

995 **Supplemental Materials:**

996 **Figs. S1 to S9:**

997 Supplemental Figure 1. UVB-driven IFN responses are mtDNA dependent and UV-induced Z-  
998 DNA derives from mtDNA.

999 Supplemental Figure 2. UVB induces oxidative DNA damage in the cytosol and mitochondrial  
1000 compartment.

1001 Supplemental Figure 3. Cytosolic Z-DNA accumulation is associated with mitochondrial  
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1003 Supplemental Figure 4. IFN $\alpha$  does not increase mitochondrial or total cellular ROS in N/TERTs.

1004 Supplemental Figure 5. ZBP1 expression does not correlate with systemic autoantibodies or  
1005 patient age.

1006 Supplemental Figure 6. mitoTEMPO rescues UVB-induced IFN expression in lupus KCs.

1007 Supplemental Figure 7. UVB leads to cytosolic shift of cGAS in N/TERTs.

1008 Supplemental Figure 8. ISGs are significantly increased after Z-DNA transfection in N/TERTs  
1009 and primary KCs.

1010 Supplemental Figure 9. Overexpression of ZBP1 results in cytosolic expression.

1011 **Tables S1 to S4:**

1012 Supplemental Table 1. Demographics and characteristics of patients and controls for primary  
1013 keratinocyte cell culture

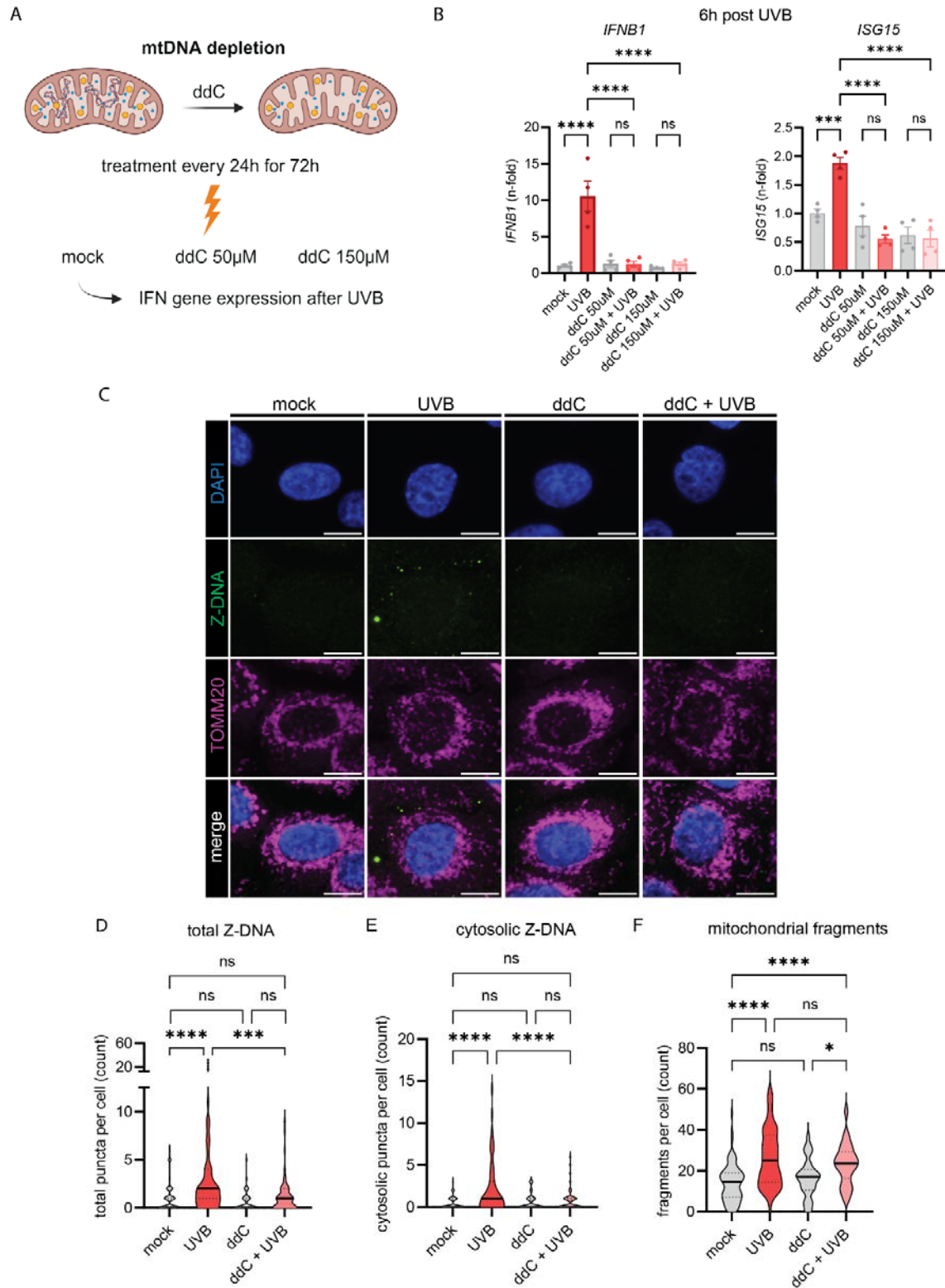
1014 Supplemental Table 2. Demographics and characteristics of lupus and dermatomyositis patients  
1015 from which skin biopsies were used for tissue immunofluorescence

1016

1017 **Supplemental Data**

1018

1019 **Supplemental Figure 1**



1020

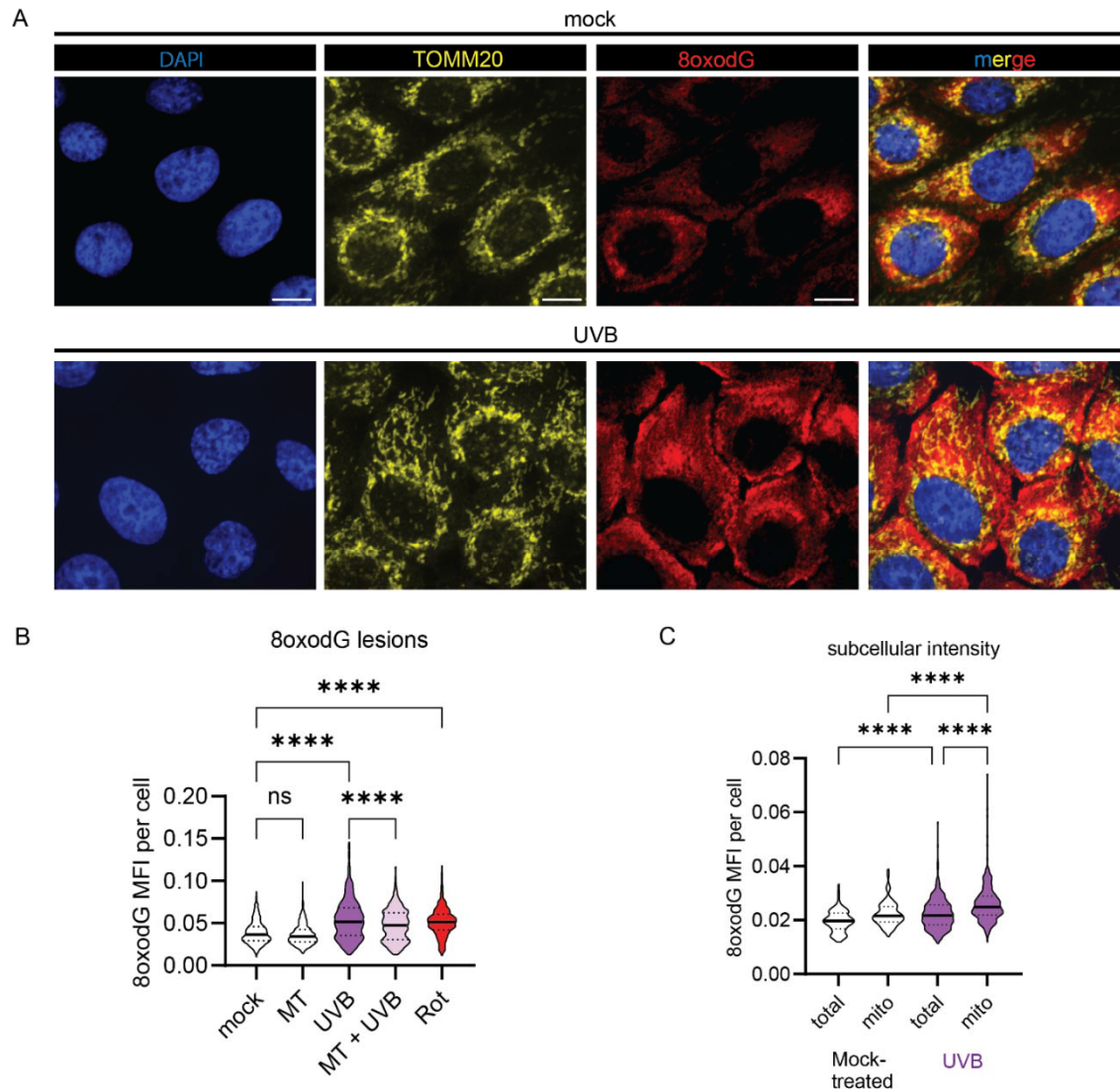
1021

1022 **Supplemental Figure 1. UVB-driven IFN responses are mtDNA dependent and UV-induced Z-DNA**  
1023 **derives from mtDNA.**

1024 **A.** Experimental approach for mtDNA depletion in N/TERTs using nucleoside 2',3' dideoxycytidine (ddC).  
1025 Treatment with ddC was performed for 72h. After irradiation, medium was changed to ddC-free medium  
1026 until gene expression analysis. **B.** Quantitative gene expression 6h after UVB exposure. n=2 for each  
1027 experiment. **C.** Representative confocal images of N/TERTs treated with +/- ddC +/- UVB 3h after UVB  
1028 exposure stained for Z-DNA, TOMM20 and DAPI. Scale bar 10µm. **D.** Quantification of Z-DNA puncta  
1029 and mitochondrial fragments using CellProfiler open-source software from conditions in (**C.**), n=3.  
1030 Comparisons were done via ordinary one-way ANOVA followed by Sidak's multiple comparison test.  
1031 Mean and SEM. \*P<0.05, \*\*P<0.01, \*\*\*P<0,001, \*\*\*\*P<0.0001.

1032

1033 **Supplemental Figure 2.**

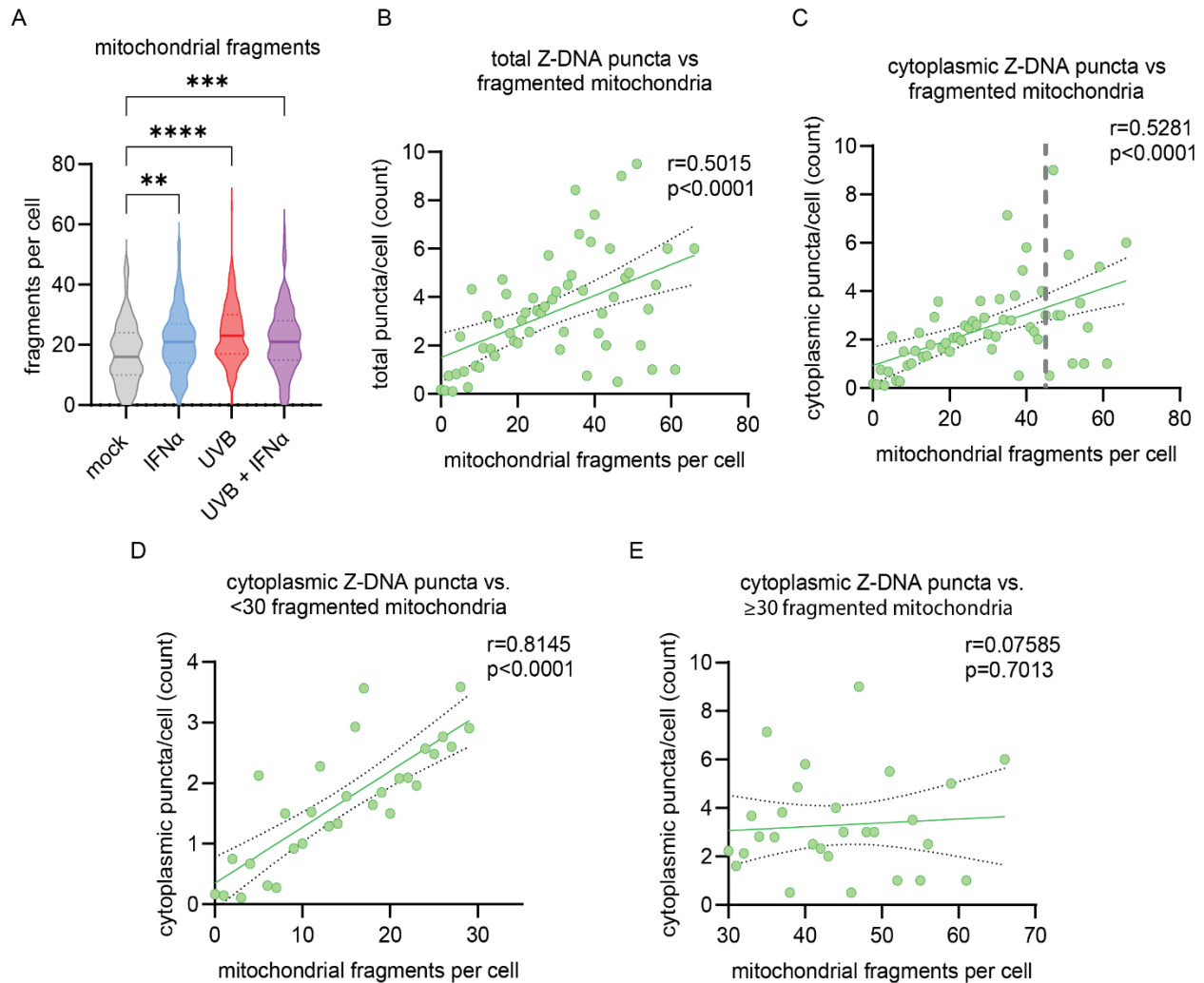


1034

1035 **Supplemental Figure 2. UVB induces oxidative DNA damage in the cytosol and mitochondrial**  
1036 **compartment.**

1037 **A.** Representative confocal microscopy images of N/TERTs 3h after UVB exposure stained for TOMM20,  
1038 8oxodG lesions and DAPI. Scale bar 20 $\mu$ m. **B.** Quantification of 8oxodG intensity per cell using open-  
1039 source software, CellProfiler, in N/TERTs treated +/- mitoTEMPO (50 $\mu$ M), +/-UVB or Rotenone (0.5 $\mu$ M)  
1040 as a positive control, n=3. **C.** Quantification of subcellular intensity of 8oxodG intensity per cell (total) or  
1041 mitochondrial (mito) assessed by TOMM20<sup>+</sup> merged area. Comparisons were done via ordinary one-way  
1042 ANOVA followed by Sidak's multiple comparison test. Mean and SEM. \*P<0.05, \*\*P<0.01, \*\*\*P<0.001,  
1043 \*\*\*\*P<0.0001.

1044 **Supplemental Figure 3.**

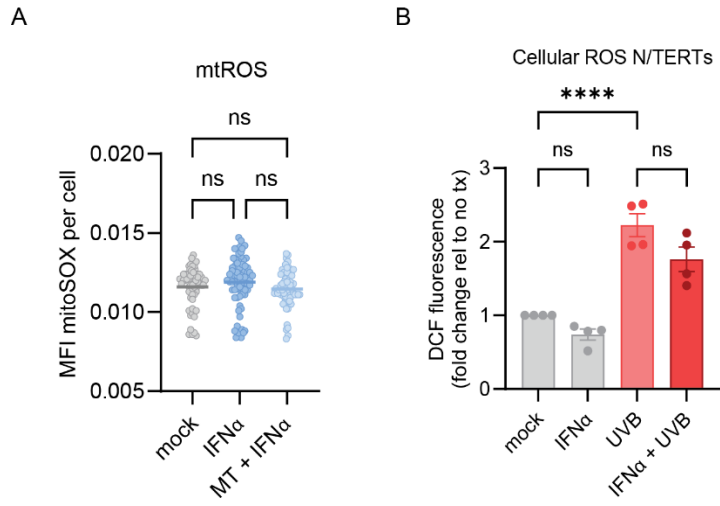


1045

1046 **Supplemental Figure 3. Cytosolic Z-DNA accumulation is associated with mitochondrial**  
 1047 **fragmentation.**

1048 **A.** Violin plots represent quantification of mitochondrial fragments (defined as TOMM20<sup>+</sup> objects smaller  
 1049 than 1 $\mu$ m) in N/TERTs after 16h of IFN $\alpha$  treatment followed by UVB (50mJ/cm<sup>2</sup>) exposure. Comparisons  
 1050 were done via ordinary one-way ANOVA followed by Sidak's multiple comparison test. \*\*P<0.01,  
 1051 \*\*\*P<0,001, \*\*\*\*P<0.0001. **B and C.** Correlation of total or cytoplasmic Z-DNA puncta and fragmented  
 1052 mitochondria with simple linear regression. **D and E.** Correlations of data in C divided by # of  
 1053 mitochondrial fragments per cell. Pearson correlation coefficient (r) and p-values for indicated correlations  
 1054 are shown in the upper right.  
 1055

1056 **Supplemental Figure 4.**



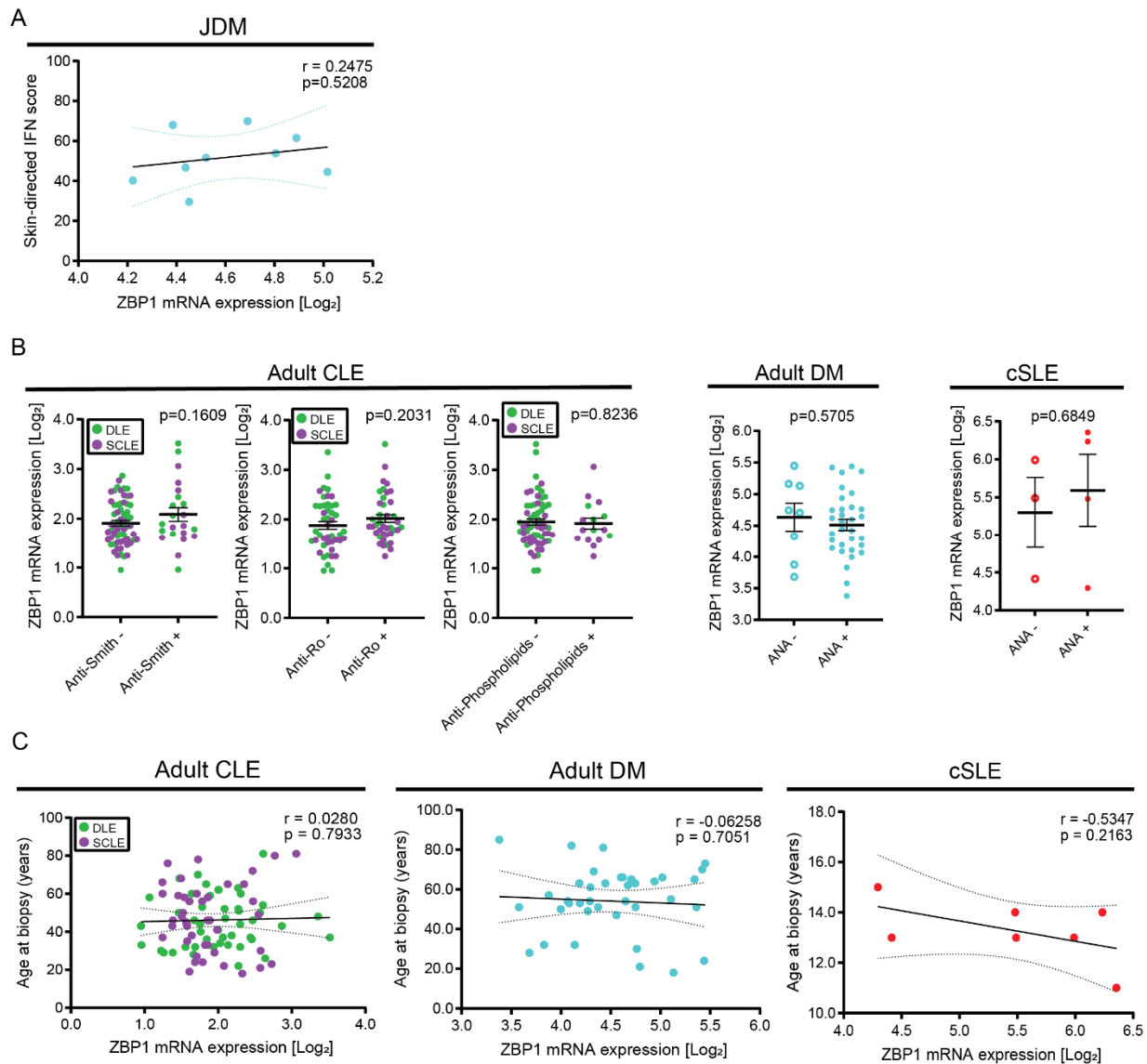
1057

1058 **Supplemental Figure 4. IFN $\alpha$  does not increase mitochondrial or total cellular ROS in N/TERTs.**

1059 **A.** Violin plots represent quantification of mitoSOX staining intensity per cell in N/TERTs stimulated with  
1060 IFN $\alpha$  (1000U/ml) for 16h compared to mock. **B.** Fold change of fluorescence of  
1061 Dichlorodihydrofluorescein (DFC) after treatment with IFN $\alpha$  for 16h +/- UVB exposure in N/TERTs 5min  
1062 after UVB exposure, n=4. Comparisons were done via ordinary one-way ANOVA followed by Sidak's  
1063 multiple comparison test. Mean and SEM. \*\*\*\*P<0.0001.

1064

1065 **Supplemental Figure 5.**



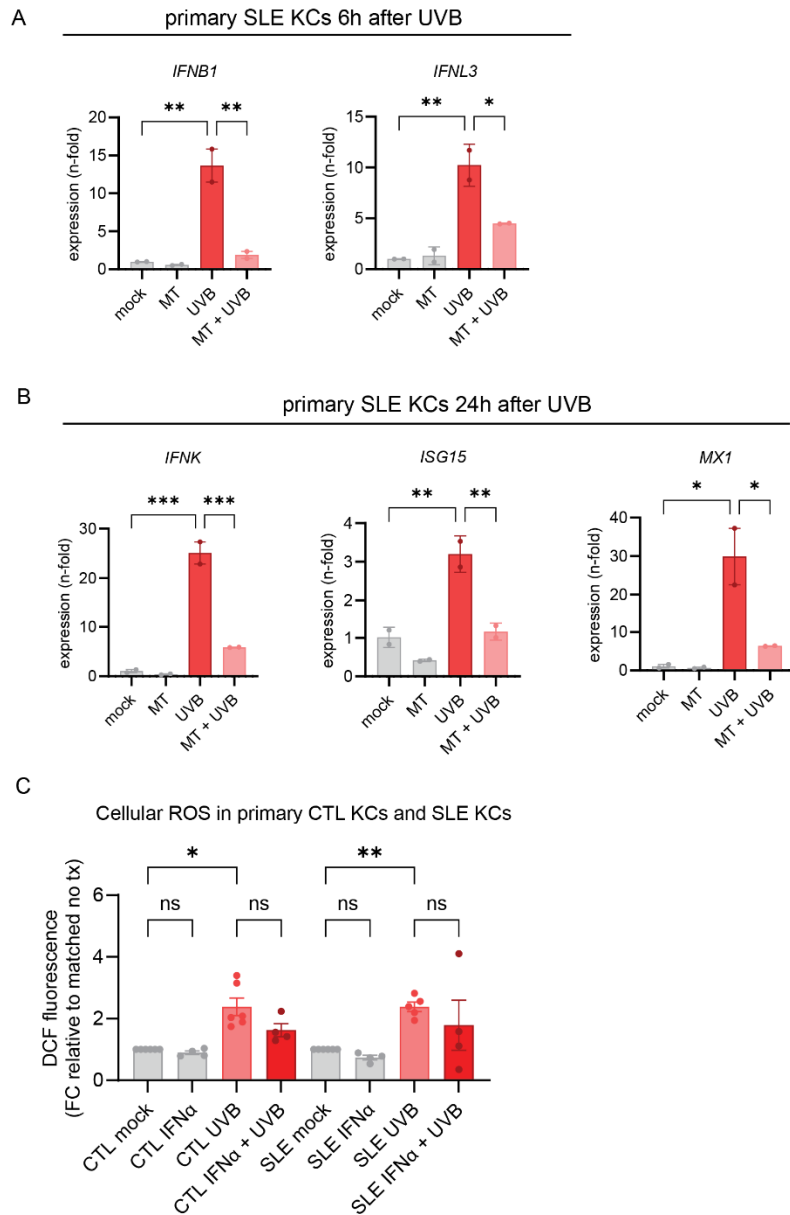
1066

1067 **Supplemental Figure 5. ZBP1 expression does not correlate with systemic autoantibodies or**  
1068 **patient age.**

1069 **A.** Correlation of cutaneous *ZBP1* expression in juvenile dermatomyositis (n=9) with skin-directed IFN  
1070 score showing no significant correlation. **B.** Comparison of cutaneous *ZBP1* expression with  
1071 autoantibodies in adult CLE, DM and childhood onset SLE (cSLE) showing independence of *ZBP1*  
1072 expression with autoantibody status. **C.** Correlation of cutaneous *ZBP1* expression with age in adult CLE,  
1073 adult DM and childhood SLE (cSLE) showing no significant correlation with age.

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1075 **Supplemental Figure 6.**



1076

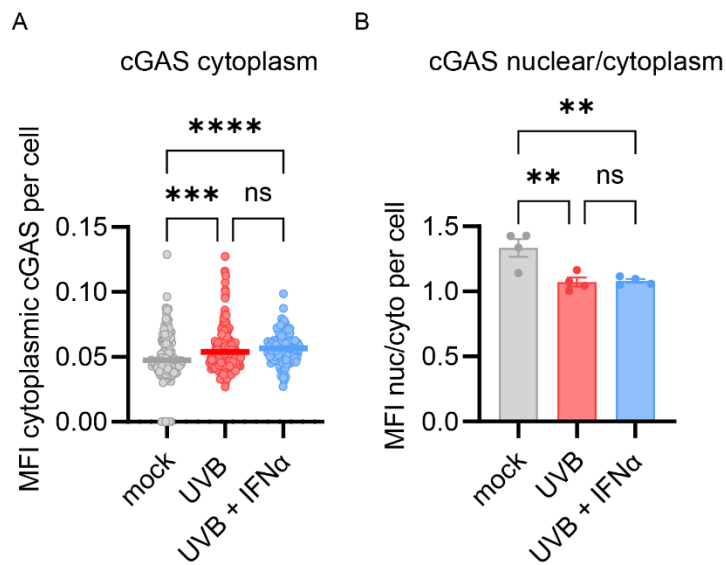
1077 **Supplemental Figure 6. mitoTEMPO rescues UVB-induced IFN expression in lupus KCs.**

1078 **A.** Nonlesional SLE KCs (n=2) were treated +/- mitoTEMPO (50μM) and irradiated with UVB. Gene  
 1079 expression was analyzed 6h after UVB exposure. **B.** Gene expression analysis 24h after UVB exposure  
 1080 was normalized to β-Actin. n=2. Mean and SEM. **C.** Measurement of cellular ROS in primary HC KCs  
 1081 (n=4) and SLE KCs (n=4) at baseline and after IFNα treatment +/- UVB exposure. Comparisons were  
 1082 done via ordinary one-way ANOVA followed by Sidak's multiple comparison test. Mean and SEM.  
 1083 \*P<0.05, \*\*P<0.01, \*\*\*P<0.001, \*\*\*\*P<0.0001.

1084



1085 **Supplemental Figure 7.**



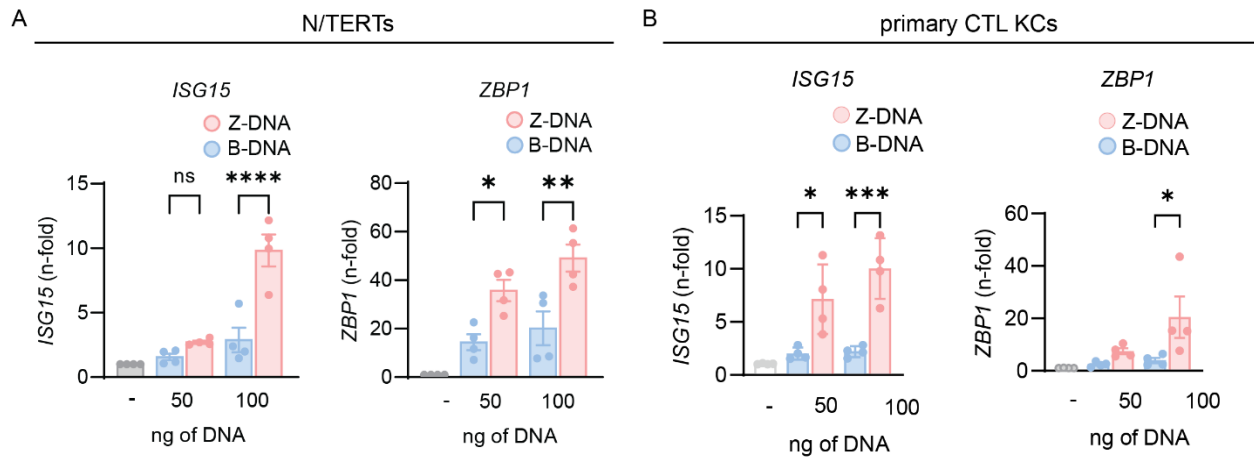
1086

1087 **Supplemental Figure 7. UVB leads to cytosolic shift of cGAS in N/TERTs.**

1088 **A.** Quantification of cytosolic mean fluorescence intensity (MFI) of cytoplasmic cGAS defined by the  
1089 DAPI-negative area in N/TERTs using open-source software CellProfiler. **B.** Ratio of nuclear and  
1090 cytoplasmic MFI per cell and shown is the mean ratio per cell of each experiment (n=4). Comparisons  
1091 were done via ordinary one-way ANOVA followed by Sidak's multiple comparison test. Mean and SEM.  
1092 \*\*P<0.01, \*\*\*P<0,001, \*\*\*\*P<0.0001.

1093

1094 **Supplemental Figure 8.**



1095

1096 **Supplemental Figure 8. ISG15 and ZBP1 are significantly increased after Z-DNA transfection vs.**

1097 **B-DNA in N/TERTs and primary KCs.**

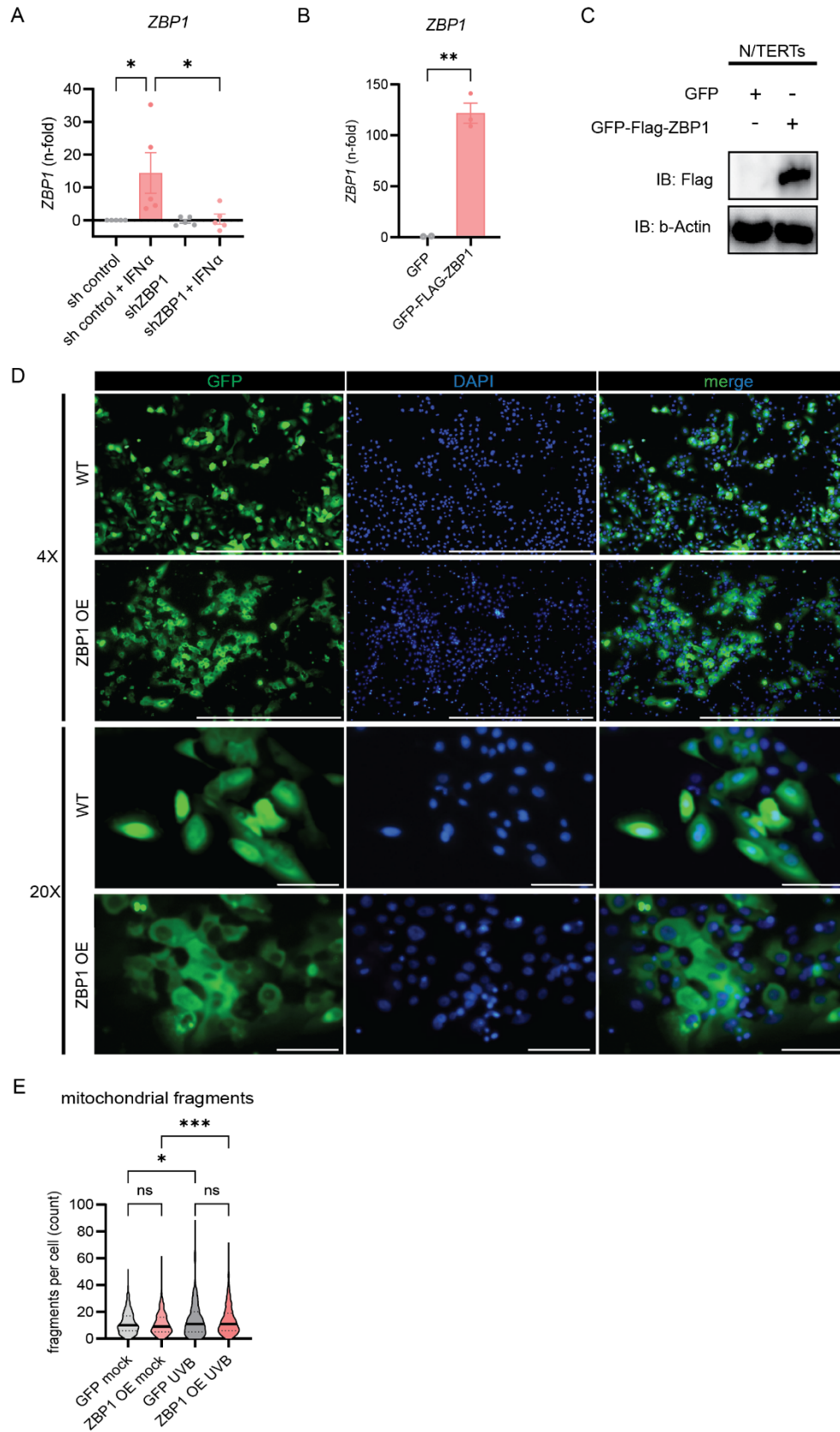
1098 **A.** Gene expression at 24h of indicated genes from N/TERTs (n=4) and primary HC KCs (n=4) treated  
1099 transfected with Z-DNA or B-DNA. Comparisons were done via ordinary one-way ANOVA followed by  
1100 Sidak's multiple comparison test. Mean and SEM. \*\*P<0.01, \*\*\*P<0.001, \*\*\*\*P<0.0001.

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1104 **Supplemental Figure 9.**



1106 **Supplemental Figure 9. Overexpression of ZBP1 results in cytosolic expression.**

1107 **A.** Confirmation of shRNA knockdown by qPCR compared to shcontrol after IFN $\alpha$  stimulation (1000U/ml)  
1108 for 16h, n=5. **B.** Quantitative gene expression of ZBP1 overexpressors compared to GFP alone, n=3.  
1109 **C.** Immunoblot against FLAG confirming FLAG-tag of ZBP1 overexpressor cells. **D.** Representative  
1110 immunofluorescence images show efficient transfection of both GFP (first line) alone and GFP-ZBP1  
1111 (second line) in 4X magnification, scale bar=1000 $\mu$ m. Detailed images reveal pancellular tag of GFP (third  
1112 line) and cytosolic overexpression of ZBP1 (fourth line). 20X, scale bar=1000 $\mu$ m. 4X, scale bar=100 $\mu$ m.  
1113 **E.** Quantification of mitochondrial fragments (TOMM20<sup>+</sup> objects <1 $\mu$ m<sup>2</sup> with circularity >0.6) in GFP-tag  
1114 N/TERTs and ZBP1 OE N/TERTs at baseline and after UVB exposure using CellProfiler software.  
1115 Comparisons were done via ordinary one-way ANOVA followed by Sidak's multiple comparison test or t-  
1116 test. \*P<0.05, \*\*P<0.01, \*\*\*P<0,001, \*\*\*\*P<0.0001.

1117

1118 **Supplemental Table 1. Demographics and characteristics of patients and controls for primary**  
 1119 **keratinocyte cell culture**

	<b>HC (N=8)</b>	<b>SLE (N=8)</b>
Median age in years (IQR)	44 (31,52)	44 (41,52)
Female sex - n (%)	4 (50%)	6 (75%)
Cutaneous lupus – n (%)	-	5 (62%)
Median SLEDAI-2k (IQR)	-	2 (0,4)
<b>Cutaneous lupus subtype – n (%)</b>		
ACLE	-	1 (12%)
SCLE	-	1 (12%)
DLE	-	3 (38%)
CLASI activity (IQR)		2 (0,3)
<b>SLE treatment – n (%)</b>		
Hydroxychloroquine	-	5 (62%)
Glucocorticoid	-	3 (38%)
Immunosuppressant	-	7 (88%)
<b>Autoantibodies – n positive (%)</b>	-	
ANA	-	8 (100%)
Anti-Ro/SSA	-	5 (62%)
Anti-dsDNA	-	4 (50%)
Anti-Sm/RNP	-	4 (50%)
<b>Site of non-lesional biopsy - n (%)</b>		
Buttock/hip	8 (100%)	7 (88%)
Arm	0	1 (12%)
HC: healthy controls; SLE: systemic lupus erythematosus; IQR: interquartile range; n: number; SLEDAI: Systemic Lupus Erythematosus Disease Activity; ACLE: acute cutaneous lupus; DLE: discoid lupus erythematosus; SCLE: subacute cutaneous lupus erythematosus; CLASI: Cutaneous Lupus Erythematosus Disease Area and Severity Index; ANA: antinuclear antibody		

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 1121

1122 **Supplemental Table 2. Demographics and characteristics of lupus and dermatomyositis**  
 1123 **patients from which skin biopsies were used for tissue immunofluorescence**

	<b>CLE/SLE (N=13)</b>		<b>DM (N=6)</b>	
Median age in years (IQR)	46 (41,51)		54 (35,61)	
Female sex - n (%)	11 (85%)		5 (83%)	
	<b>Clinical manifestations CLE/SLE</b>		<b>Clinical manifestations DM</b>	
	Cutaneous lupus only – n (%)	4 (31%)	Skin involvement	6 (100%)
	DLE	8 (62%)	Muscle involvement	4 (67%)
	SCLE	5 (38%)		
	Median CLASI activity (IQR)	4 (2,8)		
	Median SLEDAI-2k (IQR)	4 (2,8)		
<b>Autoantibodies – n positive (%)</b>				
ANA	12 (92%)		5 (83%)	
	Anti-Ro/SSA	6 (46%)	Anti-Mi-2	1 (17%)
	Anti-dsDNA	4 (31%)	Anti-TIF-1γ	1 (17%)
	Anti-Sm/RNP	3 (23%)	Anti-PL7	1 (17%)
<b>Treatment – n (%)</b>				
Hydroxychloroquine	12 (92%)		2 (33%)	
Glucocorticoid	6 (46%)		1 (17%)	
Immunosuppressant	5 (38%)		3 (50%)	
SLE: systemic lupus erythematosus; CLE: cutaneous lupus erythematosus; DM: dermatomyositis; IQR: interquartile range; n: number; DLE: discoid lupus erythematosus; SCLE: subacute cutaneous lupus erythematosus; CLASI: Cutaneous Lupus Erythematosus Disease Area and Severity Index; SLEDAI: Systemic Lupus Erythematosus Disease Activity; ANA: antinuclear antibody				