Supplementary Figures

Figure S1

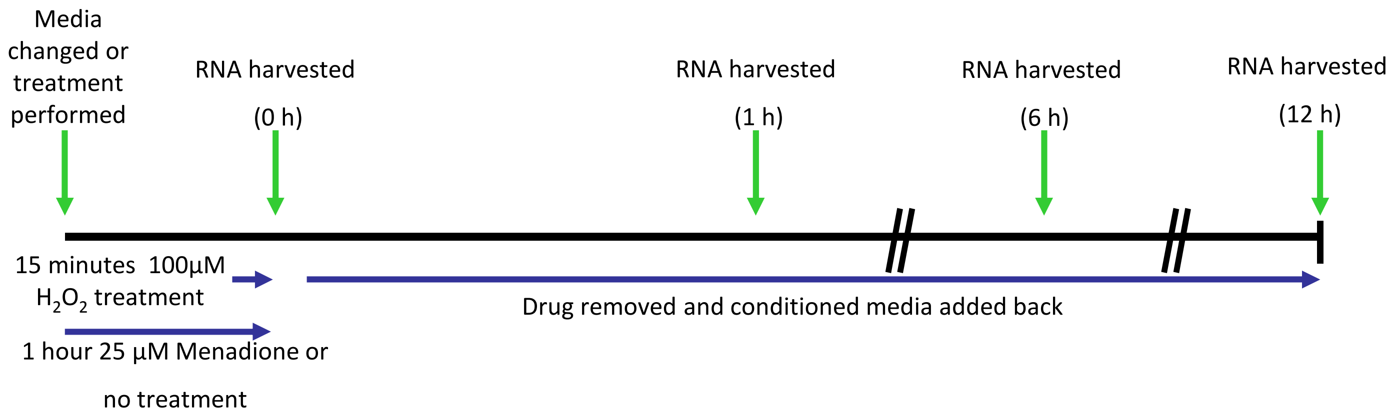
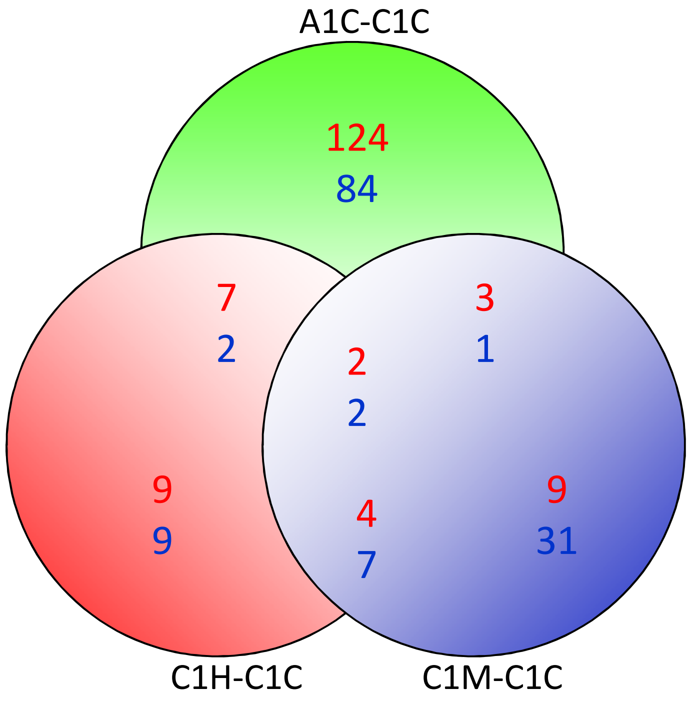

Media changed or treatment performed
RNA harvested (0 h)
RNA harvested (1 h)
RNA harvested (6 h)
RNA harvested (12 h)
15 minutes 100µM H_2O_2 treatment
1 hour 25 µM Menadione or no treatment
Drug removed and conditioned media added back

Figure S2

A


A1C-C1C
124
84
7
2
3
1
2
2
9
9
4
7
9
31
C1H-C1C
C1M-C1C

B

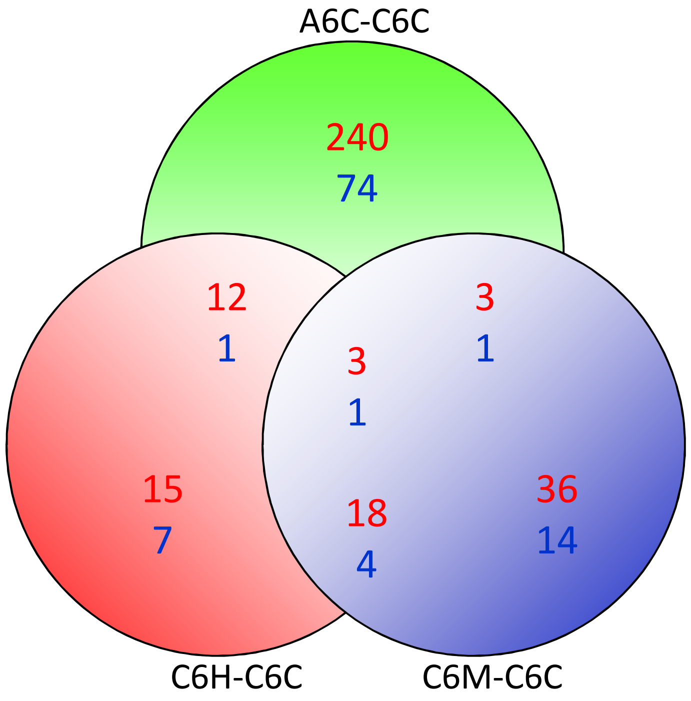

A6C-C6C
240
74
12
1
3
1
3
1
15
7
18
4
36
14
C6H-C6C
C6M-C6C

Figure S2

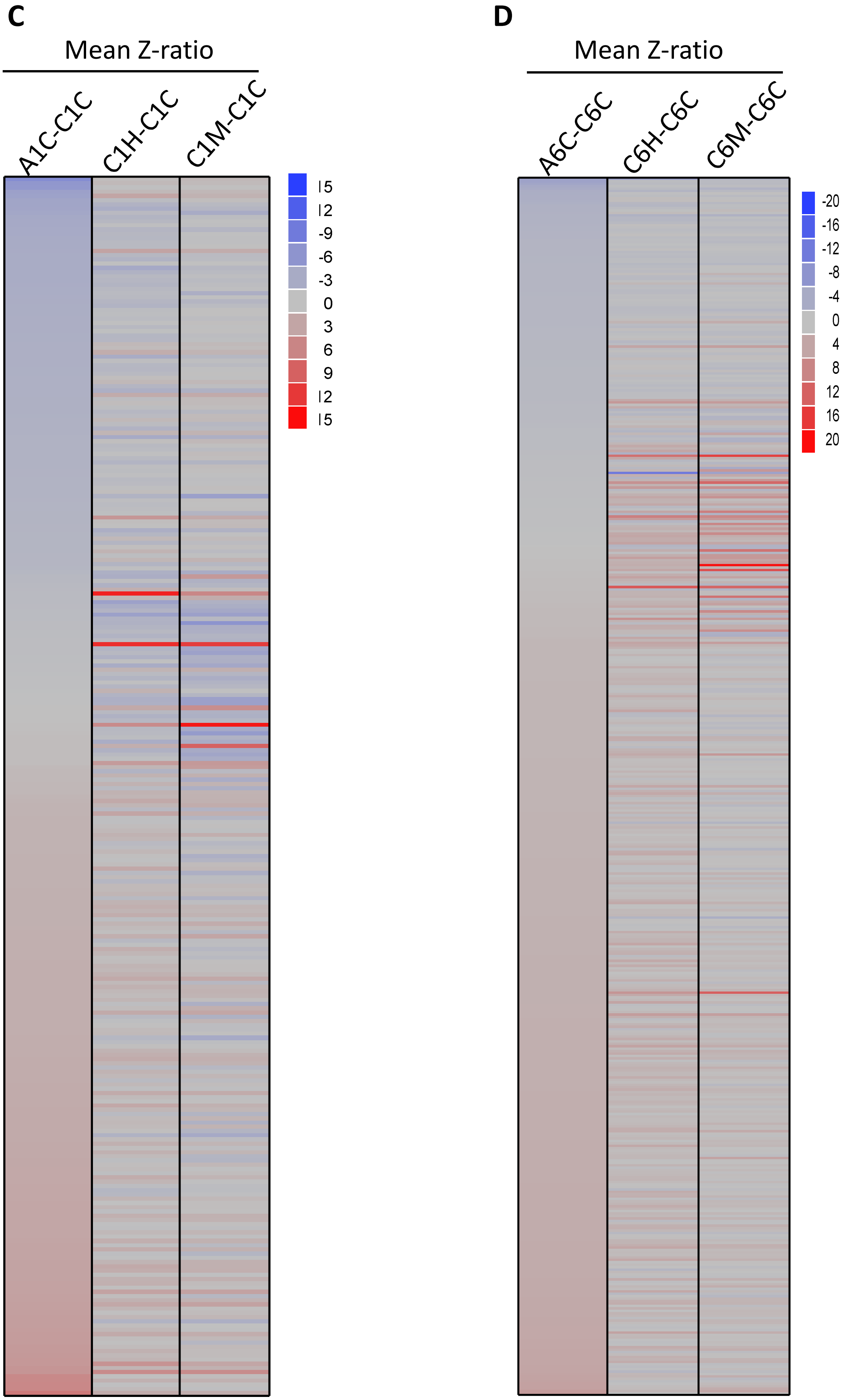

C
Mean Z-ratio
A1C-C1C
C1H-C1C
C1M-C1C
15
12
-9
-6
-3
0
3
6
9
12
15
D
Mean Z-ratio
A6C-C6C
C6H-C6C
C6M-C6C
-20
-16
-12
-8
-4
0
4
8
12
16
20

Figure S3

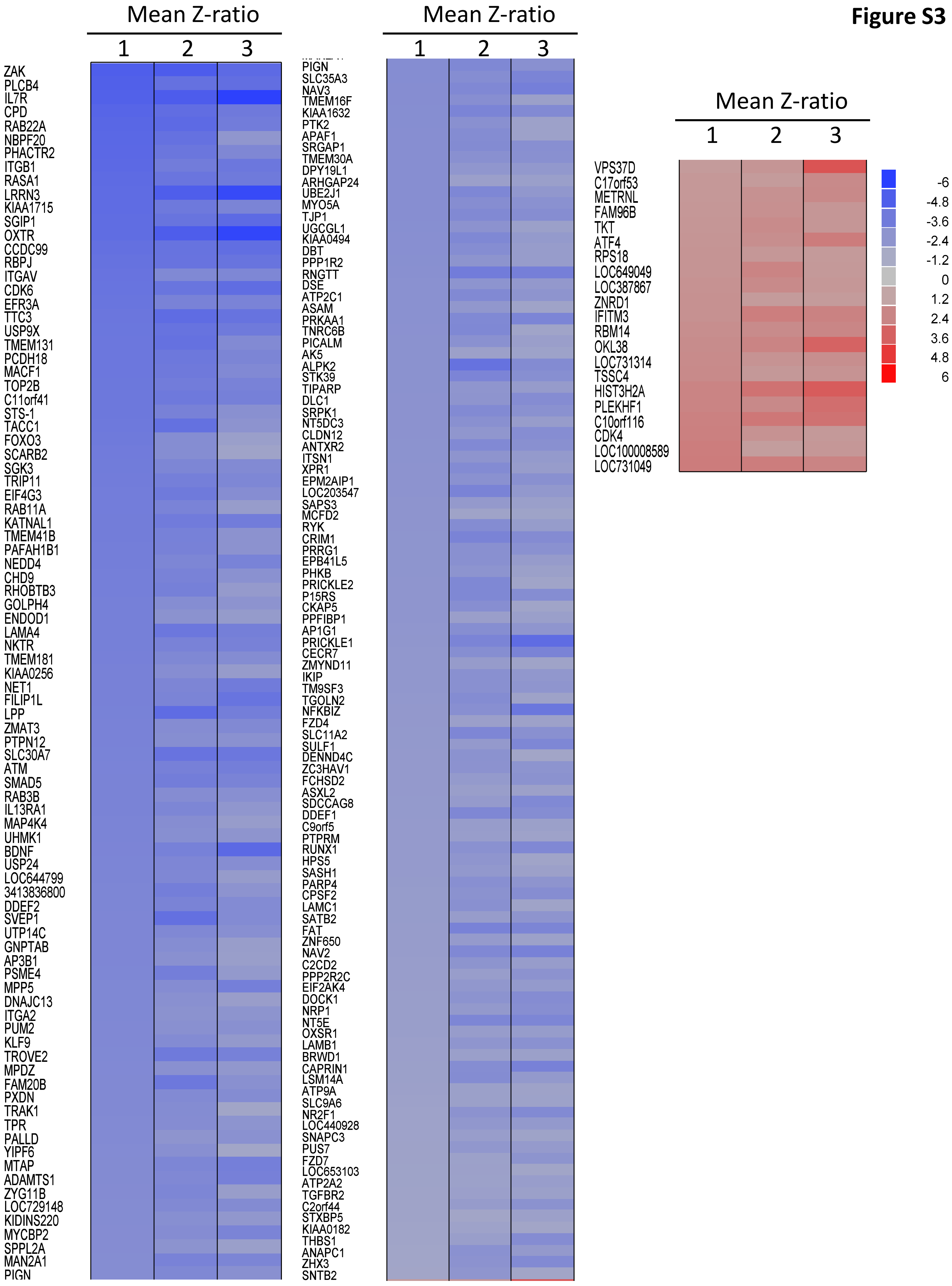

Mean Z-ratio
1
2
3
ZAK
PLCB4
IL7R
CPD
RAB22A
NBPF20
PHACTR2
ITGB1
RASA1
LRRN3
KIAA1715
SGIP1
OXTR
CCDC99
RBPJ
ITGAV
CDK6
EFR3A
TTC3
USP9X
TMEM131
PCDH18
MACF1
TOP2B
C11orf41
STS-1
TACC1
FOXO3
SCARB2
SGK3
TRIP11
EIF4G3
RAB11A
KATNAL1
TMEM41B
PAFAH1B1
NEDD4
CHD9
RHOBTB3
GOLPH4
ENDOD1
LAMA4
NKTR
TMEM181
KIAA0256
NET1
FILIP1L
LPP
ZMAT3
PTPN12
SLC30A7
ATM
SMAD5
RAB3B
IL13RA1
MAP4K4
UHMK1
BDNF
USP24
LOC644799
3413836800
DDEF2
SVEP1
UTP14C
GNPTAB
AP3B1
PSME4
MPP5
DNAJC13
ITGA2
PUM2
KLF9
TROVE2
MPDZ
FAM20B
PXDN
TRAK1
TPR
PALLD
YIPF6
MTAP
ADAMTS1
ZYG11B
LOC729148
KIDINS220
MYCBP2
SPPL2A
MAN2A1
PIGN
Mean Z-ratio
1
2
3
PIGN
SLC35A3
NAV3
TMEM16F
KIAA1632
PTK2
APAF1
SRGAP1
TMEM30A
DPY19L1
ARHGAP24
UBE2J1
MYO5A
TJP1
UGCGL1
KIAA0494
DBT
PPP1R2
RNGTT
DSE
ATP2C1
ASAM
PRKAA1
TNRC6B
PICALM
AK5
ALPK2
STK39
TIPARP
DLC1
SRPK1
NT5DC3
CLDN12
ANTXR2
ITSN1
XPR1
EPM2AIP1
LOC203547
SAPS3
MCFD2
RYK
CRIM1
PRRG1
EPB41L5
PHKB
PRICKLE2
P15RS
CKAP5
PPFIBP1
AP1G1
PRICKLE1
CECR7
ZMYND11
IKIP
TM9SF3
TGOLN2
NFKBIZ
FZD4
SLC11A2
SULF1
DENND4C
ZC3HAV1
FCHSD2
ASXL2
SDCCAG8
DDEF1
C9orf5
PTPRM
RUNX1
HPS5
SASH1
PARP4
CPSF2
LAMC1
SATB2
FAT
ZNF650
NAV2
C2CD2
PPP2R2C
EIF2AK4
DOCK1
NRP1
NT5E
OXSR1
LAMB1
BRWD1
CAPRIN1
LSM14A
ATP9A
SLC9A6
NR2F1
LOC440928
SNAPC3
PUS7
FZD7
LOC653103
ATP2A2
TGFBR2
C2orf44
STXBP5
KIAA0182
THBS1
ANAPC1
ZHX3
SNTB2
Mean Z-ratio
1
2
3
VPS37D
C17orf53
METRNL
FAM96B
TKT
ATF4
RPS18
LOC649049
LOC387867
ZNRD1
IFITM3
RBM14
OKL38
LOC731314
TSSC4
HIST3H2A
PLEKHF1
C10orf116
CDK4
LOC100008589
LOC731049
-6
-4.8
-3.6
-2.4
-1.2
0
1.2
2.4
3.6
4.8
6

Figure S4

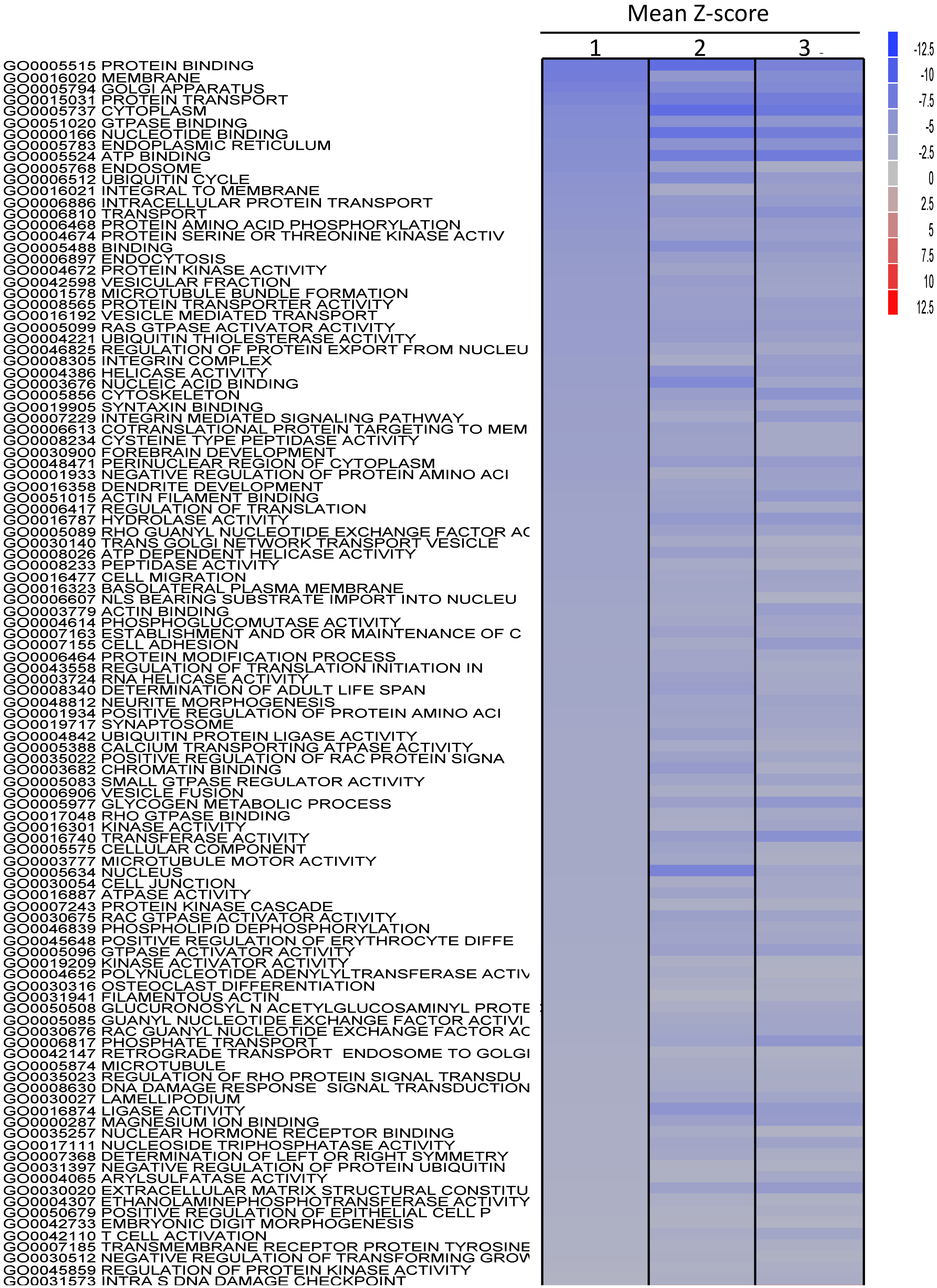

Mean Z-score
1
2
3
-12.5
-10
-7.5
-5
-2.5
0
2.5
5
7.5
10
12.5
GO0005515 PROTEIN BINDING
GO0016020 MEMBRANE
GO0005794 GOLGI APPARATUS
GO0015031 PROTEIN TRANSPORT
GO0005737 CYTOPLASM
GO0051020 GTPASE BINDING
GO0000166 NUCLEOTIDE BINDING
GO0005783 ENDOPLASMIC RETICULUM
GO0005524 ATP BINDING
GO0005768 ENDOSOME
GO0006512 UBIQUITIN CYCLE
GO0016021 INTEGRAL TO MEMBRANE
GO0006886 INTRACELLULAR PROTEIN TRANSPORT
GO0006810 TRANSPORT
GO0006468 PROTEIN AMINO ACID PHOSPHORYLATION
GO0004674 PROTEIN SERINE OR THREONINE KINASE ACTIV
GO0005488 BINDING
GO0006897 ENDOCYTOSIS
GO0004672 PROTEIN KINASE ACTIVITY
GO0042598 VESICULAR FRACTION
GO0001578 MICROTUBULE BUNDLE FORMATION
GO0008565 PROTEIN TRANSPORTER ACTIVITY
GO0016192 VESICLE MEDIATED TRANSPORT
GO0005099 RAS GTPASE ACTIVATOR ACTIVITY
GO0004221 UBIQUITIN THIOLESTERASE ACTIVITY
GO0046825 REGULATION OF PROTEIN EXPORT FROM NUCLEU
GO0008305 INTEGRIN COMPLEX
GO0004386 HELICASE ACTIVITY
GO0003676 NUCLEIC ACID BINDING
GO0005856 CYTOSKELETON
GO0019905 SYNTAXIN BINDING
GO0007229 INTEGRIN MEDIATED SIGNALING PATHWAY
GO0006613 COTRANSLATIONAL PROTEIN TARGETING TO MEM
GO0008234 CYSTEINE TYPE PEPTIDASE ACTIVITY
GO0030900 FOREBRAIN DEVELOPMENT
GO0048471 PERINUCLEAR REGION OF CYTOPLASM
GO0001933 NEGATIVE REGULATION OF PROTEIN AMINO ACI
GO0016358 DENDRITE DEVELOPMENT
GO0051015 ACTIN FILAMENT BINDING
GO0006417 REGULATION OF TRANSLATION
GO0016787 HYDROLASE ACTIVITY
GO0005089 RHO GUANYL NUCLEOTIDE EXCHANGE FACTOR AC
GO0030140 TRANS GOLGI NETWORK TRANSPORT VESICLE
GO0008026 ATP DEPENDENT HELICASE ACTIVITY
GO0008233 PEPTIDASE ACTIVITY
GO0016477 CELL MIGRATION
GO0016323 BASOLATERAL PLASMA MEMBRANE
GO0006607 NLS BEARING SUBSTRATE IMPORT INTO NUCLEU
GO0003779 ACTIN BINDING
GO0004614 PHOSPHOGLUCOMUTASE ACTIVITY
GO0007163 ESTABLISHMENT AND OR OR MAINTENANCE OF C
GO0007155 CELL ADHESION
GO0006464 PROTEIN MODIFICATION PROCESS
GO0043558 REGULATION OF TRANSLATION INITIATION IN
GO0003724 RNA HELICASE ACTIVITY
GO0008340 DETERMINATION OF ADULT LIFE SPAN
GO0048812 NEURITE MORPHOGENESIS
GO0001934 POSITIVE REGULATION OF PROTEIN AMINO ACI
GO0019717 SYNAPTOSOME
GO0004842 UBIQUITIN PROTEIN LIGASE ACTIVITY
GO0005388 CALCIUM TRANSPORTING ATPASE ACTIVITY
GO0035022 POSITIVE REGULATION OF RAC PROTEIN SIGNA
GO0003682 CHROMATIN BINDING
GO0005083 SMALL GTPASE REGULATOR ACTIVITY
GO0006906 VESICLE FUSION
GO0005977 GLYCOGEN METABOLIC PROCESS
GO0017048 RHO GTPASE BINDING
GO0016301 KINASE ACTIVITY
GO0016740 TRANSFERASE ACTIVITY
GO0005575 CELLULAR COMPONENT
GO0003777 MICROTUBULE MOTOR ACTIVITY
GO0005634 NUCLEUS
GO0030054 CELL JUNCTION
GO0016887 ATPASE ACTIVITY
GO0007243 PROTEIN KINASE CASCADE
GO0030675 RAC GTPASE ACTIVATOR ACTIVITY
GO0046839 PHOSPHOLIPID DEPHOSPHORYLATION
GO0045648 POSITIVE REGULATION OF ERYTHROCYTE DIFFE
GO0005096 GTPASE ACTIVATOR ACTIVITY
GO0019209 KINASE ACTIVATOR ACTIVITY
GO0004652 POLYNUCLEOTIDE ADENYLYLTRANSFERASE ACTIV
GO0030316 OSTEOCLAST DIFFERENTIATION
GO0031941 FILAMENTOUS ACTIN
GO0050508 GLUCURONOSYL N ACETYLGLUCOSAMINYL PROTE
GO0005085 GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVI
GO0030676 RAC GUANYL NUCLEOTIDE EXCHANGE FACTOR AC
GO0006817 PHOSPHATE TRANSPORT
GO0042147 RETROGRADE TRANSPORT ENDOSOME TO GOLGI
GO0005874 MICROTUBULE
GO0035023 REGULATION OF RHO PROTEIN SIGNAL TRANSDU
GO0008630 DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION
GO0030027 LAMELLIPODIUM
GO0016874 LIGASE ACTIVITY
GO0000287 MAGNESIUM ION BINDING
GO0035257 NUCLEAR HORMONE RECEPTOR BINDING
GO0017111 NUCLEOSIDE TRIPHOSPHATASE ACTIVITY
GO0007368 DETERMINATION OF LEFT OR RIGHT SYMMETRY
GO0031397 NEGATIVE REGULATION OF PROTEIN UBIQUITIN
GO0004065 ARYLSULFATASE ACTIVITY
GO0030020 EXTRACELLULAR MATRIX STRUCTURAL CONSTITU
GO0004307 ETHANOLAMINEPHOSPHOTRANSFERASE ACTIVITY
GO0050679 POSITIVE REGULATION OF EPITHELIAL CELL P
GO0042733 EMBRYONIC DIGIT MORPHOGENESIS
GO0042110 T CELL ACTIVATION
GO0007185 TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE
GO0030512 NEGATIVE REGULATION OF TRANSFORMING GROW
GO0045859 REGULATION OF PROTEIN KINASE ACTIVITY
GO0031573 INTRA S DNA DAMAGE CHECKPOINT

Figure S4

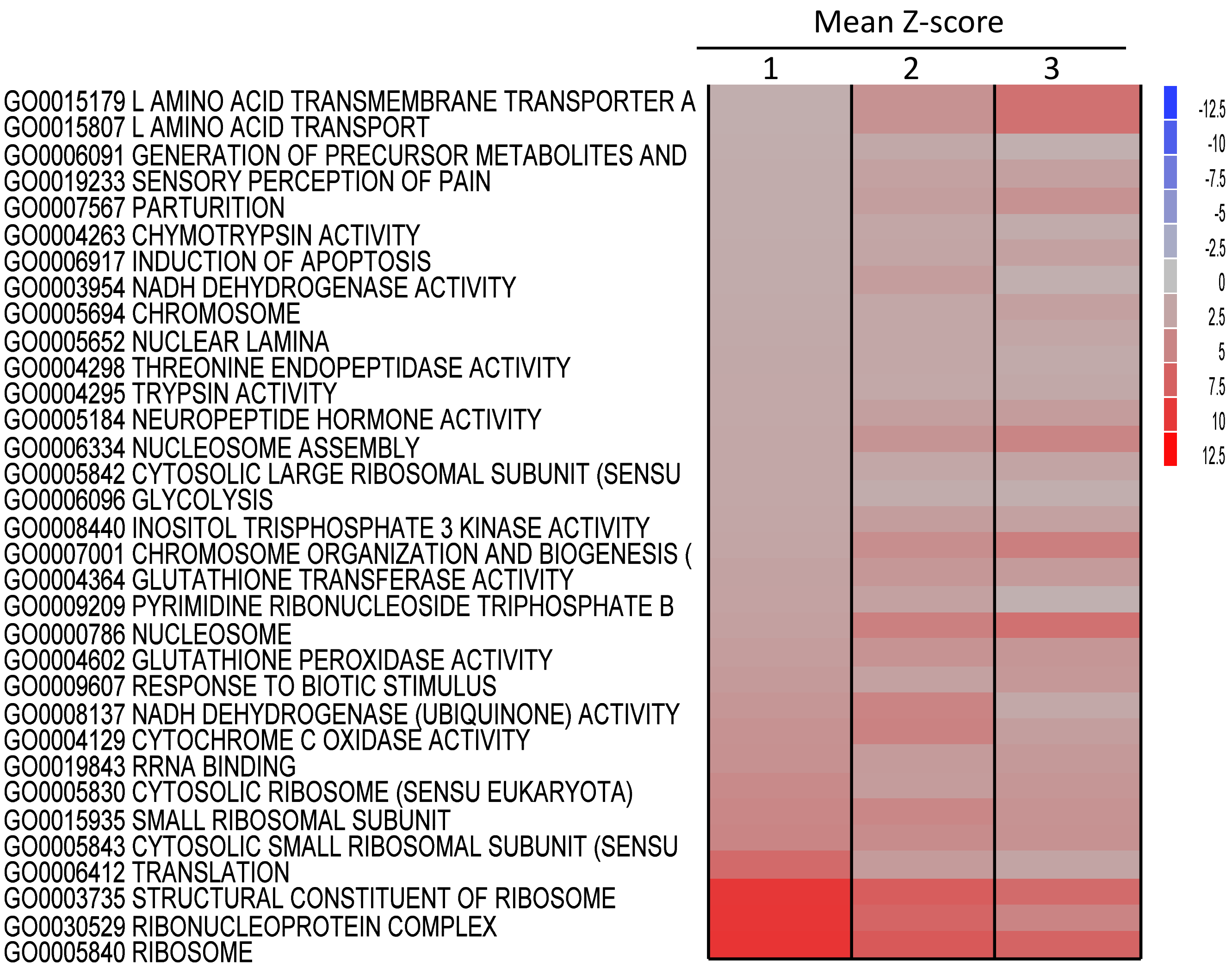

Mean Z-score
1
2
3
GO0015179 L AMINO ACID TRANSMEMBRANE TRANSPORTER A
GO0015807 L AMINO ACID TRANSPORT
GO0006091 GENERATION OF PRECURSOR METABOLITES AND
GO0019233 SENSORY PERCEPTION OF PAIN
GO0007567 PARTURITION
GO0004263 CHYMOTRYPSIN ACTIVITY
GO0006917 INDUCTION OF APOPTOSIS
GO0003954 NADH DEHYDROGENASE ACTIVITY
GO0005694 CHROMOSOME
GO0005652 NUCLEAR LAMINA
GO0004298 THREONINE ENDOPEPTIDASE ACTIVITY
GO0004295 TRYPSIN ACTIVITY
GO0005184 NEUROPEPTIDE HORMONE ACTIVITY
GO0006334 NUCLEOSOME ASSEMBLY
GO0005842 CYTOSOLIC LARGE RIBOSOMAL SUBUNIT (SENSU
GO0006096 GLYCOLYSIS
GO0008440 INOSITOL TRISPHOSPHATE 3 KINASE ACTIVITY
GO0007001 CHROMOSOME ORGANIZATION AND BIOGENESIS (
GO0004364 GLUTATHIONE TRANSFERASE ACTIVITY
GO0009209 PYRIMIDINE RIBONUCLEOSIDE TRIPHOSPHATE B
GO0000786 NUCLEOSOME
GO0004602 GLUTATHIONE PEROXIDASE ACTIVITY
GO0009607 RESPONSE TO BIOTIC STIMULUS
GO0008137 NADH DEHYDROGENASE (UBIQUINONE) ACTIVITY
GO0004129 CYTOCHROME C OXIDASE ACTIVITY
GO0019843 RRNA BINDING
GO0005830 CYTOSOLIC RIBOSOME (SENSU EUKARYOTA)
GO0015935 SMALL RIBOSOMAL SUBUNIT
GO0005843 CYTOSOLIC SMALL RIBOSOMAL SUBUNIT (SENSU
GO0006412 TRANSLATION
GO0003735 STRUCTURAL CONSTITUENT OF RIBOSOME
GO0030529 RIBONUCLEOPROTEIN COMPLEX
GO0005840 RIBOSOME
-12.5
-10
-7.5
-5
-2.5
0
2.5
5
7.5
10
12.5

Figure S5

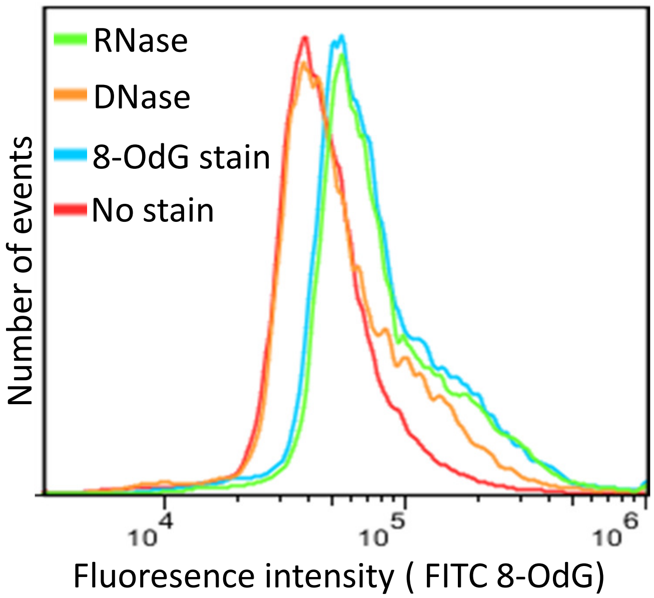

RNase
DNase
8-OdG stain
No stain
Number of events
10^4
10^5
10^6
Fluoresence intensity (FITC 8-OdG)

Table S1

Probe sets used for validation

TAQ probe	TAQ probe
APAF	Hs00559441_m1
DLC1	Hs00183436_m1
IL6	Hs00985639_m1
ATM	Hs01112307_m1
CHD9	Hs00322236_m1
PTPN12	Hs01026371_m1
TROVE2	Hs00184747_m1
EIFG3	Hs00184747_m1
18S	Hs99999999_s1