

Supplementary Table S1. Time point-based Comparison of SDTGs ($p < 0.05$ and $FC \geq 2$) distribution among sublethal IR doses

Time point	Union	Common in all Doses	Dose-unique (comparison of BSDs only)		
			1Gy	3Gy	6Gy
2h	394	58 14.72%	117 29.69%	23 5.83%	58 14.72%
d4	459	48 10.45%	159 34.64%	19 4.13%	137 29.84%
d7	455	26 5.71%	42 9.23%	9 1.97%	287 63.07%
d21	314	5 1.47%	47 14.96%	76 24.20%	118 37.57%
d28	322	19 5.90%	21 6.52%	66 20.49%	112 34.78%

Supplementary Table S2. Top SDTGs in BLD with an average fold change regulation larger than ten (Ave $FC > 10$ and $p < 0.05$) in all time points.

Symbol	Entrez Gene Name	Fold change (FC)			Location	Function
		h2	d4	d7		
Ctla2a/Ctla2b	cytotoxic T lymphocyte-associated protein 2 alpha	9.981	14.219	14.814	Plasma Membrane	other
S100A9	S100 calcium binding protein A9	7.161	11.249	12.778	Cytoplasm	other
TMEM37*	transmembrane protein 37	9.533	10.832	10.335	Plasma Membrane	ion channel
COL3A1*	collagen type III alpha 1 chain	-31.753	-26.584	-47.74	Extracellular Space	other
COL1A1	collagen type I alpha 1 chain	-24.315	-23.331	-35.277	Extracellular Space	other
COL1A2*	collagen type I alpha 2 chain	-22.209	-20.323	-31.159	Extracellular Space	other
FA2H	fatty acid 2-hydroxylase	-20.851	-16.568	-23.311	Cytoplasm	enzyme
Mup1 (includes others)	major urinary protein 1	-17.097	-15.839	-20.242	Extracellular Space	other
DHCR24	24-dehydrocholesterol reductase	-14.088	-12.843	-14.346	Cytoplasm	enzyme
KRT1	keratin 1	-12.075	-11.79	-14.346	Cytoplasm	other
LUM	lumican	-12.706	-9.105	-13.944	Extracellular Space	other
RNASE2	ribonuclease A family member 2	-11.398	-10.353	-12.541	Cytoplasm	enzyme
KRT79	keratin 79	-11.132	-10.281	-10.57	Extracellular Space	other
CIDEA	cell death inducing DFFA like effector a	-11.378	-9.54	-10.169	Cytoplasm	other
MGLL	monoglyceride lipase	-9.456	-9.85	-11.687	Plasma Membrane	enzyme
KRT75*	keratin 75	-10.52	-9.371	-10.211	Cytoplasm	other

*Denote genes that are unique to the 20Gy lethal dose (i.e., not significantly differentially regulated in any sublethal doses).

Supplementary Figure S1. Significantly ($\text{Abs } z\text{-score} \geq 2$ and $-\log p \geq 1.3$) modulated pathways in at least one time point from the analysis of SDTGs ($p \leq 0.05$ and $\text{Abs FC} \geq 2$) at h2, d4, and d7 TPs in lethal (20Gy) and sublethal IR doses (1, 3, 6Gy). Color of squares ranges according to modulation intensity from dark blue for inactivation to dark red for activation prediction based on z-score values.

