



Irradiation triggers molecular and transcriptional shifts in tumor endothelial cells, supporting their activation and enhancing immune response

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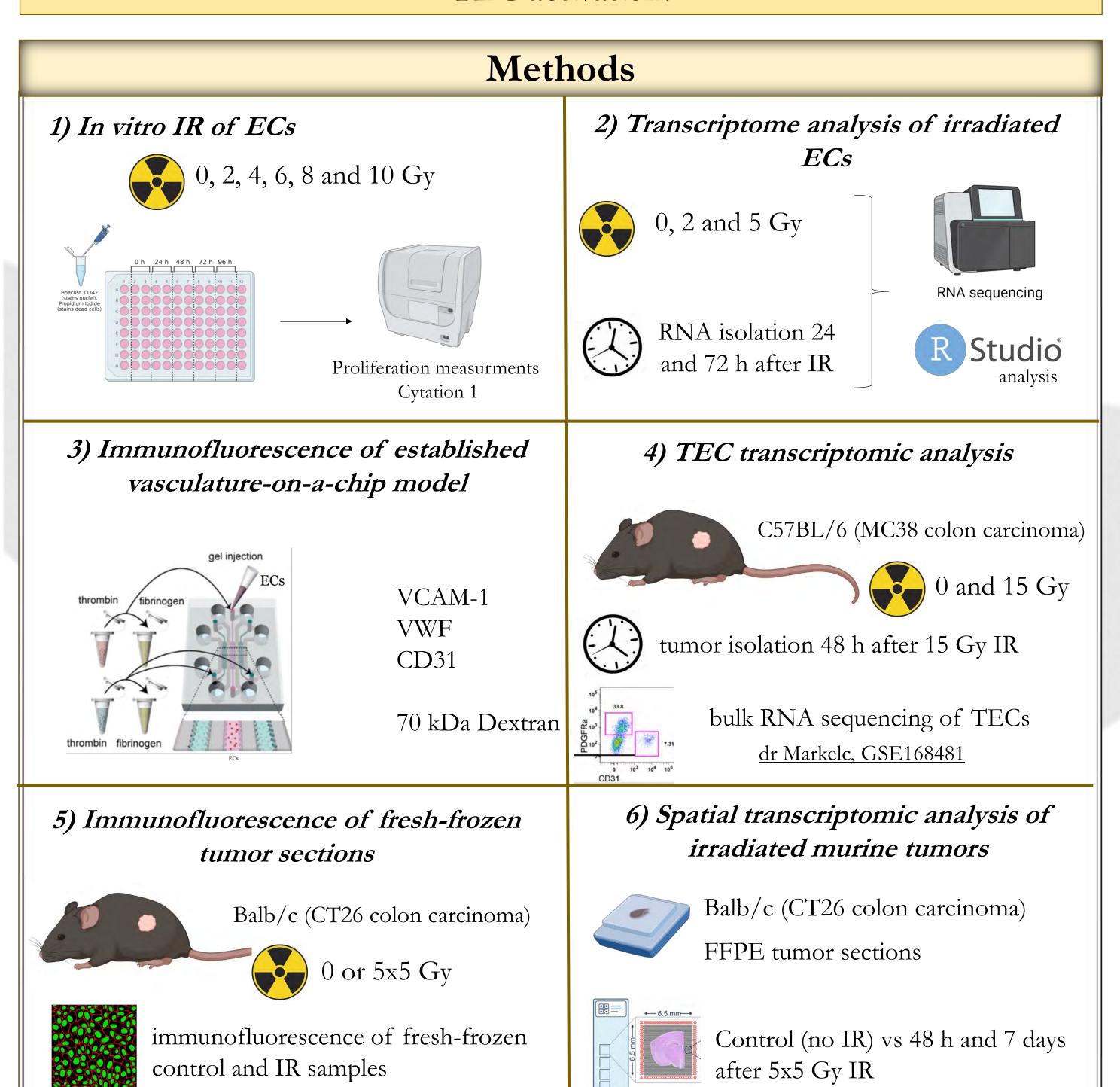
Background

Abnormal tumor vasculature is marked by inadequate blood flow and oxygen delivery, causing the formation of hypoxic areas, resistant to radiotherapy (RT). Irradiation (IR) affects not only cancer cells but also the tumor microenvironment, including tumor blood vessels. Intriguingly, besides triggering apoptosis of tumor endothelial cells (TECs), IR can also lead to vascular normalization/remodeling or TEC activation, potentially alleviating immune cell infiltration. However, the role of IR-induced alterations of tumor vasculature and TECs on the tumor response to RT remains poorly understood.

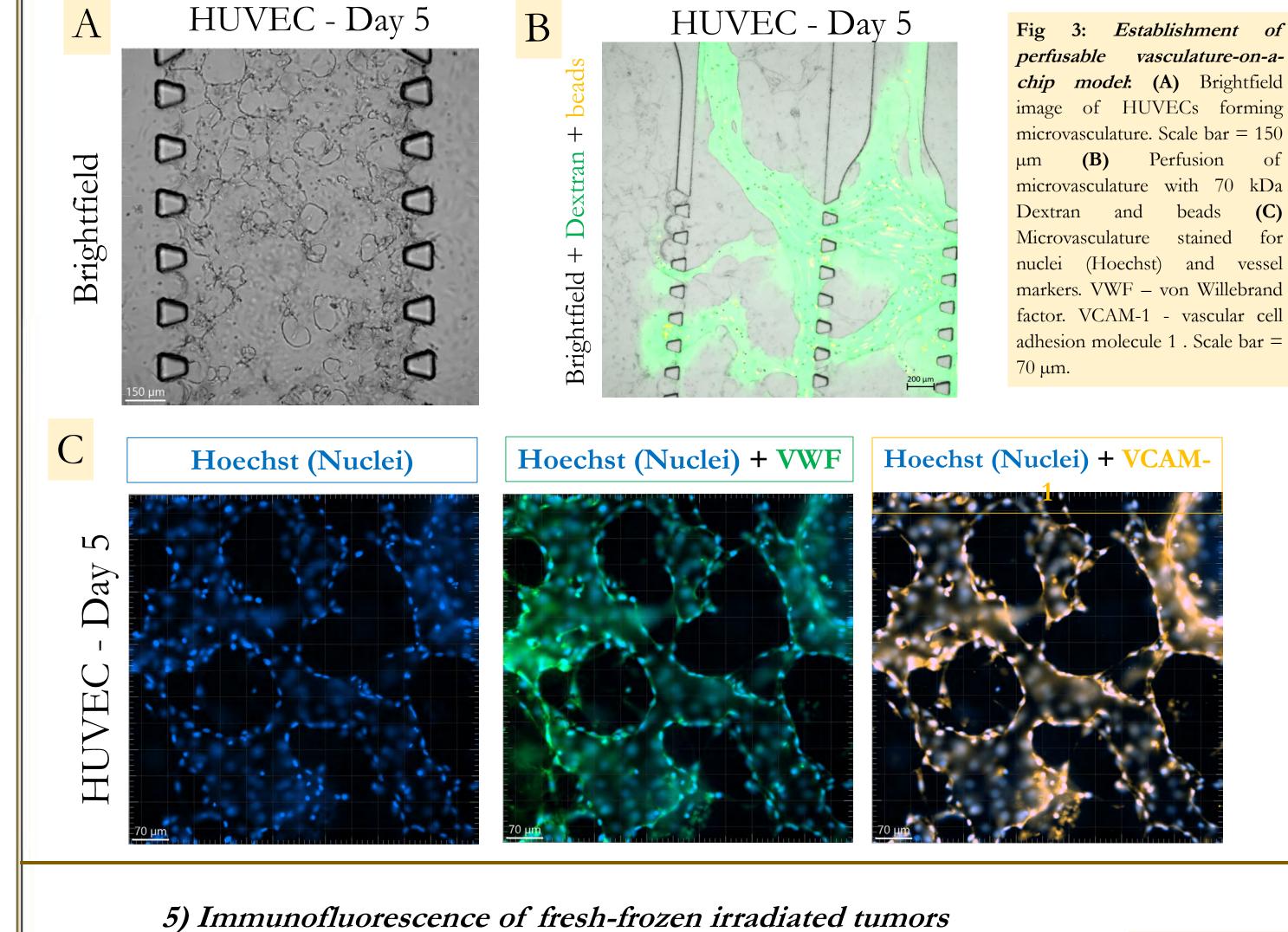
Irradiation:

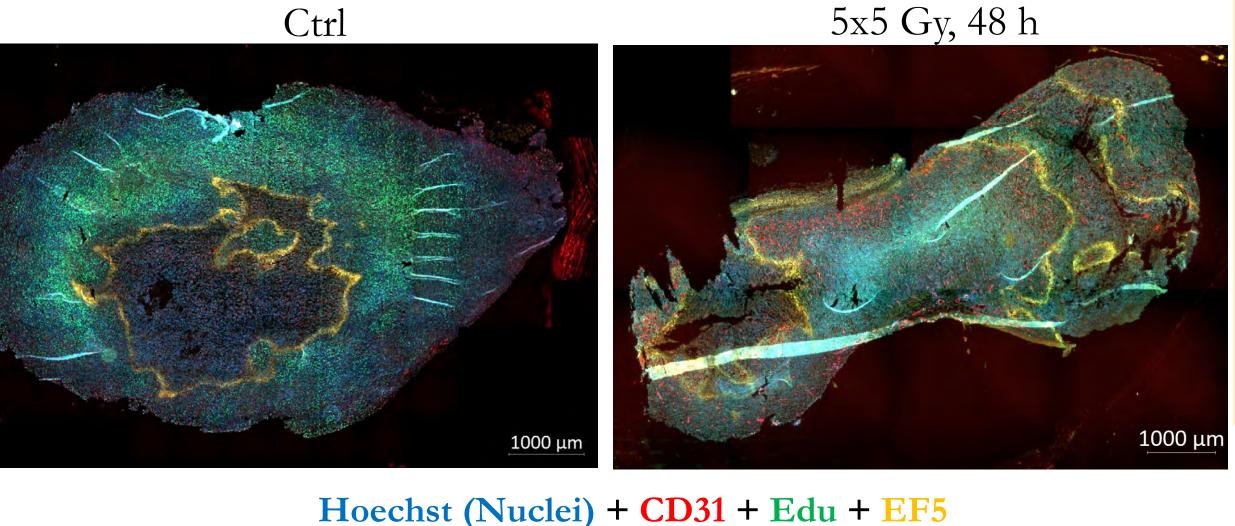
Aim

To clarify how vasculature responds to IR, focusing on its remodeling and TEC activation.



3) Immunofluorescence of established vasculature-on-a-chip





for hypoxia Scale bar

proliferation marker, EF5

molecule-1, NTAN1 - N-

terminal asparagine amidase,

differentiation 8

reduces EC proliferation and survival

alters TEC gene expression and usage of pathways, supporting TEC activation and augmented anti-tumor immune response

Conclusions

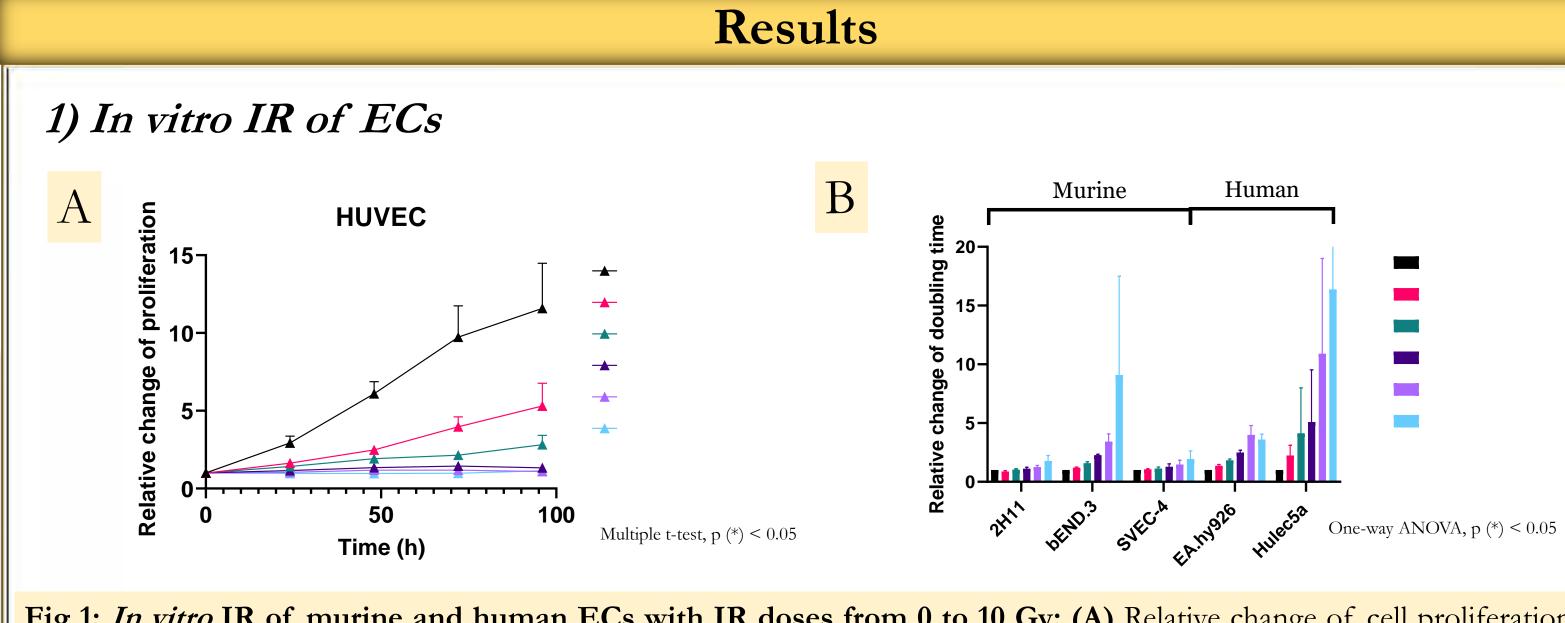
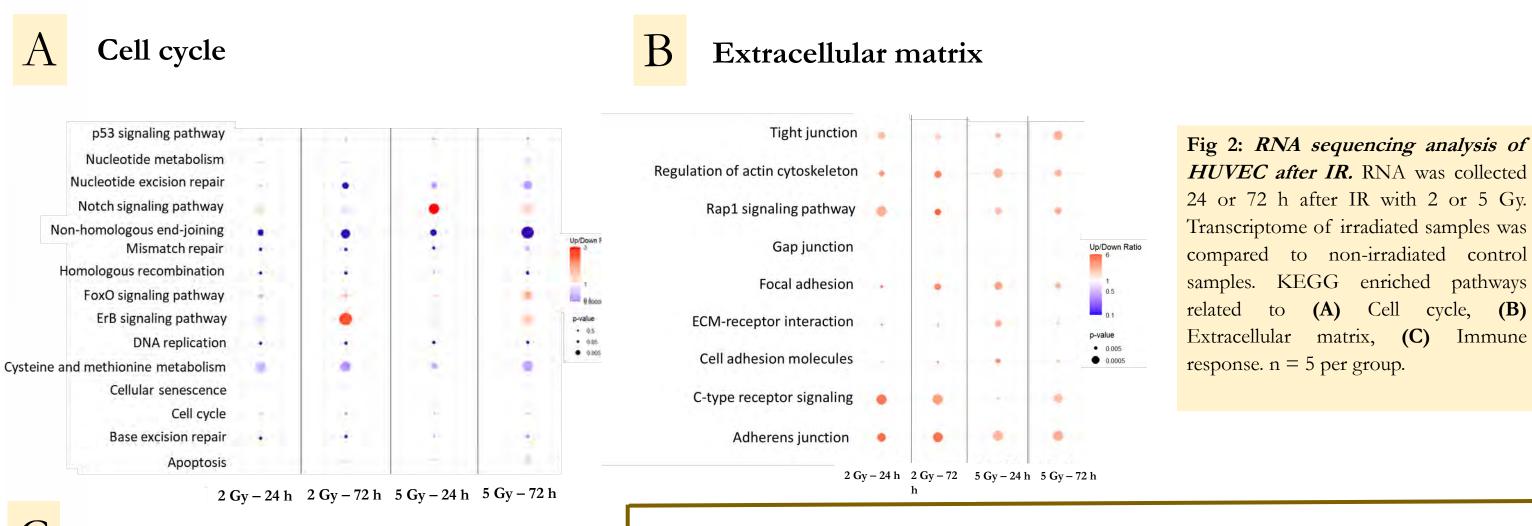
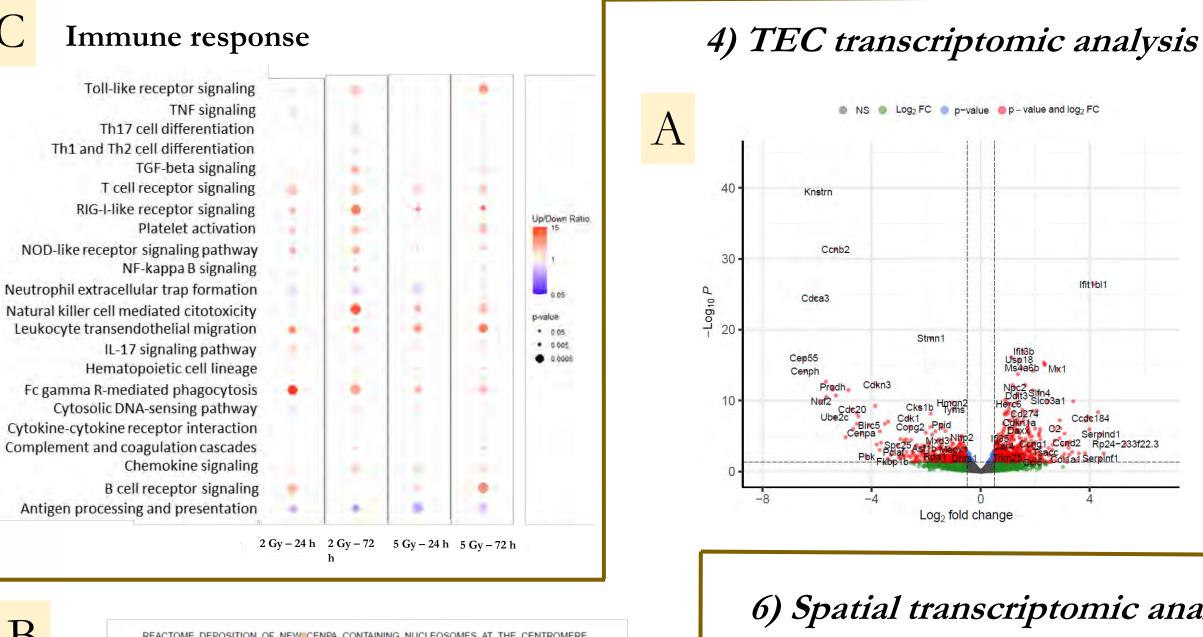


Fig 1: In vitro IR of murine and human ECs with IR doses from 0 to 10 Gy: (A) Relative change of cell proliferation of human endothelial cell line HUVEC. (B) Relative change of doubling time after IR.

2) Transcriptome analysis of irradiated ECs in vitro





■ CHST4+ ■ GLYCAM1+ ■ NTAN1+

analysis of TECs isolated from MC38 tumor, 48 h after IR with 15 Gy: (A) Differential gene analysis. significantly up-regulated and 236 significantly down-regulated genes. P-value < 0.05 and \log_2 fold change > |0.5| considered as significance limits (B) Gene set enrichment analysis (GSEA). Immune response-related upregulated and cell cycle-related down-regulated pathways. Adjusted P-value < 0.05 was considered as significance limit. n = 5 per group.

Fig 4: Bulk RNA sequencing

