptide 8               | CYP2C8        | 000770                | 1,35 (b)   |
| Cytocrome p450 family 2 subfamily c polypeptide 9               | CYP2C9        | 000771                | 1,35 (b)   |
| Cytocrome p450 family 2 subfamily d polypeptide 6               | CYP2D6        | 000106                | -1,22 (b)  |

|  |          |         |           |
|--|----------|---------|-----------|
| Cytocrome p450 family 2 subfamily e polypeptide 1              | CYP2E1   | 000773  | -1,20 (b) |
| Cytocrome p450 family 2 subfamily f polypeptide 1              | CYP2F1   | 000774  | 1,35 (b)  |
| Cytocrome p450 family 2 subfamily j polypeptide 2              | CY2J2    | 000775  | 1,75 (b)  |
| Cytocrome b5 reductase 3                                       | CYB5R3   | 007326  | 1,88 (b)  |
| Epoxide hydrolase 1 microsomal (xenobiotic)                    | EPHX1    | 000120  | 1,10 (b)  |
| Fat acide hydrolase  | FAAH     | 001441  | -1,29 (b) |
| Fructose 1,6 biphosphatase 1                                   | FBP1     | 000507  | 1,94 (b)  |
| Glutamate decarboxylase 1 (brain 67 kda)                       | GAD1     | 000817  | 1,35 (b)  |
| Glucokinase (exokinase) regulator                              | GCKR     | 001486  | -1,71 (b) |
| Gamma glutamil tranferase 1                                    | GGT1     | 005265  | -1,10 (b) |
| Glucose 6 phosphate isomerase                                  | GPI      | 000175  | 1,46 (b)  |
| Glutathione peroxidase 1 (gastrointestinal)                    | GPX2     | 000581  | -1,27 (b) |
| Glutathione peroxidase (plasma)                                | GPX3     | 002083  | 2,36 (a)  |
| Glutathione peroxidase 5 (epididymal androgen-related protein) | GPX5     | 002085  | 1,35 (b)  |
| Glutathione s-transferase alpha 4                              | GSTA4    | 001512  | -1,73 (b) |
| Glutathione s-transferase mu 3 (brain)                         | GSTM3    | 000849  | 2,29 (a)  |
| Glutathione s-transferase mu 5                                 | GSTM5    | 000851  | -1,22 (b) |
| Glutathione s-transferase p 1                                  | GSTP1    | 000852  | 1,24 (b)  |
| Glutathione s-transferase t 1                                  | GSTT1    | 000853  | 1,20 (b)  |
| Glutathione s-transferase z 1                                  | GSTZ1    | 001513  | 1,05 (b)  |
| Hydroxisteroid (17 beta) dehydrogenase 2                       | HSD17 B2 | 002153  | 1,24 (b)  |
| Hydroxisteroid (17 beta) dehydrogenase 3                       | HSD17 B3 | 000197  | -2,37 (a) |
| Lactoperoxidase  | LPO      | 006151  | -2,59 (a) |
| Myristoidated alanine rich protein kinase c substrate          | MARCKS   | 002356  | 1,12 (b)  |
| Microsomal glutathione s-transferase 1                         | MGST1    | 0203000 | 1,45 (b)  |
| Microsomal glutathione s-transferase 2                         | MGST2    | 002413  | 1,55 (b)  |
| Microsomal glutathione s-transferase 3                         | MGST3    | 004528  | 1,11 (b)  |
| Myeloperoxidase  | MPO      | 000250  | 1,48 (b)  |
| Metallotioneine 2a   | MT2A     | 005953  | 2,69 (a)  |
| Metallotioneine 3  | MT3      | 005954  | 1,35 (b)  |
| Methileneteraydropholate reductase (nadph)                     | MTHFR    | 005957  | 1,35 (b)  |
| N-acetiltransferase 1 (arilamina n-acetiltrasnferase)          | NAT1     | 000662  | 2,82 (a)  |
| N-acetiltransferase 2 (arilamina n-acetiltrasnferase)          | NAT2     | 000015  | 1,29 (b)  |
| Nitric oxide synthase 3 (endotelial cell)                      | NOS3     | 000603  | 2,51 (a)  |

|  |           |        |           |
|--|-----------|--------|-----------|
| Nadph dehydrogenase quinone 1  | NQO1      | 000903 | 1,22 (b)  |
| Piruvate kinase liver and rbc  | PKLR      | 000298 | 1,08 (b)  |
| Piruvate kinase (muscle)   | PKM2      | 002654 | -1,67 (b) |
| Paraoxonase 1  | PON1      | 000446 | 1,35 (b)  |
| Paraoxonase 2  | PON2      | 000305 | -1,84 (b) |
| Paraoxonase 3  | PON3      | 000940 | -2,07 (a) |
| Swi-snf related matrix associated actin dependent regulator of cromatin subfamily a-like 1         | SMARCAL 1 | 014140 | -1,04 (b) |
| Stannin  | SNN       | 003498 | -1,18 (b) |
| Steroid 5 alpha reductase alpha polipeptide 1 (3-oxo-5-alpha-steroid delta 4-dehydrogenase alpha1) | SRD5A1    | 001047 | 1,20 (b)  |
| Steroid 5 alpha reductase alpha polipeptide 2 (3-oxo-5-alpha-steroid delta 4-dehydrogenase alpha2) | SRD5A2    | 000348 | 1,35 (b)  |