

Figure S1. Analysis of cell growth and cell cycle dynamics of mESCs deficient for PKC δ . **A)** The growth of the $Pkc\delta^{-/-}$ and $Pkc\delta^{+/+}$ mESC lines was analyzed along two consecutive cell passages. To obtain the growth rate, the natural logarithm of the expansion factor (cell population divided by the number of cells initially plated) was in turn divided by the number of days. **B) Left panel:** Murine $Pkc\delta^{-/-}$ and $Pkc\delta^{+/+}$ mESCs were dissociated and stained with 25 $\mu\text{g/ml}$ propidium iodide (Sigma Cat#P4864) with 25 $\mu\text{g/ml}$ RNase (Roche Cat#10109142001) and their cell cycle distribution was analyzed using a BD FACSVerse flow cytometer. **Right panel:** Murine $Pkc\delta^{-/-}$ and $Pkc\delta^{+/+}$ ESCs received 10 μM EdU pulse for 1h before being dissociated and processed for EdU detection with the Click-iTTM Plus EdU Alexa FluorTM 555 Flow Cytometry Assay Kit (ThermoFisher Cat#C10638). The samples were analyzed in a LSR-Fortessa flow cytometer to obtain the percentage of EdU⁺ cells.

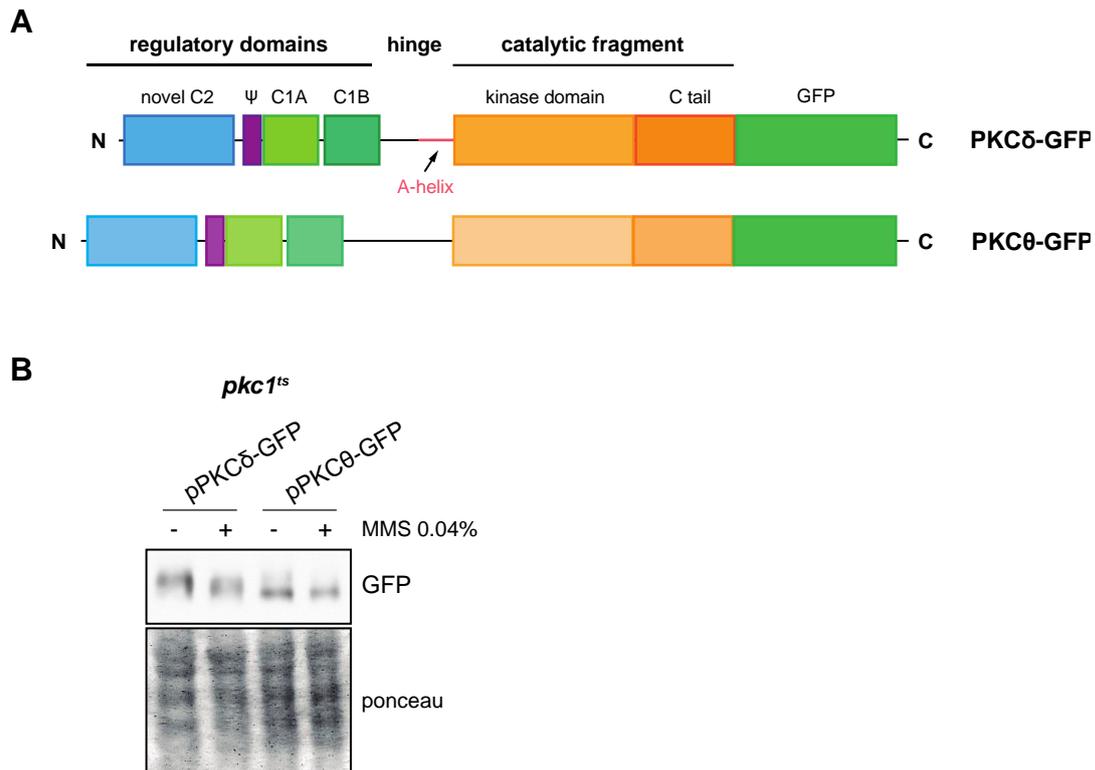


Figure S2. Protein level analysis of PKCδ and PKCθ. **A)** Schematic representation of GFP-tagged PKCδ and PKCθ proteins. **B)** Exponentially growing cultures of the *pkc1^{ts}* (JC6-3a) strain transformed with plasmids pPKCδ-GFP and pPKCθ-GFP were transferred to 37°C for 3 hours and then incubated in the absence or presence of MMS 0.04% for 1 hour. Protein levels of GFP-tagged PKCδ and PKCθ were detected by western blot. Ponceau staining of the membrane is shown as loading control.

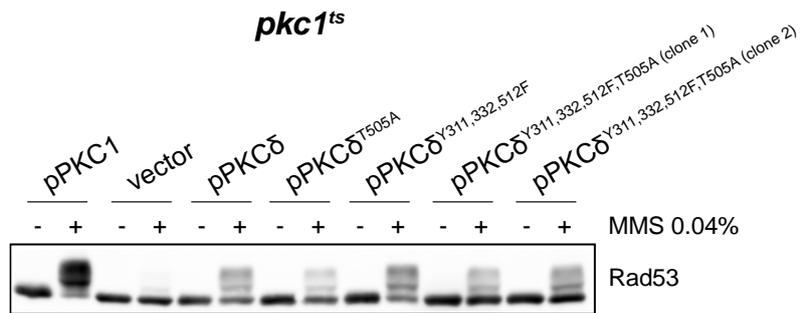


Figure S3. Analysis of DNA integrity checkpoint activation in key Tyr mutants in PKC δ oxidative stress response. Exponentially growing cultures of the *pkc1^{ts}* (JC6-3a) strain transformed with plasmids pPKC1, pPKC δ , pPKC δ ^{Y311F, Y332F, Y512F}, pPKC δ ^{Y311F, Y332F, Y512F, T505A} or with an empty vector were transferred to 37°C for 3 hours and then incubated in the absence or presence of MMS 0.04% for 1 hour. The activation of Rad53 was analyzed by western blot.

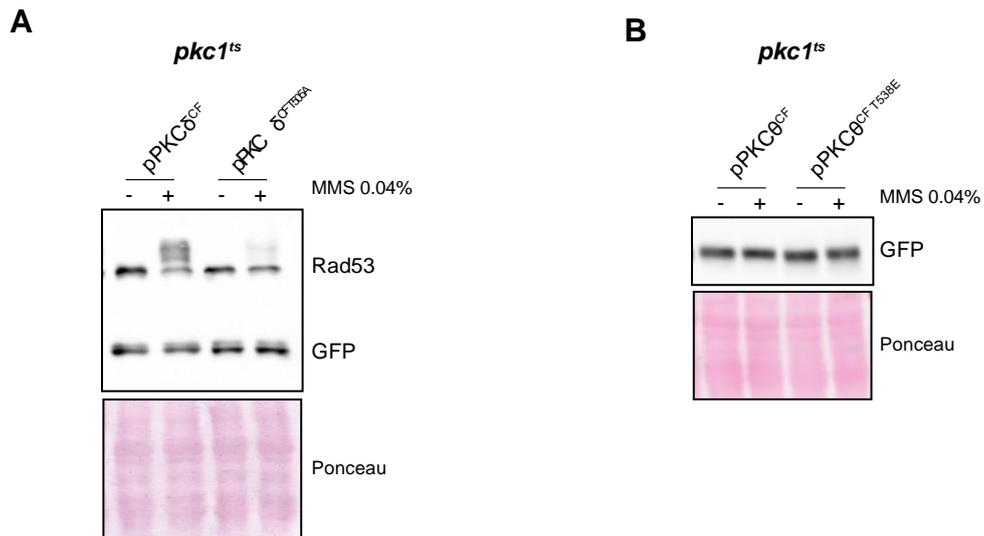


Figure S4. Protein level analysis of PKC δ^{CF} and PKC θ^{CF} mutants. Exponentially growing cultures of the *pkc1^{ts}* (JC6-3a) strain transformed with plasmids **A)** pPKC δ^{CF} -GFP and pPKC $\delta^{CF T505A}$ -GFP or **B)** pPKC θ^{CF} -GFP and pPKC $\theta^{CF T538E}$ -GFP were transferred to 37°C for 3 hours and then incubated in the absence or presence of MMS 0.04% for 1 hour. The activation of Rad53 and protein levels of GFP-tagged proteins were detected by western blot. Ponceau staining of the membrane is shown as loading control.

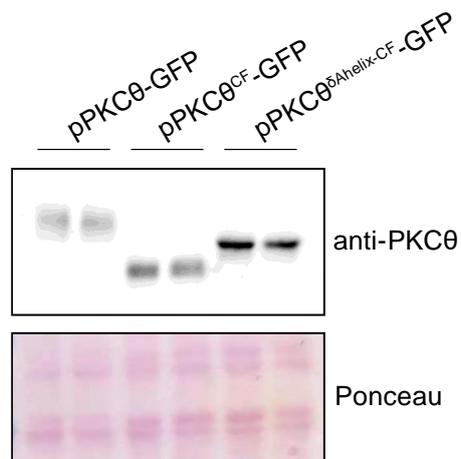


Figure S5. Protein level analysis of PKCθ truncated versions. Exponentially growing cultures of the *pkc1^{ts}* (JC6-3a) strain transformed with plasmids pPKCθ-GFP, pPKCθ^{CF}-GFP and pPKCθ^{CF^{T538E}}-GFP were transferred to 37°C for 3 hours and then incubated in the absence or presence of MMS 0.04% for 1 hour. Protein levels were detected by western blot with a rabbit mAb anti-PKCθ antibody (Cell Signaling Cat#13643). Ponceau staining of the membrane is shown as loading control.

Table S1. Comparison of amino acids between novel PKCs. PKC δ residues involved in the A-helix dependent mechanism of activation loop stabilization and the corresponding residues of the PKC θ and PKC ϵ isoforms.

nPKC	Contact 1		Contact 2		Contact 3	
δ	Tyr ³³²	Phe ⁴⁹⁸	Trp ³³⁶	Arg ³⁹⁷	Ile ⁴⁹⁷	Phe ⁵²⁵
θ	Gln	Leu	Trp	Arg	Met	His
ϵ	Asn	Met	Arg	Arg	Ile	Pro

Table S2. Mutant versions of PKC δ and PKC θ proteins.

Protein	Mutant version
PKCδ	PKC δ ^{T505A}
	PKC δ ^{E500G}
	PKC δ ^{T505A,E500G}
	PKC δ ^{Y311,332,512F}
	PKC δ ^{Y311,332,512F,T505A}
PKCδ^{CF}	PKC δ ^{CF T505A}
	PKC δ ^{CF E500G}
	PKC δ ^{CF T505A,E500G}
PKCδ^{Ahelix-CF}	PKC δ ^{Ahelix-CF T505A}
	PKC δ ^{Ahelix-CF E500G}
	PKC δ ^{Ahelix-CF T505A,E500G}
	PKC δ ^{Ahelix-CF T505A,E500G,Y332Q,W336R,I497M,F498L,F525H}
	PKC δ ^{Ahelix-CF T505A,I497A,F498A,F525A}
PKCθ	PKC θ ^{T538A}
PKCθ^{CF}	PKC θ ^{CF T538E}

Table S3. Oligonucleotides used for site-directed mutagenesis. Mutated nucleotides are highlighted in bold.

Point mutation	Oligonucleotide	Sequence (5'-3')
PKC δ Y311F	forward	CTGTCGGAATAT TT CAGGGATTTGAGAAG
	reverse	CTTCTCAAATCCCTG AA ATATTCCGACAG
PKC δ Y332F	forward	CAACGGGACCT TT GGCAAGATCTGGG
	reverse	CCCAGATCTTGCCA AA GGTCCCGTTG
PKC δ Y332Q	forward	CTAGACAACAACGGGACCC CA AGGCAAGATCTGGG
	reverse	CCCAGATCTTGC CT GGGTCCCGTTGTTGTCTAG
PKC δ W336R	forward	GACCTATGGCAAGATCCGGGAGGGGAGCAC
	reverse	CGGGTGCTCCCTCCCGGATCTTGCCATAG
PKC δ I497M	forward	CAAAGAGAATAT G TTTGGGGAG
	reverse	CTCCCCAAACATATTCTCTTTG
PKC δ I497A	forward	GTGCAAAGAGAAT G CTTTTGGGGAGG
	reverse	CCTCCCCAAA AG CATTCTCTTTGCAC
PKC δ F498L	forward	GAATATAT G GGGGAGGGCCGG
	reverse	CCGGCCCTCCCC CA ATATATTC
PKC δ F498A	forward	GTGCAAAGAGAATAT G CTGGGGAGGGG
	reverse	GCCCTCCCC AG CTATATTCTCTTTGCAC
PKC δ E500G	forward	GAATATATTTGGGG G TGGCCGGGCCAG
	reverse	CTGGCCCGGCC AC CCCCAAATATATTC
PKC δ T505A	forward	GGCCGGGCCAG G CTTTCTGCGGC
	reverse	GCCGCAGAA AG CGCTGGCCCGGCC
PKC δ Y512F	forward	GGCACTCCTGACT TT ATCGCCCCTG
	reverse	CAGGGGCGAT AA AGTCAGGAGTGCC
PKC δ F525H	forward	GGCCTGAAGTACTCC CA TTCCGGTGGACTG
	reverse	GTCCACCGA AT GAGTACTTCAG
PKC δ F525A	forward	GGCCTGAAGTACTCC G TTCCGGTGGACTG
	reverse	CAGTCCACCGA AG CGGAGTACTTCAGGCC
PKC θ T538A	forward	GCGAAGACAAAT G CTTTCTGTG
	reverse	CACAGAAAG C ATTTGTCTTCGC
PKC θ T538E	forward	GAAGACAAAT GA ATTCTGTGGAATC
	reverse	GAGTTCCACAGA AT TCATTTGTCTTC