TABLES as WORD Editable Document

Table S1

pathway	pval	padj
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0,001040583	0,00794155
HALLMARK_MYC_TARGET	0,00104612	0,00794155
HALLMARK_ DNA_REPAIR	0,001108647	0,00794155
HALLMARK_ REACTIVE_OXIGEN_SPECIES_PATHWAY	0,001270648	0,00794155
HALLMARK_ADIPOGENESIS	0,001072961	0,00794155
HALLMARK_ FATTY ACID METABOLISM	0,00116195	0,009238729
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0,001146789	0,00794155
HALLMARK_XENOBIOTIC_METABOLISM	0,002107802	0,009238729
HALLMARK_MTORC1_SIGNALING	0.002162162	0,009238729
HALLMARK_E2F_TARGETS	0,002202643	0,009238729
HALLMARK_UV RESPONSE_UP	0,002217295	0,009238729
HALLMARK_COAGULATION	0,001183432	0,00794155
HALLMARK_GLICOLYSIS	0,004338395	0,015494267
HALLMARK_HYPOXIA	0,00867679	0,016287
HALLMARK_MYOGENESIS	0,01818188	0,037037037
HALLMARK_MYC_TARGETS_V2	0,016290727	0,037024379
HALLMARK_P53_PATHWAY	0,023809524	0,044091711
HALLMARK_PEROXISOME	0,025	0,044642857

Table S2

pathway	pval	padj
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0,00103	0,007135
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0,001031	0,007135
HALLMARK_INTERFERON_ALPHA_RESPONSE	0,001142	0,007135
HALLMARK_DNA_REPAIR	0,001063	0,007135
HALLMARK_COAGULATION	0,01142	0,007135
HALLMARK_GLYCOLYSIS	0,001062	0,007135
HALLMARK_ INTERFERON_GAMMA_RESPONSE	0,001044	0,007135
HALLMARK_APICAL JUNCTION	0,001089	0,007135
HALLMARK_ADIPOGENESIS	0,002079	0,010893
HALLMARK_FATTY ACID METABOLISM	0,002179	0,010893
HALLMARK_ANGIOGENESIS	0,011952	0,037707

HALLMARK_P53_PATHWAY	0,003128	0,013034
HALLMARK_MYC_TARGETS_V1	0,003093	0,013034
HALLMARK_HYPOXIA	0,019958	0,049895
HALLMARK_ALLOGRAFT_REJECTION	0,012586	0,037707

Table S3 (left side)

RA CXCL12 Synovial Fibroblast Pathway = FIGURE2	**pval**	**padj**
HALLMARK_OXIDATIVE_PHOSPHORYLATION	**0,001040583**	**0,00794155**
HALLMARK_MYC_TARGET	0,00104612	0,00794155
HALLMARK_ DNA_REPAIR	0,001108647	0,00794155
HALLMARK_ REACTIVE_OXIGEN_SPECIES_PATHWAY	0,001270648	0,00794155
HALLMARK_ADIPOGENESIS	**0,001072961**	**0,00794155**
HALLMARK_ FATTY ACID METABOLISM	**0,00116195**	**0,009238729**
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0,001146789	0,00794155
HALLMARK_XENOBIOTIC_METABOLISM	0,002107802	0,009238729
HALLMARK_MTORC1_SIGNALING	0.002162162	0,009238729
HALLMARK_E2F_TARGETS	0,002202643	0,009238729
HALLMARK_UV RESPONSE_UP	0,002217295	0,009238729
HALLMARK_COAGULATION	**0,001183432**	**0,00794155**
HALLMARK_GLICOLYSIS	**0,004338395**	**0,015494267**
HALLMARK_HYPOXIA	**0,00867679**	**0,016287**
HALLMARK_MYOGENESIS	0,01818188	0,037037037
HALLMARK_MYC_TARGETS_V2	**0,016290727**	**0,037024379**
HALLMARK_P53_PATHWAY	**0,023809524**	**0,044091711**
HALLMARK_PEROXISOME	0,025	0,044642857

Table S3 (right side)

HER2+ Fb2 Fibroblast Pathway	**pval**	**padj**
HALLMARK_OXIDATIVE_PHOSPHORYLATION	**0,00103**	**0,007135**
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0,001031	0,007135
HALLMARK_INTERFERON_ALPHA_RESPONSE	0,001142	0,007135
HALLMARK_DNA_REPAIR	0,001063	0,007135
HALLMARK_COAGULATION	**0,01142**	**0,007135**
HALLMARK_GLYCOLYSIS	**0,001062**	**0,007135**
HALLMARK_ INTERFERON_GAMMA_RESPONSE	0,001044	0,007135
HALLMARK_APICAL JUNCTION	0,001089	0,007135

HALLMARK_ADIPOGENESIS	**0,002079**	**0,010893**
HALLMARK_FATTY ACID METABOLISM	**0,002179**	**0,010893**
HALLMARK_ANGIOGENESIS	0,011952	0,037707
HALLMARK_P53_PATHWAY	**0,003128**	**0,013034**
HALLMARK_MYC_TARGETS_V1	**0,003093**	**0,013034**
HALLMARK_HYPOXIA	**0,019958**	**0,049895**
HALLMARK_ALLOGRAFT_REJECTION	0,012586	0,037707

Table S4

Basal cell pathway	pval	padj
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0,001059	0,006127
HALLMARK_INTERFERON_ALPHA_RESPONSE	0,001131	0,006127
HALLMARK_INTERFERON_GAMMA_RESPONSE	0,001053	0,006127
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0,001032	0,006127
HALLMARK_APOPTOSIS	0,001089	0,006127
HALLMARK_COAGULATION	0,001144	0,006127
HALLMARK_P53_PATHWAY	0,001042	0,006127
HALLMARK_ALLOGRAFT_REJECTION	0,001115	0,006127
HALLMARK_ADIPOGENESIS	0,001059	0,006127
HALLMARK_UV RESPONSE_UP	0,00216	0,008999
HALLMARK_COMPLEMENT	0,002146	0,008999
HALLMARK_FATTY_ ACID_ METABOLISM	0,003341	0,011136
HALLMARK_ DNA_REPAIR	0,003236	0,011136
HALLMARK_ REACTIVE_OXIGEN_SPECIES_PATHWAY	0,001225	0,006127
HALLMARK_INFLAMMATORY_RESPONSE	0,003304	0,011136
HALLMARK_IL6_JAK_STAT3_SIGNALING	0,003695	0,011546
HALLMARK_XENOBIOTIC_METABOLISM	0,013187	0,0333333
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0,008343	0,024539
HALLMARK_HYPOXIA	0,016949	0,037481

Table S5 (left side)

Basal cell pathway	pval	padj
HALLMARK_OXIDATIVE_PHOSPHORYLATION	**0,001059**	**0,006127**
HALLMARK_INTERFERON_ALPHA_RESPONSE	**0,001131**	**0,006127**
HALLMARK_INTERFERON_GAMMA_RESPONSE	**0,001053**	**0,006127**

HALLMARK_TNFA_SIGNALING_VIA_NFKB	0,001032	0,006127
HALLMARK_APOPTOSIS	0,001089	0,006127
HALLMARK_COAGULATION	**0,001144**	**0,006127**
HALLMARK_P53_PATHWAY	**0,001042**	**0,006127**
HALLMARK_ALLOGRAFT_REJECTION	0,001115	0,006127
HALLMARK_ADIPOGENESIS	**0,001059**	**0,006127**
HALLMARK_UV RESPONSE_UP	0,00216	0,008999
HALLMARK_COMPLEMENT	0,002146	0,008999
HALLMARK_FATTY_ ACID_ METABOLISM	**0,003341**	**0,011136**
HALLMARK_ DNA_REPAIR	0,003236	0,011136
HALLMARK_ REACTIVE_OXIGEN_SPECIES_PATHWAY	0,001225	0,006127
HALLMARK_INFLAMMATORY_RESPONSE	0,003304	0,011136
HALLMARK_IL6_JAK_STAT3_SIGNALING	0,003695	0,011546
HALLMARK_XENOBIOTIC_METABOLISM	0,013187	0,0333333
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0,008343	0,024539
HALLMARK_HYPOXIA	**0,016949**	**0,037481**

Table S5 (right side)

Basal cell cluster pathway	pval	padj
HALLMARK_OXIDATIVE_PHOSPHORYLATION	**0,00103**	**0,007135**
HALLMARK_EPITHELIAL_MESENKIMAL_TRANSITION	0,001031	0,007135
HALLMARK_INTERFERON_ALPHA_RESPONSE	**0,001142**	**0,007135**
HALLMARK_ DNA_REPAIR	0,001063	0,007135
HALLMARK_ COAGULATION	**0,001142**	**0,007135**
HALLMARK_GLYCOLYSIS	0,001062	0,007135
HALLMARK_INTERFERON_GAMMA_RESPONSE	**0,001044**	**0,007135**
HALLMARK_APICAL_JUNCTION	0,001089	0,007135
HALLMARK_ADIPOGENESIS	**0,002079**	**0,010893**
HALLMARK_ FATTY_ ACID_ METABOLISM	**0,002179**	**0,010893**
HALLMARK_ANGIOGENESIS	0,011952	0,037707
HALLMARK_P53_PATHWAY	**0,003128**	**0,013034**
HALLMARK_MYC_TARGETS	0,003093	0,013034
HALLMARK_HYPOXIA	**0,019958**	**0,049896**
HALLMARK_ ALLOGRAFT_REJECTION	0,012588	0,037707

Table S6 (left side)

HER2+ Fb2 Fibroblast Pathway	**pval**	**padj**
HALLMARK_OXIDATIVE_PHOSPHORYLATION	**0,00103**	**0,007135**
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	**0,001031**	**0,007135**
HALLMARK_INTERFERON_ALPHA_RESPONSE	**0,001142**	**0,007135**
HALLMARK_DNA_REPAIR	**0,001063**	**0,007135**
HALLMARK_COAGULATION	0,01142	0,007135
HALLMARK_GLYCOLYSIS	**0,001062**	**0,007135**
HALLMARK_ INTERFERON_GAMMA_RESPONSE	**0,001044**	**0,007135**
HALLMARK_APICAL JUNCTION	0,001089	0,007135
HALLMARK_ADIPOGENESIS	0,002079	0,010893
HALLMARK_FATTY ACID METABOLISM	0,002179	0,010893
HALLMARK_ANGIOGENESIS	0,011952	0,037707
HALLMARK_P53_PATHWAY	**0,003128**	**0,013034**
HALLMARK_MYC_TARGETS_V1	**0,003093**	**0,013034**
HALLMARK_HYPOXIA	**0,019958**	**0,049895**
HALLMARK_ALLOGRAFT_REJECTION	**0,012586**	**0,037707**

Table S6 (right side)

UNC1 Cell Cluster Pathways	**pval**	**padj**
HALLMARK_OXIDATIVE_PHOSPHORYLATION	**0,001148**	**0,012903**
HALLMARK_INTERFERON GAMMA RESPONSE	**0,001183**	**0,012903**
HALLMARK_HYPOXIA	0,001229	0,012903
HALLMARK_ALLOGRAFT_REJECTION	0,01255	0,012903
HALLMARK_INTERFERON_ALPHA_RESPONSE	**0,00129**	**0,012903**
HALLMARK_MYC_TARGETS	0,002222	0,015152
HALLMARK_P53_PATHWAY	0,002424	0,015152
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0,002317	0,015152
HALLMARK_DNA_REPAIR	0,004957	0,027793
HALLMARK_ REACTIVE_OXIGEN_SPECIES_PATHWAY	0,007267	0,027793
HALLMARK_GLYCOLYSIS	**0,007782**	**0,027793**
HALLMARK_INFLAMMATORY_RESPONSE	0,013263	0,009384
HALLMARK_KRAS_SIGNALING_UP	0,013459	0,039585
HALLMARK_IL6_JAK_STAT3_SIGNALING	0,012931	0,039585

Table S7 (left side)

B Cell Cluster Pathways	**pval**	**padj**
HALLMARK_ INTERFERON_GAMMA_RESPONSE	**0,001182**	**0,009411**
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0,001135	0,009411
HALLMARK_ALLOGRAFT_REJECTION	**0,01202**	**0,009411**
HALLMARK_INTERFERON_ALPHA_RESPONSE	0,001318	0,009411
HALLMARK_UV_RESPONSE_UP	0,001252	0,009411
HALLMARK_MTORC1_SIGNALING	0,001145	0,009411
HALLMARK_HYPOXIA	**0,001186**	**0,009411**
HALLMARK_INFLAMMATORY_RESPONSE	**0,002635**	**0,016469**
HALLMARK_FATTY_ACID_METABOLISM	0,004087	0,022707
HALLMARK_APOPTOSIS	**0,007151**	**0,034722**
HALLMARK_IL2_STAT5_SIGNALING	**0,008235**	**0,034722**

Table S7 (left side bottom)

Plasma Cell Cluster Pathways	**pval**	**padj**
HALLMARK_INTERFERON_ALPHA_RESPONSE	**0,00137**	**0,034247**
HALLMARK_ALLOGRAFT_REJECTION	**0,001252**	**0,034247**

Table S7 (right side)

Natural Killer Cell Cluster Pathways	**pval**	**padj**
HALLMARK_ALLOGRAFT_REJECTION	**0,01189**	**0,005746**
HALLMARK_INTERFERON GAMMA RESPONSE	**0,001193**	**0,005746**
HALLMARK_TNFA_SIGNALING_VIA_NFKB	**0,001155**	**0,005746**
HALLMARK_INTERFERON_ALPHA_RESPONSE	**0,001264**	**0,005746**
HALLMARK_UV_RESPONSE_UP	0,001233	0,005746
HALLMARK_IL2_STAT5_SIGNALING	**0,001192**	**0,005746**
HALLMARK_MTORC1_SIGNALING	0,001166	0,005746
HALLMARK_APOPTOSIS	**0,001193**	**0,005746**
HALLMARK_INFLAMMATORY_RESPONSE	**0,001252**	**0,005746**
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0,001193	0,005746
HALLMARK_HYPOXIA	**0,001221**	**0,005746**
HALLMARK_COMPLEMENT	0,004969	0,019111
HALLMARK_P53_PATHWAY	0,005967	0,020704
HALLMARK_IL6_JAK_STAT3_SIGNALING	0,015048	0,03762
HALLMARK_BILE_ACID_METABOLISM	0,01385	0,036448

Supplementary Material

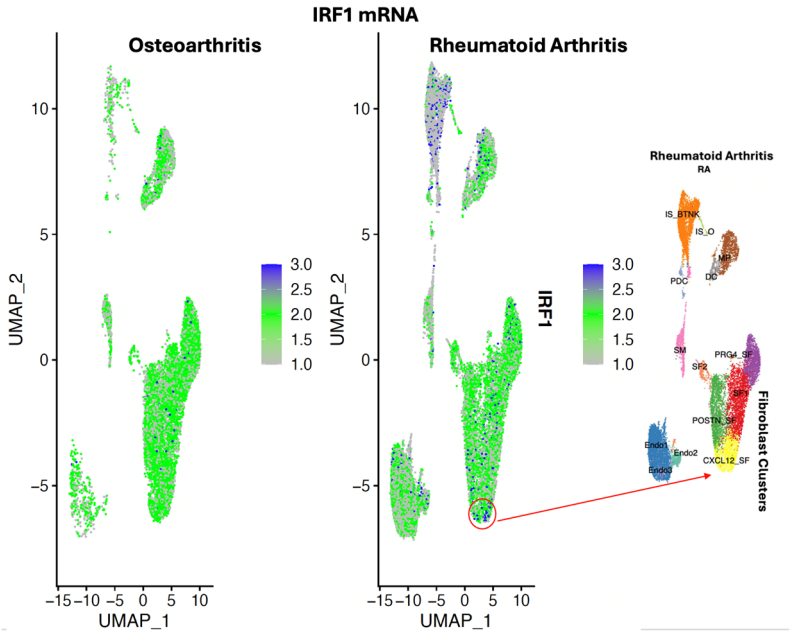
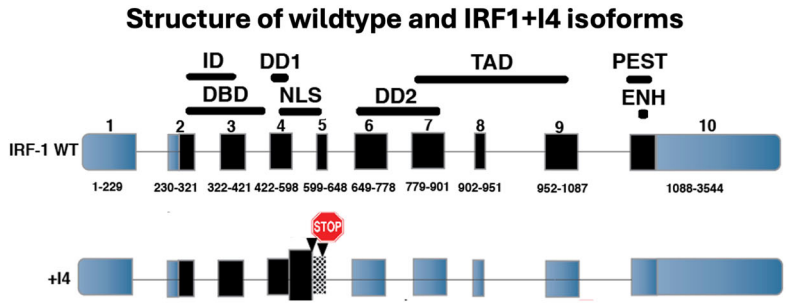


Figure S1.



Abbreviations:
DBD: DNA Binding Domain
ID: Inhibitory Domain
NLS: Nuclear Localisation Domain
DD1: Dimerization Domain (homodimers)
DD2: Dimerization Domain (heterodimers)
TAD: Transactivation Domain
ENH: Enhancement Domain
PEST: Protein Degradation Signal

Figure S2.

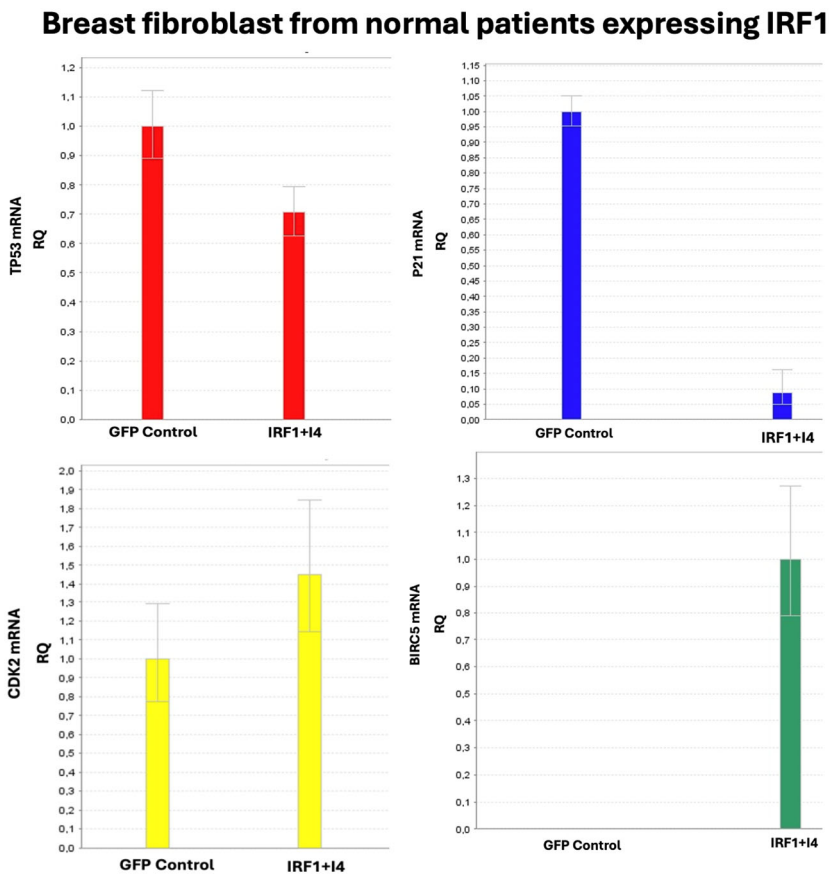

Breast fibroblast from normal patients expressing IRF1+I4
TP53 mRNA RQ
GFP Control
IRF1+I4
P21 mRNA RQ
GFP Control
IRF1+I4
CDK2 mRNA RQ
GFP Control
IRF1+I4
BIRC5 mRNA RQ
GFP Control
IRF1+I4

Figure S3.

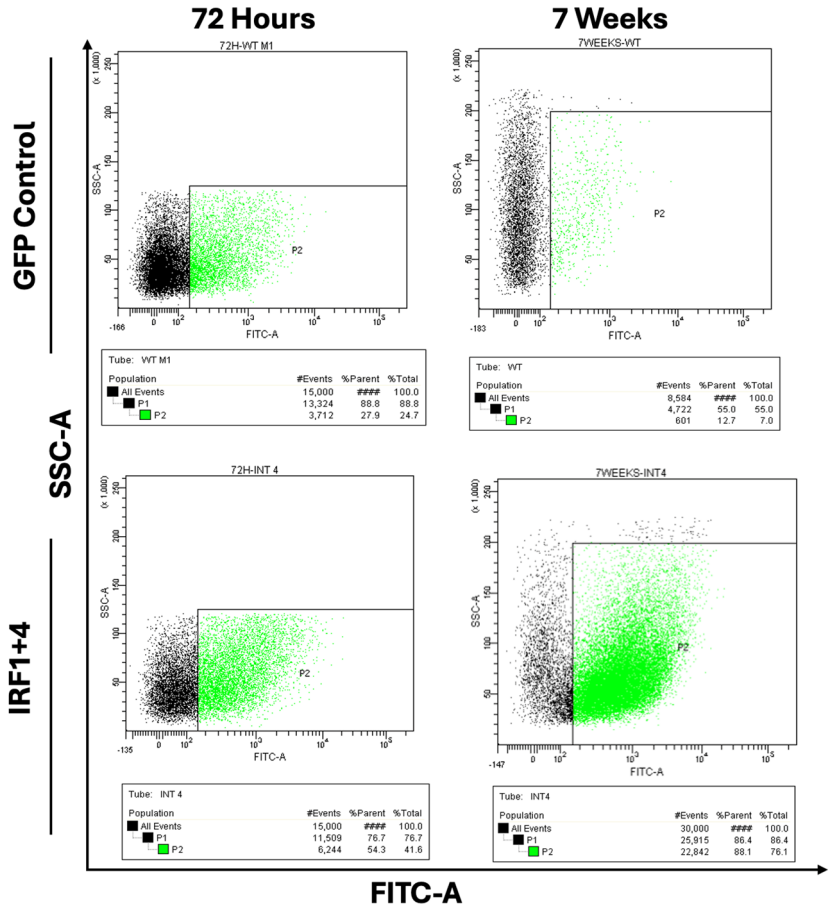
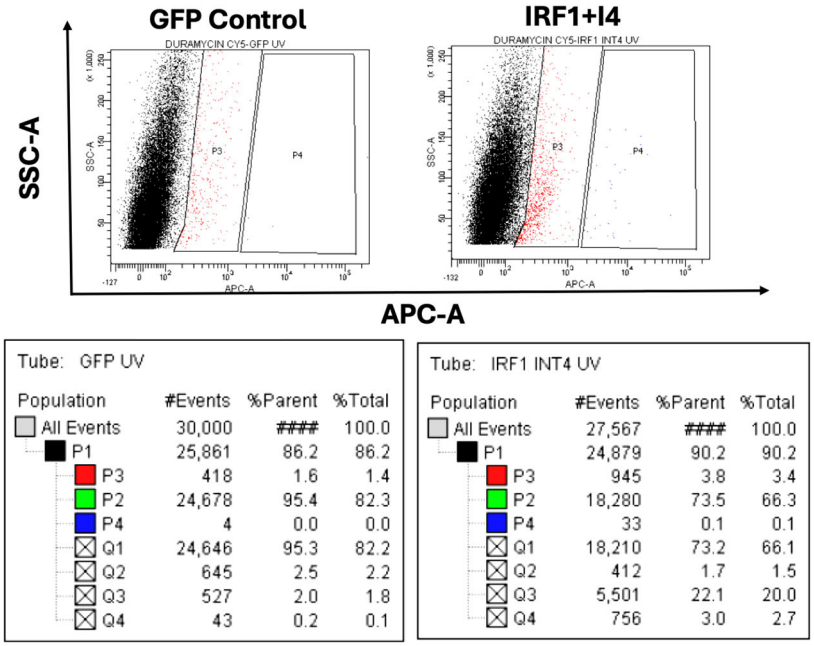


Figure S4.



Flow cytometry assay of breast fibroblast cells apoptosis induced by UV-C treatment. Cells overexpressing IRF-1 isoforms were treated with 50 J/m2 UV-C. Cy5-flurophores and Duramycin were used to measure apoptotic cells during the early stages of apoptosis. IRF-1 WT cells result to be the most affected (P3 Population).

Figure S5.

Supplementary Material - Primers for Quantitative real time PCR

Gene	Gene ID	Primer Fwd Sequence 5'→3'	Primer Rev Sequence 5'→3'
P21 (CDKN1A)	1026	TGGAGACTCTCAGGGTCGAAA	GGCGTTTGGAGTGGTAGAAATC
CDK2	1017	CCTCATCAAGAGCTATCTGTTCCA	ACCCGATGAGAATGGCAGAA
CCNE1	898	TGCGAGCAATTCTTCTGGATT	CAACATTTTCTTGTGTCGCCAT
Tp53	7157	TCAACAAGATGTTTTGCCAACTG	ATGTGCTGTGACTGCTTGTAGATG
BIRC5	332	GGACCACCGCATCTCTACAT	AGTCTGGCTCGTTCTCAGTG
HPRT1	3251	TTTGCTGACCTGCTGGATTACA	GGTCATTACAATAGCTCTTCAGTCTGAT

Supplementary Material. Patient cohort information

normal breast tissue samples (GSE235326)	(https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc= GSE19566 data subset GSE235326)					
	Age	menopause status	Tissue source	parity	Etnicity	Treatment
GSM7500385hbcac76	> 50	pre	Reduction Mammoplasty	0	caucasian	none
GSM7500386hbcac77	> 50	pre	Reduction Mammoplasty	0	caucasian	none
GSM7500417hbcac108	> 50	pre	Reduction Mammoplasty	0	caucasian	none
GSM7500426hbcac117	> 50	pre	Prophylactic Mastectomy	0	caucasian	unknown
GSM7500458hbcac149	> 50	pre	Reduction Mammoplasty	0	caucasian	none

HER2 breast cancer patient tissue samples (GSE176078)	(https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE176078)					
sample ID	Age	Cancer Grade	Cancer type	HER2	Treatment	
CID3586	43	3	IDC	3+	no	
CID3838	49	3	IDC	3+	no	
CID3921	60	3	IDC	3+	no	
CID4066	41	3	IDC	3+	no	
CID45171	58	3	IDC	3+	no	

A. Tissue samples ID and clinical metadata of the samples selected for this stufdy from the 126 breast samples included in the breast atlas project. The columns list the age of the women, the menopause status (pre/post), the procedure from which the tissue source was collected (reduction mammoplastiesor prophylactic mastectomies), the parity status as positive (1) or negative (0), the ethnicity , whether the woman received any prior treatment before the tissue was collected.

B tissue samples ID and clinical metadata of the samples selected in this stufdy from the 26 primary tumors included in the breast cancer atlas project. The columns list the age of the women, the grade of the tumors , the cancer type, the HER2 degree, whether the woman received any prior treatment before the tissue was collected.