

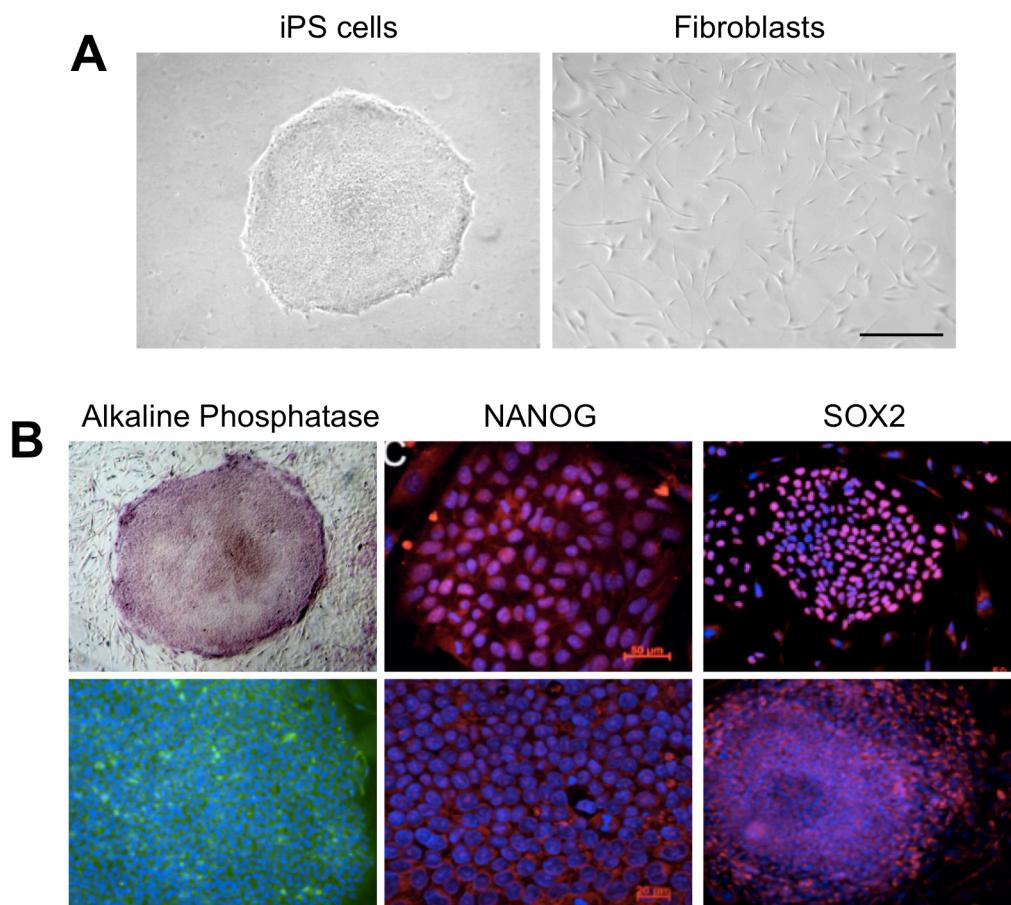
**Stem Cell Reports, Volume 4**

**Supplemental Information**

**High Glutathione and Glutathione Peroxidase-2  
Levels Mediate Cell-Type-Specific DNA Damage  
Protection in Human Induced Pluripotent Stem Cells**

**Benjamin Dannenmann, Simon Lehle, Dominic G. Hildebrand, Ayline Kübler, Paula Grondona, Vera Schmid, Katharina Holzer, Mirjam Fröschl, Frank Essmann, Oliver Rothfuss, and Klaus Schulze-Osthoff**

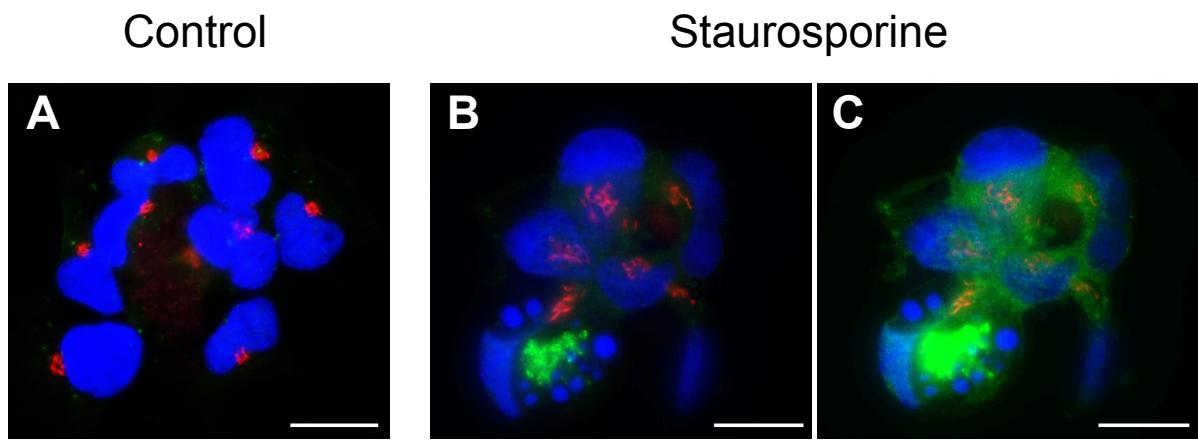
## Supplementary Figures



**Figure S1: Characterization of employed human iPS cells and fibroblasts.**

(A) Microscopical images of human dermal fibroblasts and iPS cells that were generated by retroviral transduction with *OCT4*, *SOX2*, *KLF4* and *c-MYC*. Scale bar = 200 µM.

(B) Alkaline phosphatase staining and expression of pluripotency markers NANOG, SOX2, TRA1-60, TRA1-81, and SSEA-4. Nuclei were visualized by blue DAPI staining. Exemplarily, L2 iPS cells (P25) and fibroblasts (P7) are shown.



**Figure S2: Human iPS cells do not maintain a constitutively active form of BAX at the Golgi.**

Human iPS (iPSC L1) cells were either left untreated (A) or stimulated with 100 nM staurosporine (B, C) for 2 h to undergo apoptosis. Immunohistochemistry reveals that active Bax (green staining) is hardly detectable in healthy untreated cells and not present at the Golgi (red staining). An apoptotic cell shown in (B) reveals typical BAX clustering and nuclear fragmentation (blue staining). A brighter illumination of the picture (C) shows in pre-apoptotic cells an even cytosolic distribution of BAX but no localization at the Golgi. Scale bar = 20  $\mu$ M. For indirect immunofluorescence cells were fixed in 4% formaldehyde and permeabilized in immunofluorescence buffer (PBS, 4% BSA, 0.05% saponin) for 1 h followed by over-night incubation at 4°C with conformation-specific anti-BAX-NT and the Golgi marker anti-GM130. Subsequently cells were washed and secondary antibodies were applied for 3 h at RT. Nuclei were stained for 5 min in PBS containing DAPI (10 ng/mL).

## Supplementary Tables

**Table S1: List of primary antibodies.**

Specificity	Origin	Provider	Cat #/Address
Actin	Mouse	Sigma	A2228
Anti-mouse Alexa Fluor 488	Chicken	Invitrogen	A-21200
Anti-mouse Alexa Fluor 568	Rabbit	Invitrogen	A-11061
Anti-mouse Alexa Fluor 647	Chicken	Invitrogen	A-21463
Anti-rabbit Alexa Fluor 594	Chicken	Invitrogen	A-21442
Anti-rat Alexa Fluor 488	Chicken	Invitrogen	A-21470
BAD	Mouse	BD Transduction Laboratories	610391
BAK	Rabbit	Millipore (Upstate)	06-536
BAX	Mouse	Trevigen	2281-MC
BAX-NT (active BAX)	Rabbit	Millipore (Upstate)	06-499
BCL-2	Mouse	Santa Cruz	sc-7382
Bcl-X	Rabbit	BD	610212
BID	Goat	R&D	AF860
BIM	Rabbit	Stressgen	ADI-AAP-330-E
GM130	Rabbit	Abcam	EP892Y
GPX2	Rabbit	Anna P. Kipp	DIFE, Postdam-Rehbrücke, Germany
GSTA2	Rabbit	John Hayes	University of Dundee, UK
MCL-1	Mouse	BD Pharmingen	559027
NANOG	Rabbit	Abcam	ab21624
p53	Mouse	Calbiochem	OP43
Sox2	Rabbit	Abcam	ab59776
SSEA-4	Rat	Chemicon	MAB4303
TRA1-60	Mouse	Chemicon	MAB4360
TRA1-81	Mouse	Chemicon	MAB4381

**Table S2: LORD-Q primers applied in DNA damage quantification experiments.**

Locus	Base pairs	Efficiency	Primer Denotation	Primer Sequence
mtDNA (L)	3724	1.643	CL5.F	5'-ATCGTAGCCTTCTCCACTTC-3'
			AS2.R	5'-TGGTTAGGCTGGTGTAGGG-3'
mtDNA (S)	50	1.989	AS2.F	5'-GGCCACAGCACTAACACACA-3'
			AS2.R	5'-TGGTTAGGCTGGTGTAGGG-3'
nDNA: GAPDH (L)	3653	1.660	GAPDH.F (1598)	5'-AGTCCCCAGAACAGGAGGT-3'
			GAPDH.R (5250)	5'-GGCTGAGCTCCACTAACCGAG-3'
nDNA: GAPDH (S)	45	1.995	GAPDH.F (4076)	5'-GCCTCACTCCTTTGCAGAC-3'
			GAPDH.R (4128)	5'-GTCTTCTGGGTGGCAGTGAT-3'
nDNA: TP53 (L)	3075	1.649	TP53.F	5'-CATACCAGCAAATGGGAAAC-3'
			TP53.R (3075)	5'-CGGGACGTGAAAGGTTAGAA-3'
nDNA: TP53 (S)	45	1.991	TP53.F	5'-CATACCAGCAAATGGGAAAC-3'
			TP53.R (45)	5'-CGTCCTTTGATGGCCTT-3'

**Table S3: Primers used in qRT-PCR experiments.**

ACTB.F	5'-CATGTACGTTGCTATCCAGGC-3'
ACTB.R	5'-CTCCTTAATGTCACGCACGAT-3'
ALAS1.F	5'-CGCCGCTGCCATTCTTAT-3'
ALAS1.R	5'-TCTGTTGGACCTTGGCCTTAG-3'
CAT.F	5'-TGTGCTGGAGAATCGGGTTC-3'
CAT.R	5'-TCCCAGTTACCATCTTCTGTGTA-3'
GAPDH.F	5'-GGAGCGAGATCCCTCCAAAAT-3'
GAPDH.R	5'-GGCTGTTGTCATACTTCTCATGG-3'
GCLC.F	5'-GGAGGAAACCAAGCGCCAT-3'
GCLC.R	5'-CTTGACGGCGTGGTAGATGT-3'
GCLM.F	5'-TGTCTTGGAAATGCACTGTATCTC-3'
GCLM.R	5'-CCCAGTAAGGCTGTAAATGCTC-3'
GDF3.F	5'-GCCATCAAAGAAAGGGAAC-3'
GDF3.R	5'-TCTGGCACAGGTGTCTTCAG-3'
GPX1.F	5'-CAGTCGGTGTATGCCTTCTCG-3'
GPX1.R	5'-GAGGGACGCCACATTCTCG-3'
GPX2.F	5'-GGTAGATTCAATACGTTCCGGG-3'
GPX2.R	5'-TGACAGTTCTCCTGATGTCCAAA-3'
GPX3.F	5'-AGAGCCGGGGACAAGAGAA-3'
GPX3.R	5'-ATTGCCAGCATACTGCTTGA-3'
GPX4.F	5'-GAGGCAAGACCGAAGTAAACTAC-3'
GPX4.R	5'-CCGAACCTGGTTACACGGGAA-3'
GPX7.F	5'-CCCACCACTTAACGTGCTC-3'
GPX7.R	5'-GGCAAAGCTCTCAATCTCCTT-3'
GSR.F	5'-TTCCAGAACATACCAACGTCAAAGG-3'
GSR.R	5'-GTTTCGGCCAGCAGCTATTG-3'
GSTA1.F	5'-CTGCCGTATGTCCACCTG-3'
GSTA1.R	5'-AGCTCCTCGACGTAGTAGAGA-3'
GSTA2.F	5'-TACTCCAATATACGGGGCAGAA-3'
GSTA2.R	5'-TCCTCAGGTTGACTAAAGGGC-3'
GSTA4.F	5'-CCGGATGGAGTCCGTGAGAT-3'
GSTA4.R	5'-GGGCACTTGTTGGAACAGGC-3'
GSTM1.F	5'-TCTGCCCTACTTGATTGATGGG-3'
GSTM1.R	5'-TCCACACGAATCTTCTCCTCT-3'
GSTM2.F	5'-TGTGCGGGGAATCAGAAAAGG-3'
GSTM2.R	5'-CTGGGTCATAGCAGAGTTGG-3'
GSTM3.F	5'-TCGTGCGAGTCGTCTATGGT-3'
GSTM3.R	5'-TCTCCTCATAGAGGTATCCGTG-3'
GSTM4.F	5'-AGAGGAGAAGATTCGTGTGGA-3'
GSTM4.R	5'-TGCTGCATCATTGTAGGAAGTT-3'
GSTM5.F	5'-CCATCCTGCGCTACATTGC-3'
GSTM5.R	5'-CCAGCTCCATGTGGTTATCCAT-3'
GSTO1.F	5'-GAACGGCTGGAAGCAATGAAG-3'
GSTO1.R	5'-TGCCATCCACAGTTTCAGTT-3'

<i>GSTO2.F</i>	5'-TGCCCCTATTCTCACAGGACC-3'
<i>GSTO2.R</i>	5'-TCCAGGTACTCACAAGCAATAAC-3'
<i>GSTT1.F</i>	5'-TGCGCGCTGTTACATCTT-3'
<i>GSTT1.R</i>	5'-GTGCTGACCTTAATCAGATCCA-3'
<i>GSTT2.F</i>	5'-TGGCATCCCCCTAGAGCTG-3'
<i>GSTT2.R</i>	5'-CTTGAGCGTCGGCAGTTTC-3'
<i>GSTZ1.F</i>	5'-GCCAGAACGCCATCACTT-3'
<i>GSTZ1.R</i>	5'-CTACACAGTATATGCCGCTG-3'
<i>MGST1.F</i>	5'-ATGACAGAGTAGAACGTGTACGC-3'
<i>MGST1.R</i>	5'-TACAGGAGGCCAATTCCAAGA-3'
<i>MGST2.F</i>	5'-TCGGCCTGTCAGCAAAGTTAT-3'
<i>MGST2.R</i>	5'-TGCCCAGAAATACTCTCTCAAAC-3'
<i>MGST3.F</i>	5'-GGCCCACCTAGCCATCAATG-3'
<i>MGST3.R</i>	5'-CGCTGAATGCAGTTGAAGATGT-3'
<i>NANOG.F</i>	5'-ACTCTCCAACATCCTGAACCTC-3'
<i>NANOG.R</i>	5'-GCCTTCTGCGTCACACCA-3'
<i>PRDX1.F</i>	5'-CATTCTTGGTATCAGACCCG-3'
<i>PRDX1.R</i>	5'-CCCTGAACGAGATGCCTTCAT-3'
<i>PRDX2.F</i>	5'-GAAGCTGTCGGACTACAAAGG-3'
<i>PRDX2.R</i>	5'-TCGGTGGGGCACACAAAAG-3'
<i>PRDX3.F</i>	5'-GAGACTACGGTGTGCTGTTAGA-3'
<i>PRDX3.R</i>	5'-GTTGACGCTCAAATGCTTGATG-3'
<i>PRDX4.F</i>	5'-AGAGGAGTGCCACTTCTACG-3'
<i>PRDX4.R</i>	5'-GGAAATCTCGCTTGCTTAGGT-3'
<i>PRDX6.F</i>	5'-GTTGCCACCCCAGTTGATTG-3'
<i>PRDX6.R</i>	5'-TGAAGACTCCTTCGGGAAAAGT-3'
<i>SOD1.F</i>	5'-GGTGGGCCAAAGGATGAAGAG-3'
<i>SOD1.R</i>	5'-CCACAAGCCAAACGACTTCC-3'
<i>SOD2.F</i>	5'-GCTCCGGTTTGGGTATCTG-3'
<i>SOD2.R</i>	5'-GCGTTGATGTGAGGTTCCAG-3'
<i>SOD3.F</i>	5'-ATGCTGGCGCTACTGTGTT-3'
<i>SOD3.R</i>	5'-CTCCGCCAGTCAGAGTTG-3'
<i>TMX1.F</i>	5'-AGTATGTCAGCACTTTCAGC-3'
<i>TMX1.R</i>	5'-CACACTGGCAATCCAAGGTCT-3'
<i>TXN.F</i>	5'-GTGAAGCAGATCGAGAGCAAG-3'
<i>TXN.R</i>	5'-CGTGGCTGAGAAGTCAACTACTA-3'
<i>TXNIP.F</i>	5'-GGTCTTAACGACCCTGAAAAGG-3'
<i>TXNIP.R</i>	5'-ACACGAGTAACTCACACACCT-3'