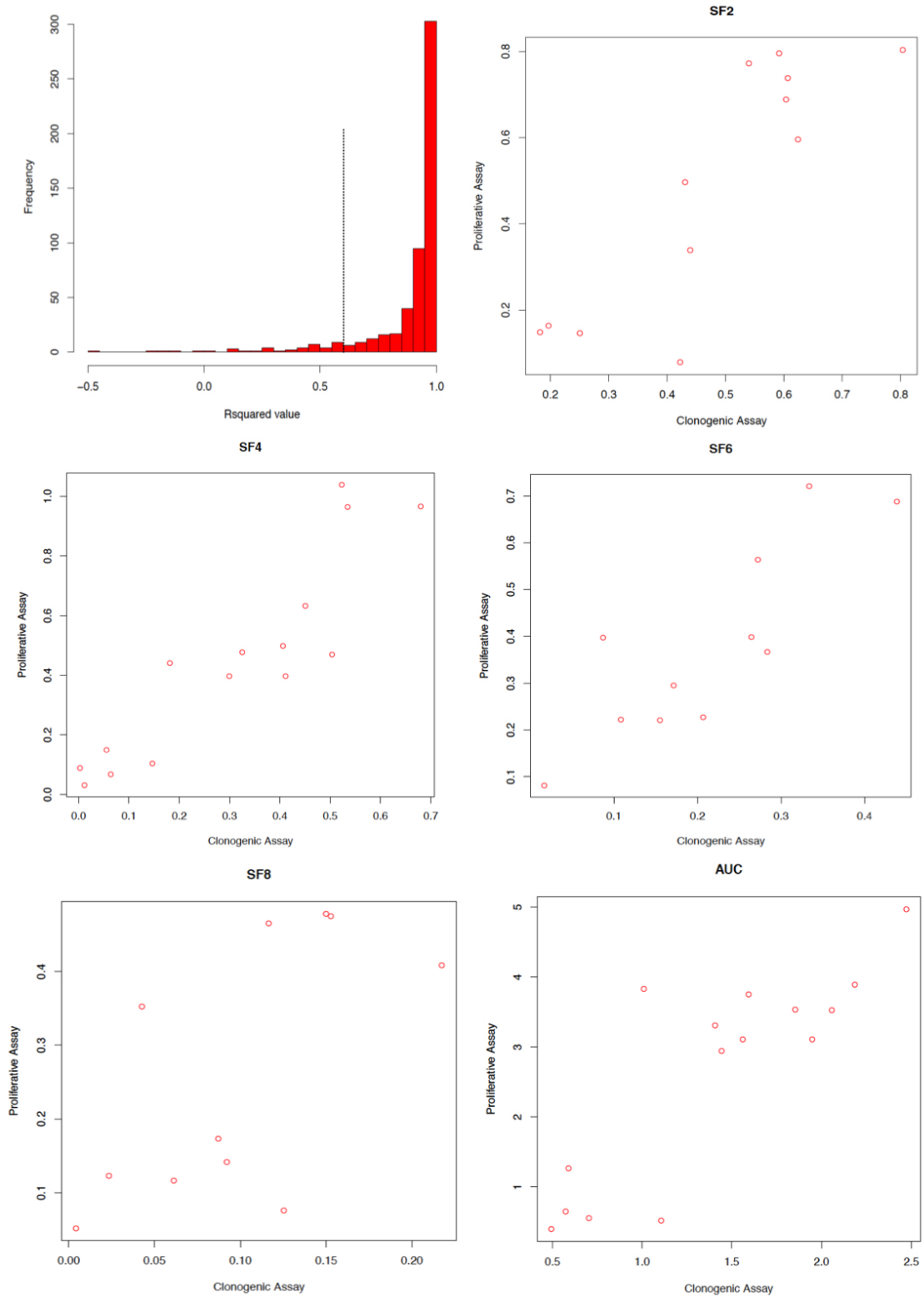


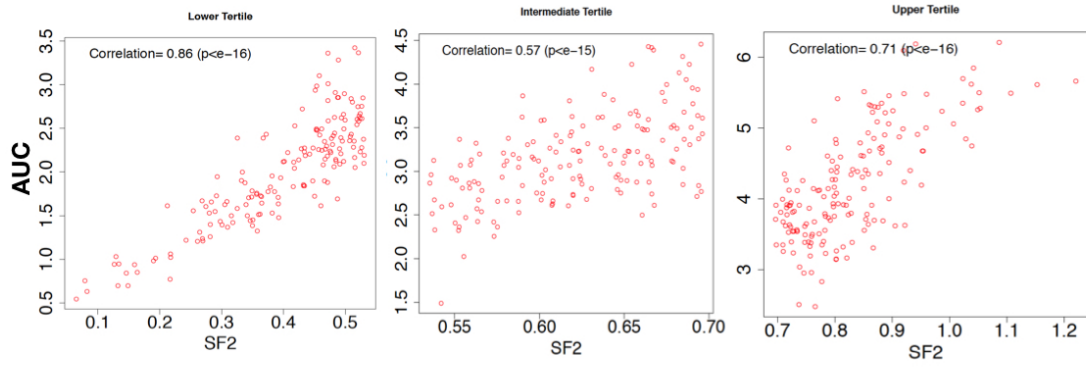
Supplementary Figure 1: Design of RadioGx platform.

Supplementary Figure 2: Comparison of cancer cell line survival following ionizing radiation using the clonogenic assay vs. the 9-day viability (proliferative) assay published by Yard et al. (2016).

Goodness of fit by the LQ model

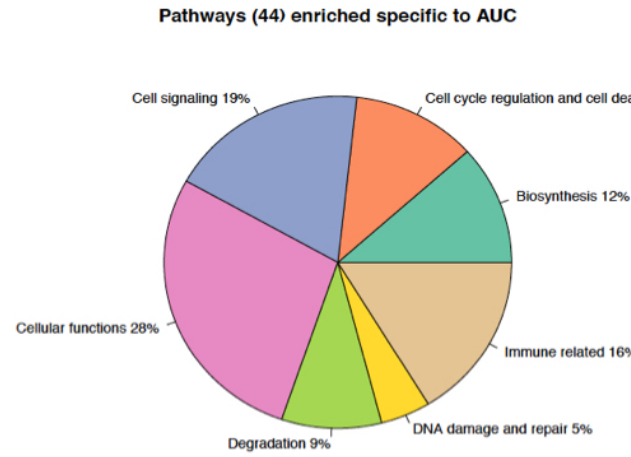
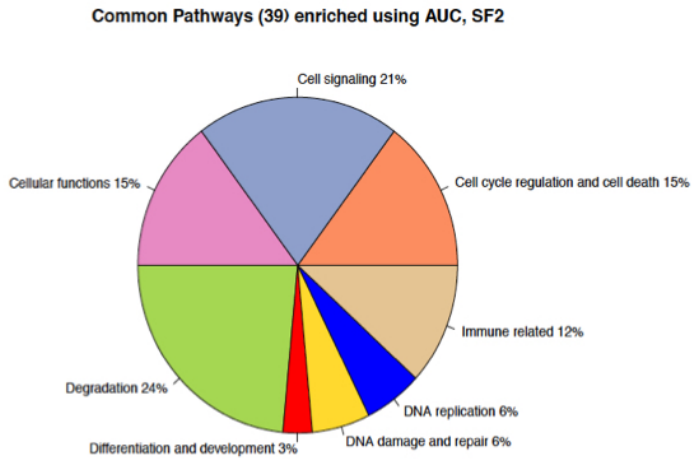


SF2 vs. AUC based on Tertiles

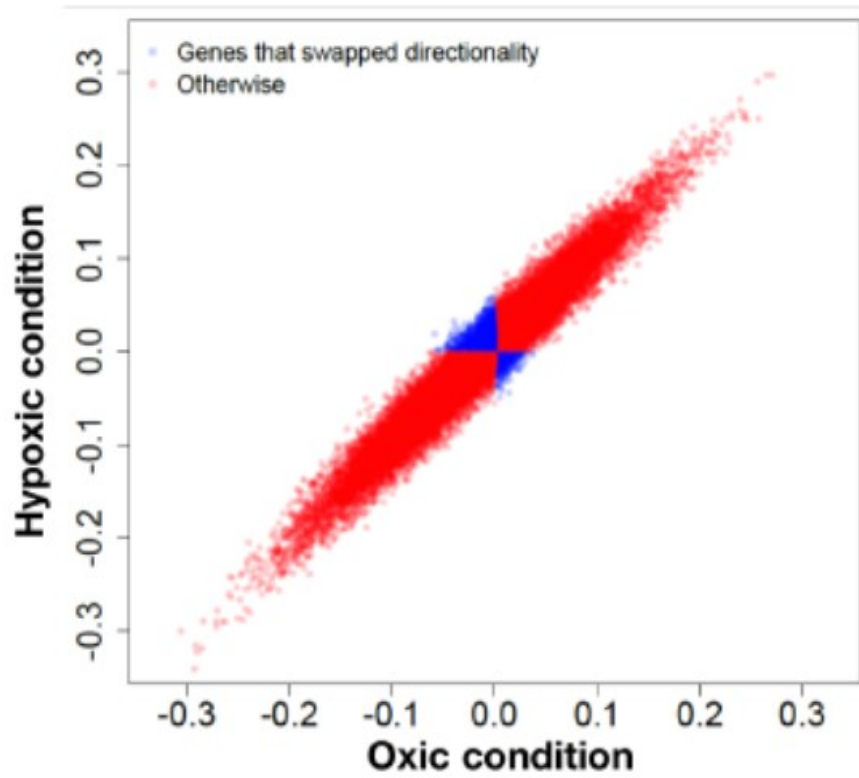


Supplementary Figure 3: Comparison of SF2 and AUC based on tertiles.

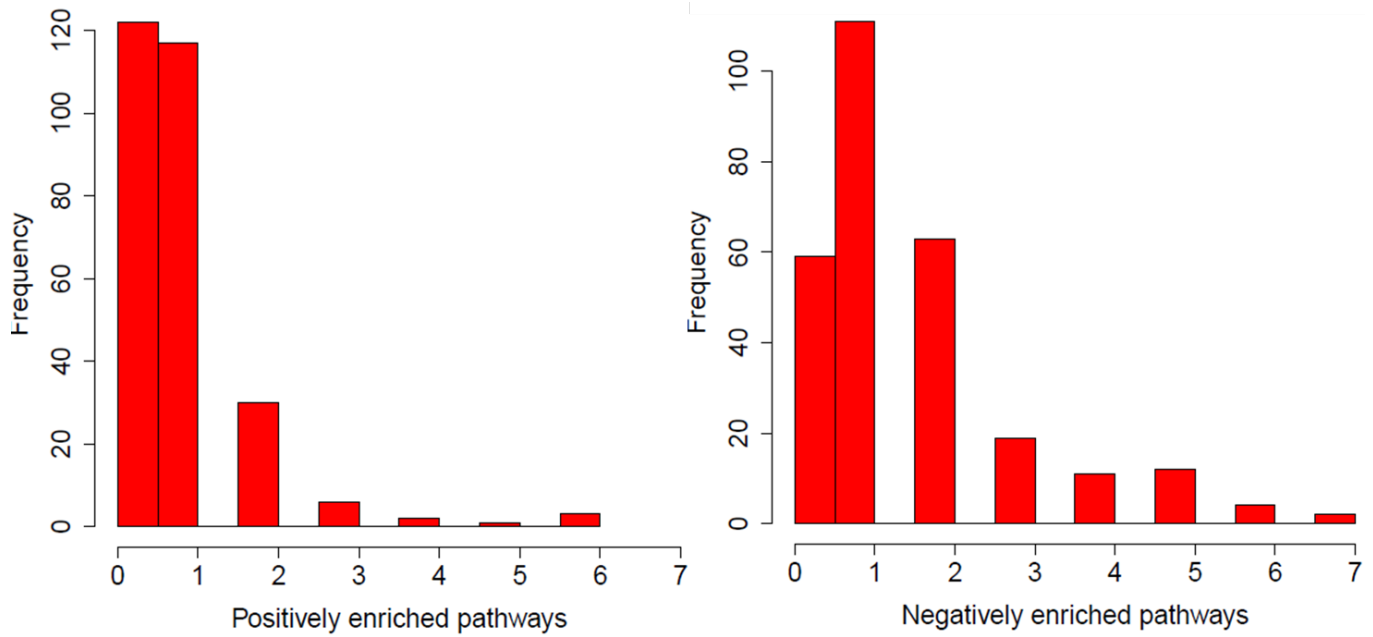
**Pathways: SF2 vs. AUC**



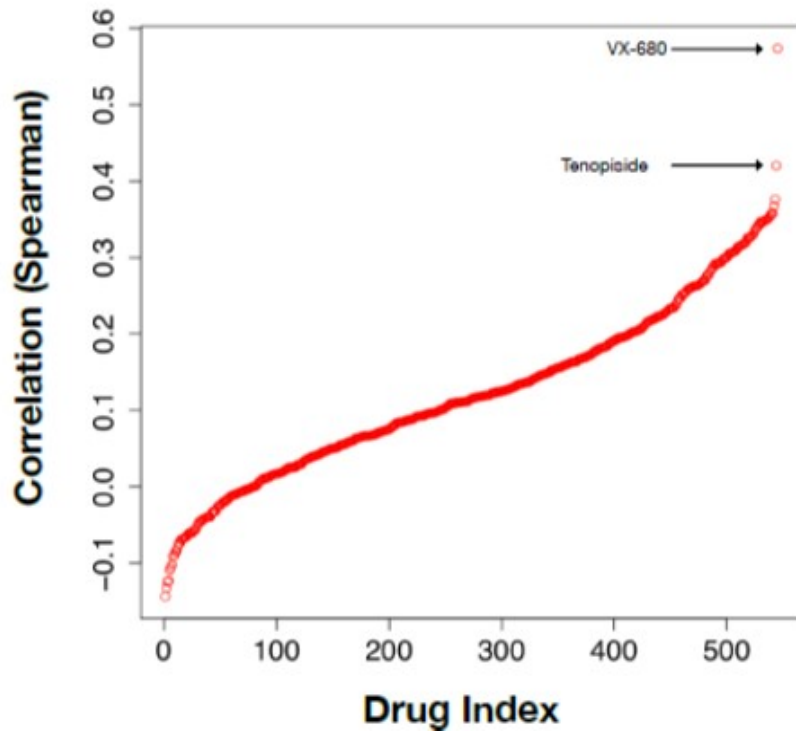
Supplementary Figure 4: Pathway analysis comparison: SF2 vs. AUC.



Supplementary Figure 5: Univariate correlation between radiation response associated genes under oxic and modeled hypoxic conditions.

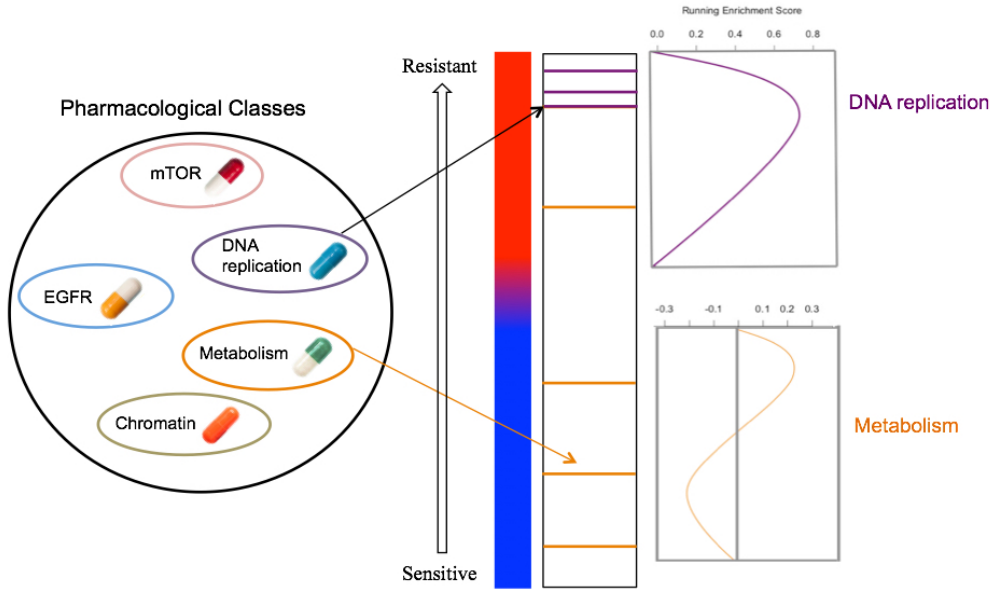


Supplementary Figure 6: The tumour types (n=12) represented by a minimum of 15 cell lines were considered for analysis. A total of 281 pathways are enriched for  $FDR < 5\%$ . Number of positively and negatively enriched pathways in each tissue.



Supplementary Figure 7: Replication of Figure 1 from Yard et al 2016, demonstrating the correlation between drug response and radiation response. Figure produced using RadioGx package.

PCL Enrichment Analysis Methodology



Supplementary Figure 8: Methodology for pharmacological enrichment analysis.