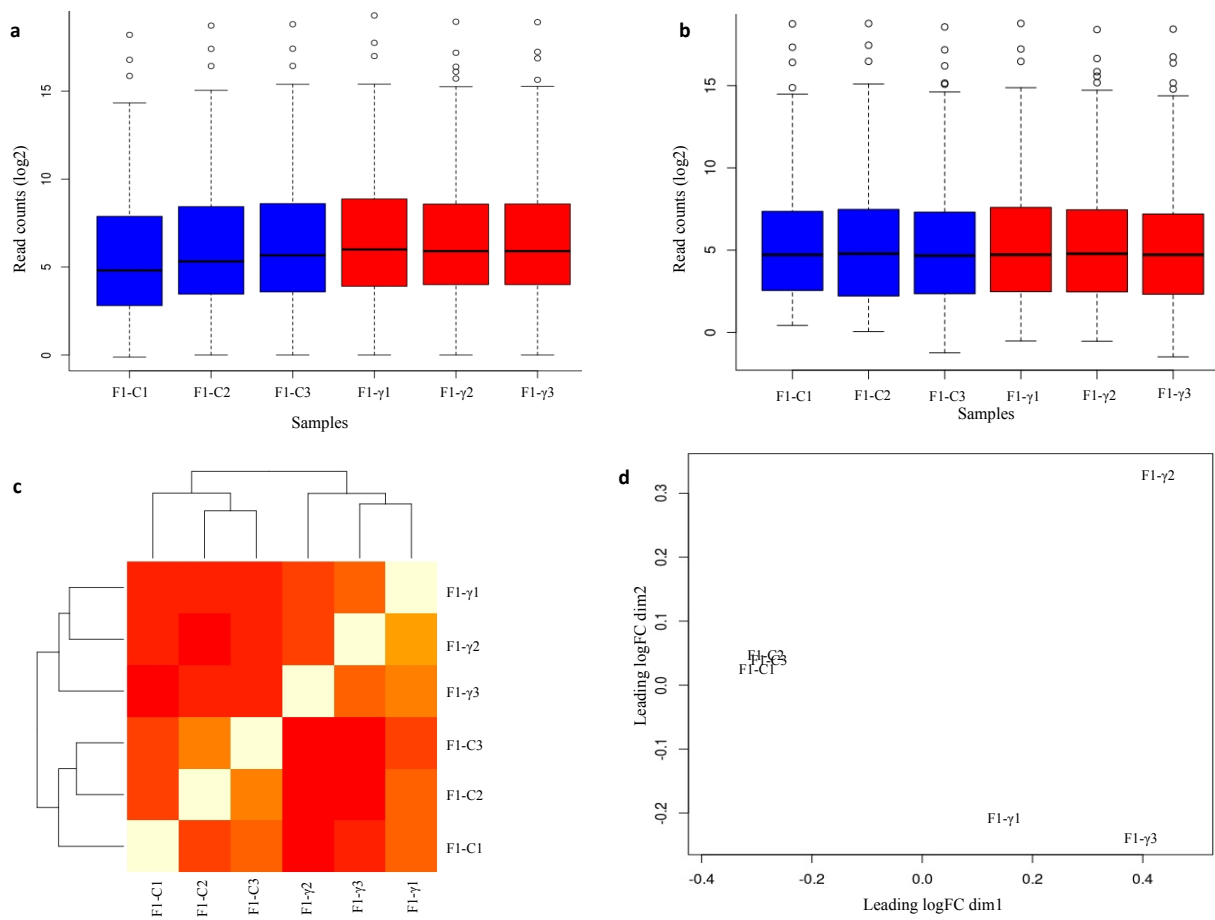
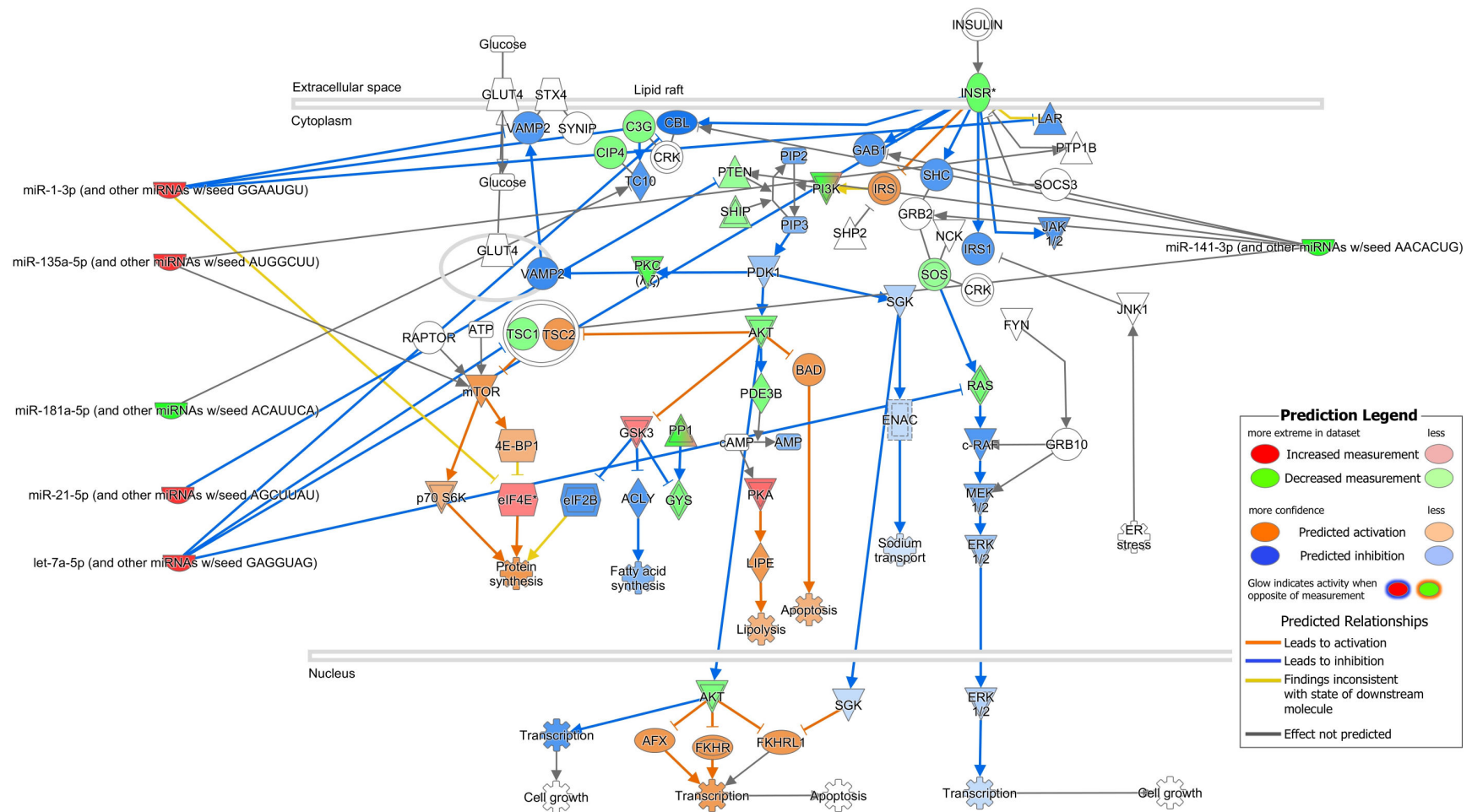


Altered non-coding RNA expression profile in F₁ progeny one year after parental irradiation is linked to adverse effects in zebrafish

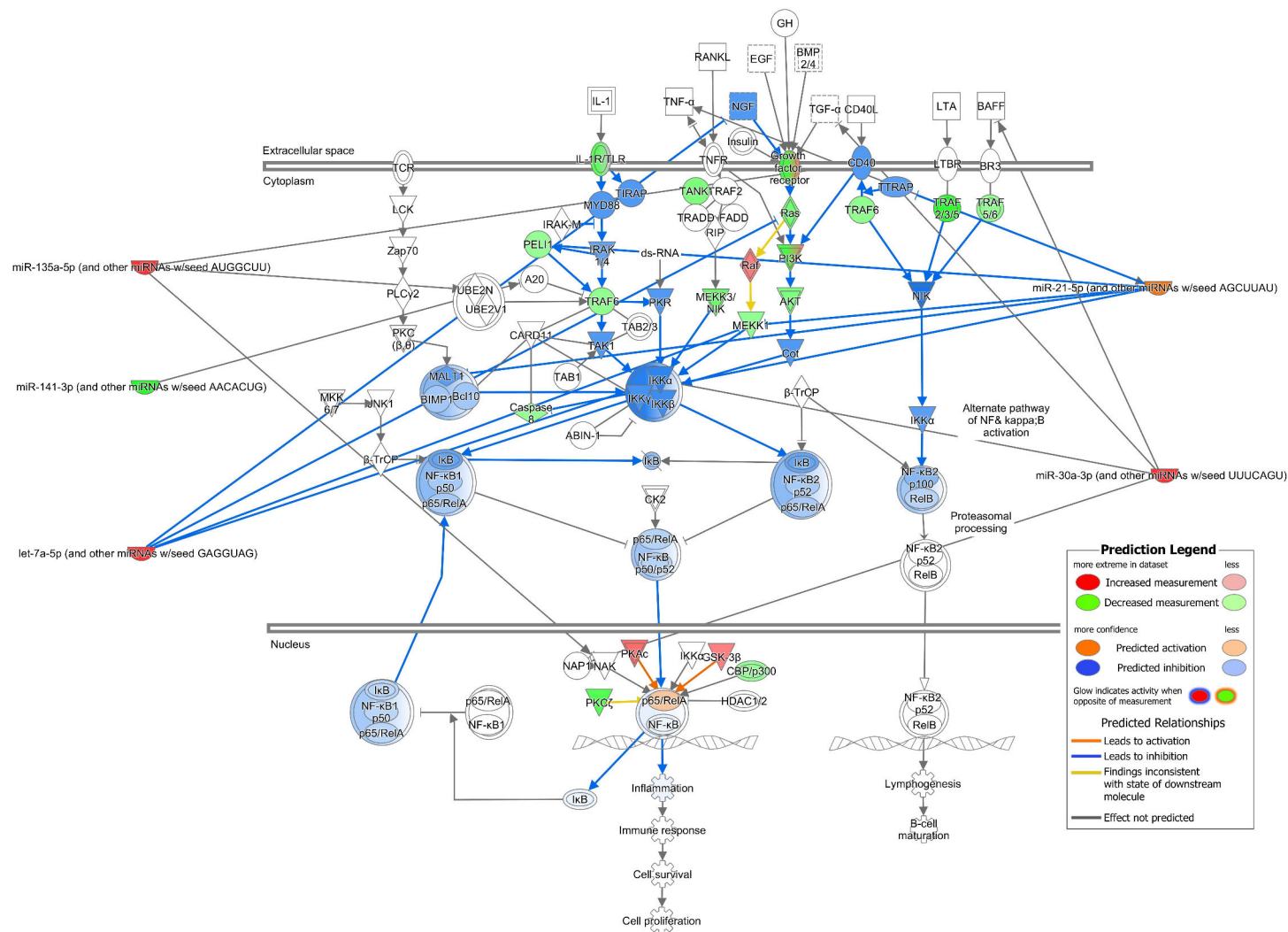
Leonardo Martín, Jorke H Kamstra, Selma Hurem, Leif C Lindeman, Dag A Brede, Håvard Aanes, Igor Babiak, Amilcar Arenal, Deborah Oughton, Brit Salbu, Jan Ludvig Lyche, Peter Aleström.



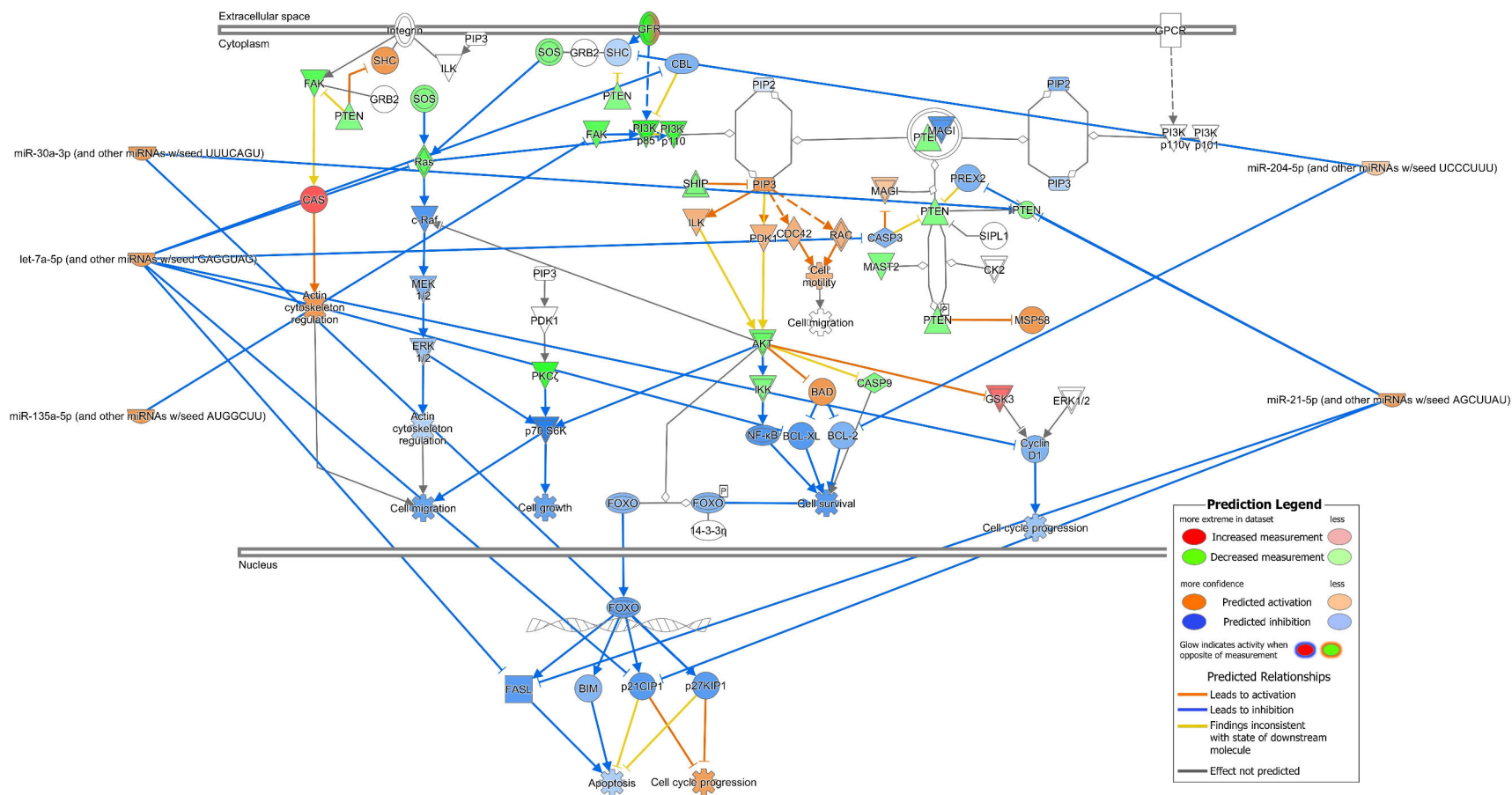
Supplementary Figure S1. Statistical exploration of miRNA expression dataset in generation F₁ from parents exposed to 8.7 mGy/h γ -radiation (F₁- γ) and F₁ from control parents (F₁-C) (n = 3). Median comparison before normalization A). After TMM normalization: Median comparison B). Heatmap of Pearson's correlation coefficient C), and Multidimensional scaling plot D).



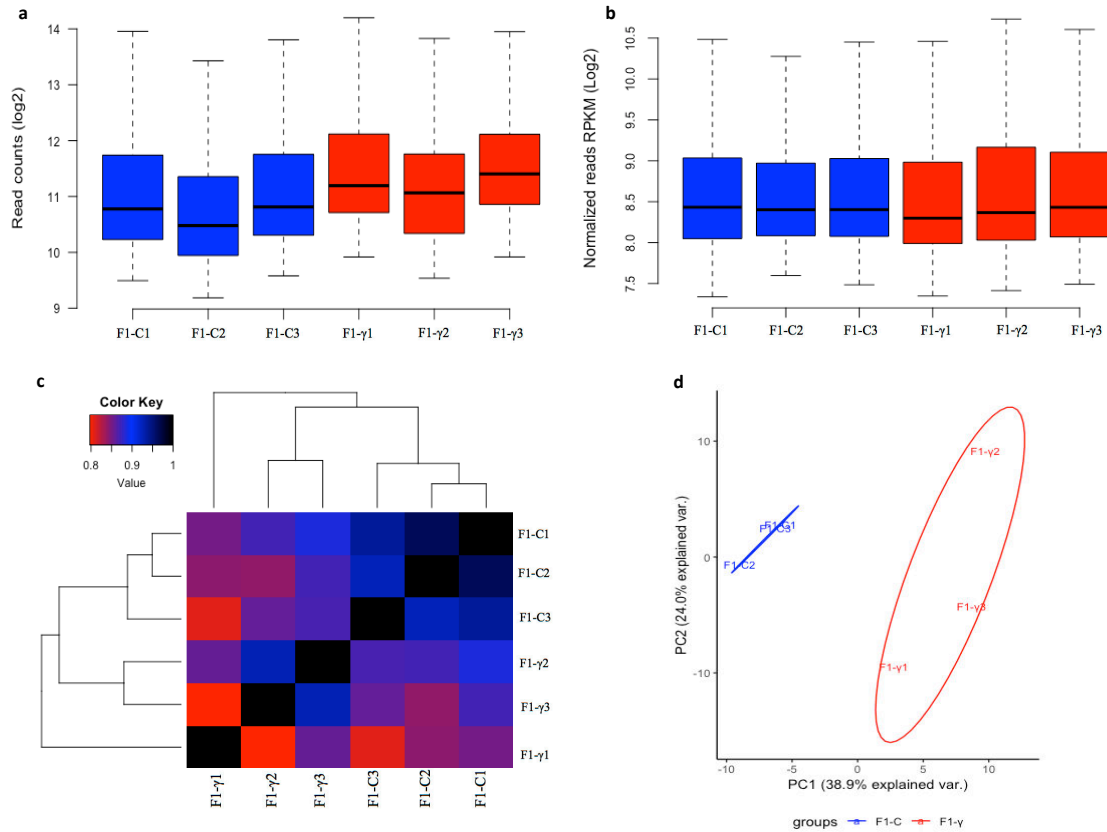
Supplementary Figure S2: Pathway analysis including molecule activity prediction, showing the insulin receptor-signaling pathway, with added miRNAs involved in the different nodes.



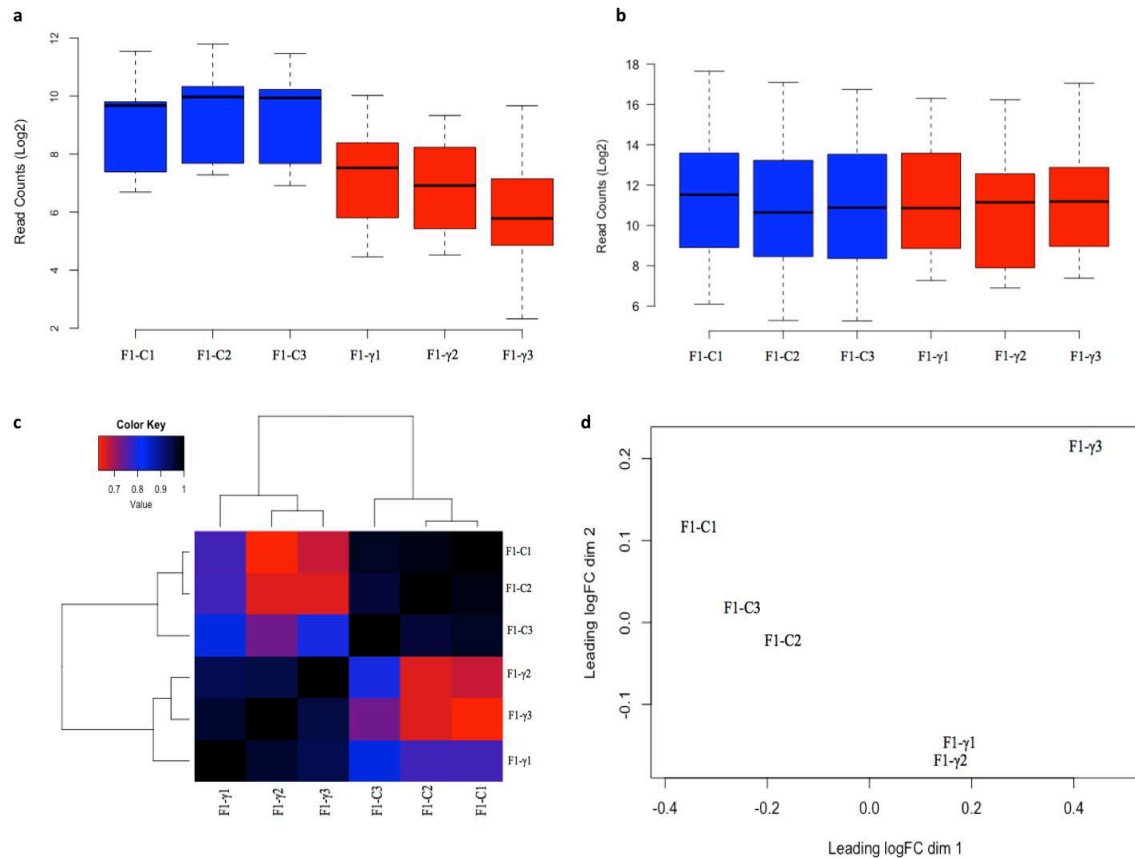
Supplementary Figure S3: Pathway analysis including molecule activity prediction, showing the NFκB signaling pathway, with added miRNAs involved in the different nodes.



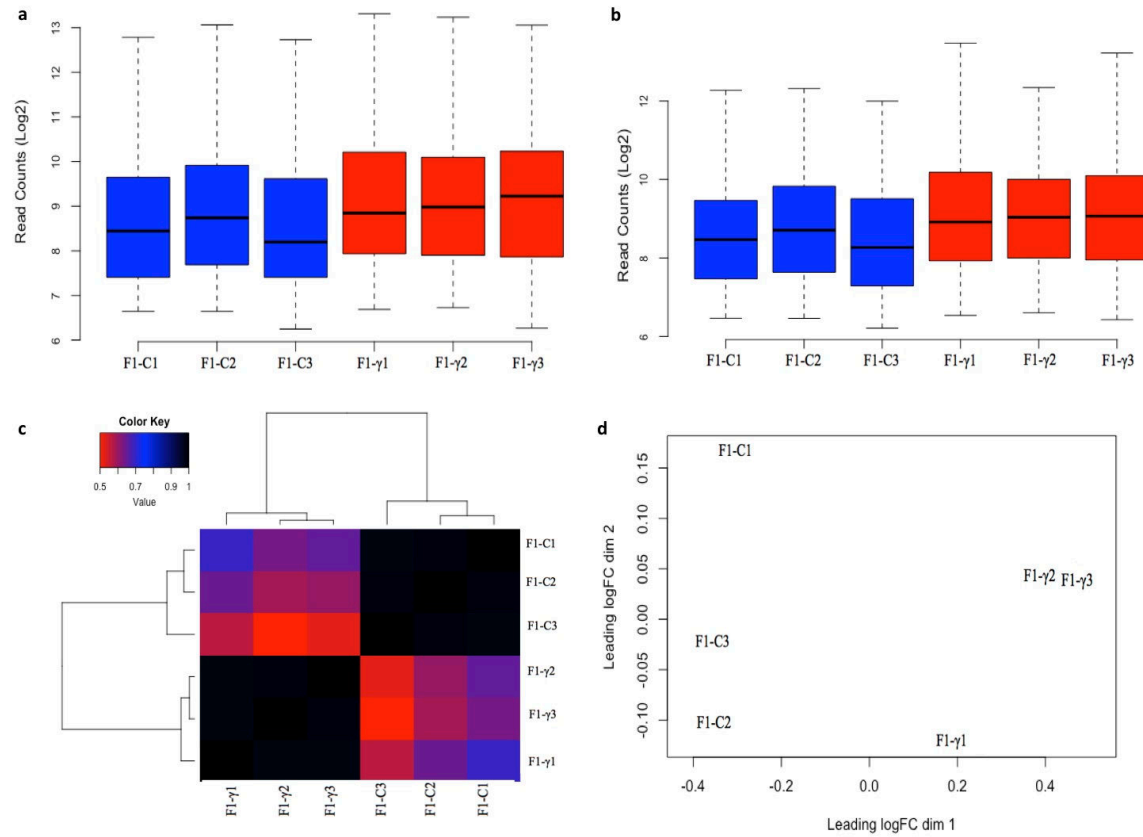
Supplementary Figure S4: Pathway analysis including molecule activity prediction, showing the PTEN signaling pathway, with added miRNAs involved in the different nodes.



Supplementary Figure S5. Statistical exploration of piRNA clusters expression in generation F₁ from parents exposed to 8.7 mGy/h γ -radiation (F₁- γ) and F₁ from control parents (F₁-C) (n = 3). A) Median comparison before normalization. After RPKM normalization: Median comparison (B). Heatmap of Pearson's correlation coefficient (C), and Principal Component Analysis (D).



Supplementary Figure S6. Statistical exploration of snRNA expression in generation F_1 from parents exposed to 8.7 mGy/h γ -radiation (F_1 - γ) and F_1 from control parents (F_1 -C) ($n = 3$). A) Median comparison before normalization. After TMM normalization: Median comparison (B). Heatmap of Pearson's correlation coefficient (C), Multi-dimensional scaling plot (D).



Supplementary Figure S7. Statistical exploration of lincRNA expression in generation F₁ from parents exposed to 8.7 mGy/h γ -radiation (F₁- γ) and F₁ from control parents (F₁-C) (n = 3). A) Median comparison before normalization. After TMM normalization: Median comparison (B). Heatmap of Pearson's correlation coefficient (C), Multi-dimensional scaling plot (D).

<i>miRNA Details</i>			
Name:	hsa-let-7g-5p		
Sequence:	ugagguaguaguuuuguacaguu		
MirBase ID:	MIMAT0000414 ↗		
Related Diseases:	↗		
Binding Category	Transcript Position	Binding Score	Conservation
6mer	4980-4997	0.002	4 ^
Position on chromosome:	11:65502740-65502758		
Conserved Species:	panTro2,rheMac2,canFam2,monDom5		
Binding area:	AGGCAGAAA AGAUAU UUUGAUG G AUGUCA AUGGAG U C		

<i>miRNA Details</i>			
Name:	hsa-miR-21-5p		
Sequence:	uagcuuauacagacugauguuga		
MirBase ID:	MIMAT0000076 ↗		
Related Diseases:	↗		
Binding Category	Transcript Position	Binding Score	Conservation
7mer	1113-1132	0.005	2 ^
Position on chromosome:	11:65498873-65498893		
Conserved Species:	panTro2,rheMac2		
Binding area:	UGUAGUUU GCAUU UGUAG U CA UCAG AC CC AUAAGCUG U		

Supplementary Figure S8. Predicted interaction of hsa-let-7g-5p (top) and hsa-miR-21-5p (bottom) orthologs of dre-let-7g-5p and dre-miR-21-1-3p respectively, with MALAT1 (ENST00000534336). DIANA-lncBase (v2).