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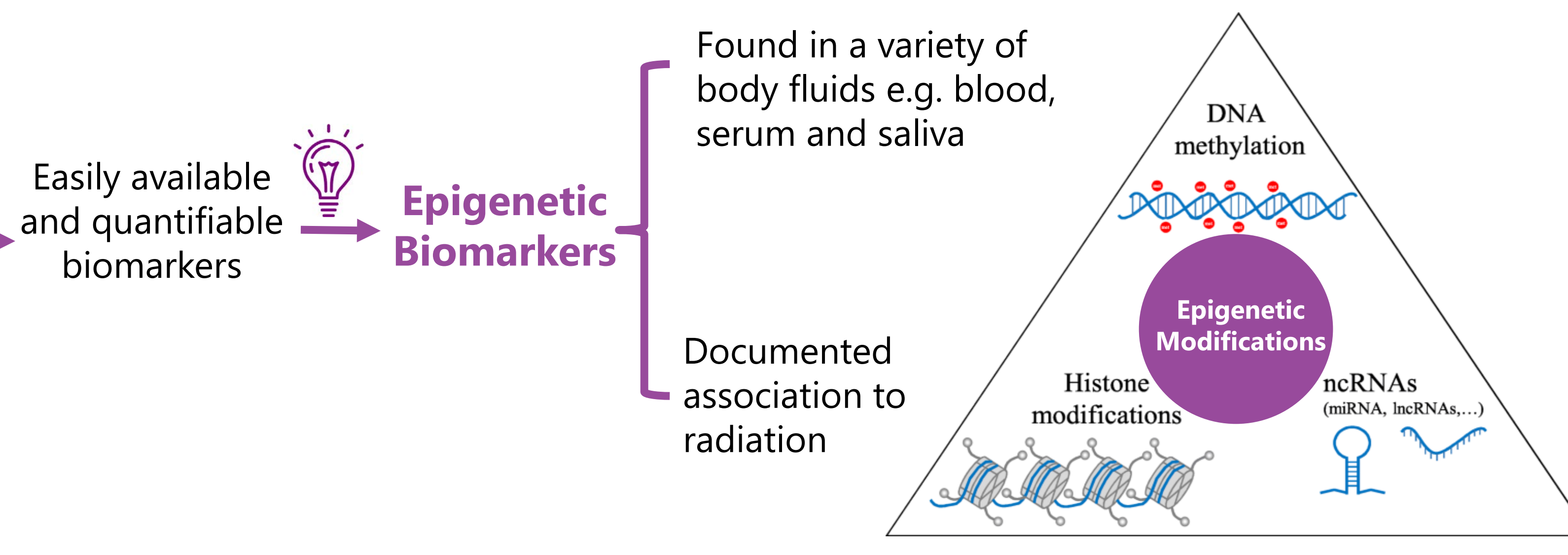
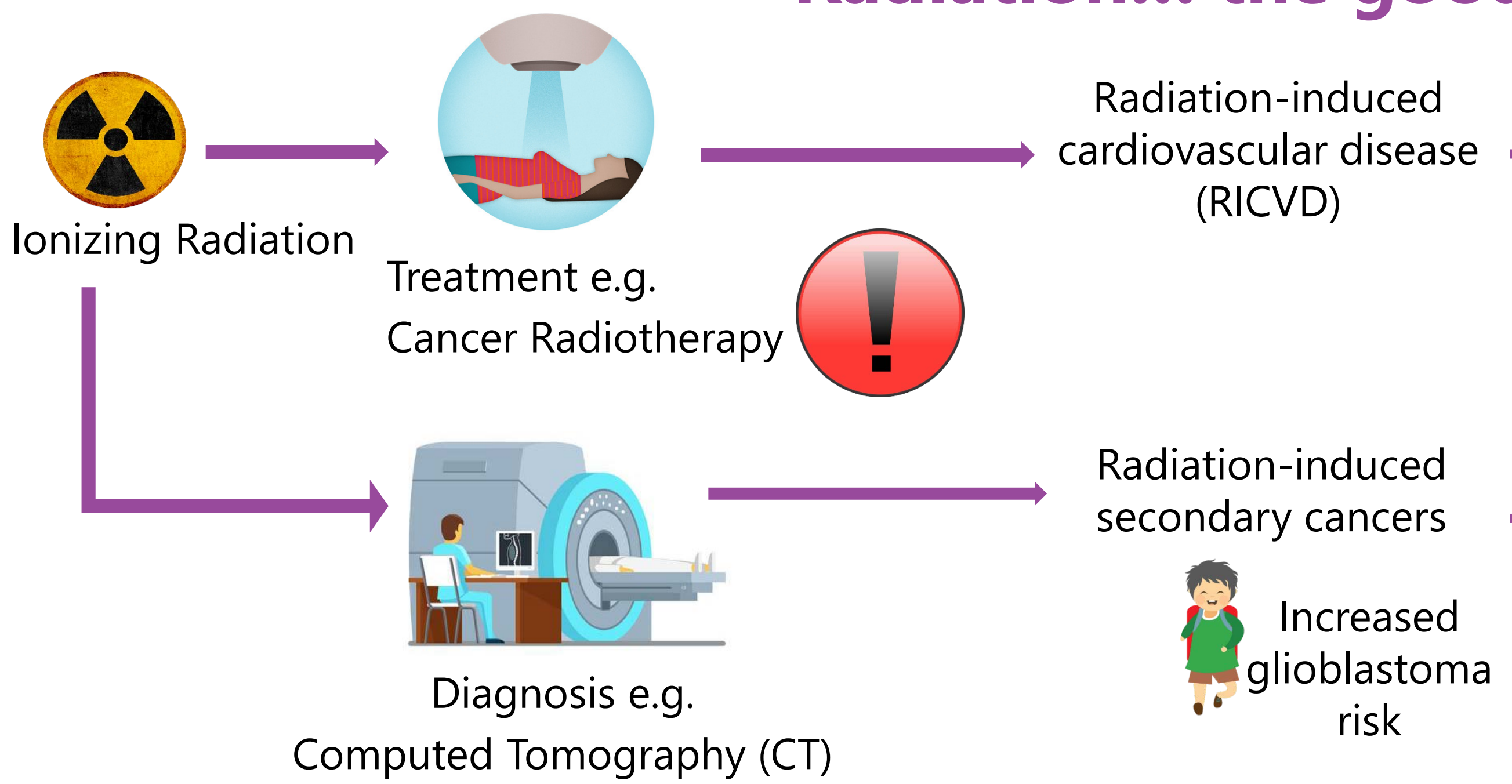
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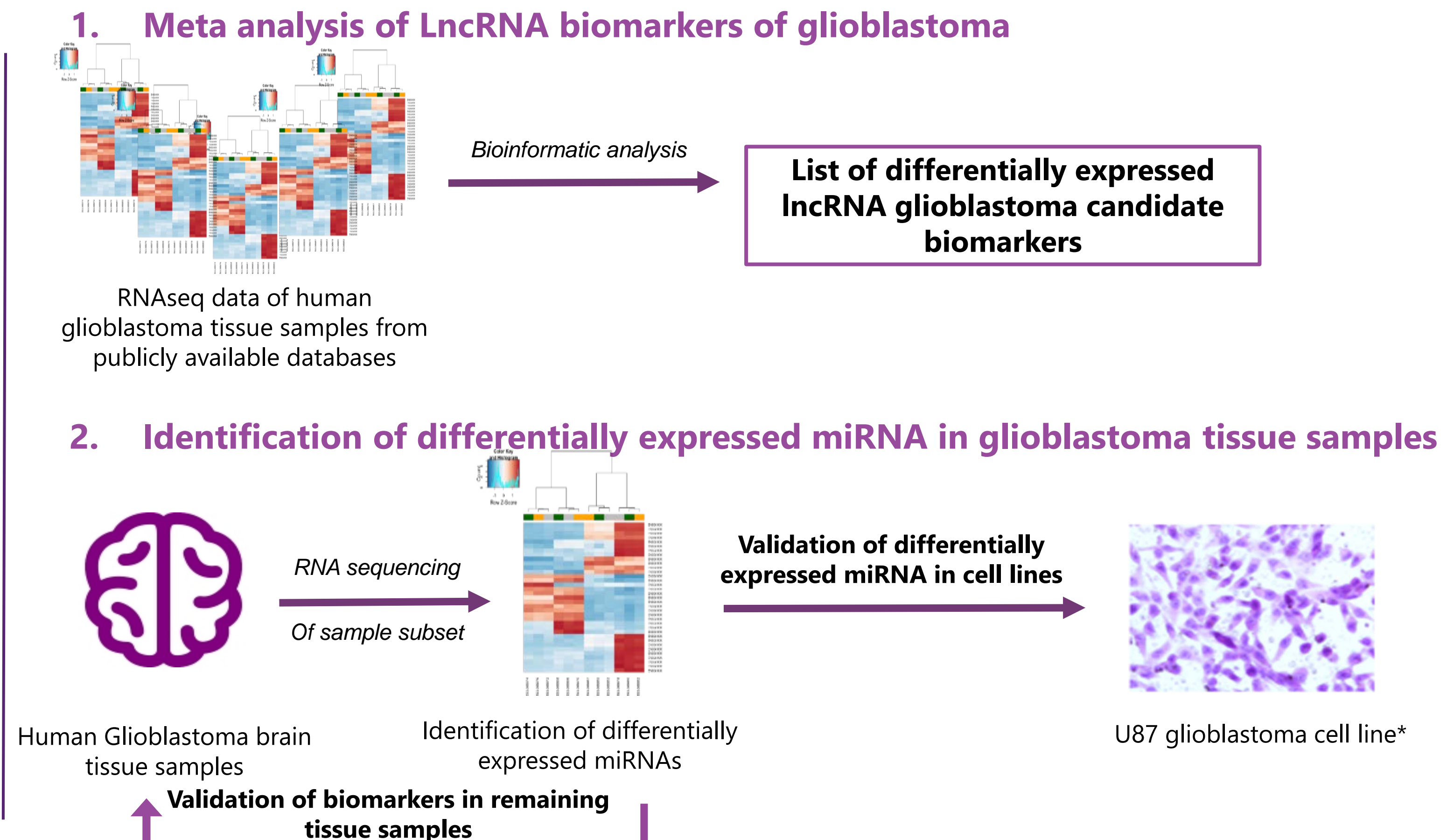
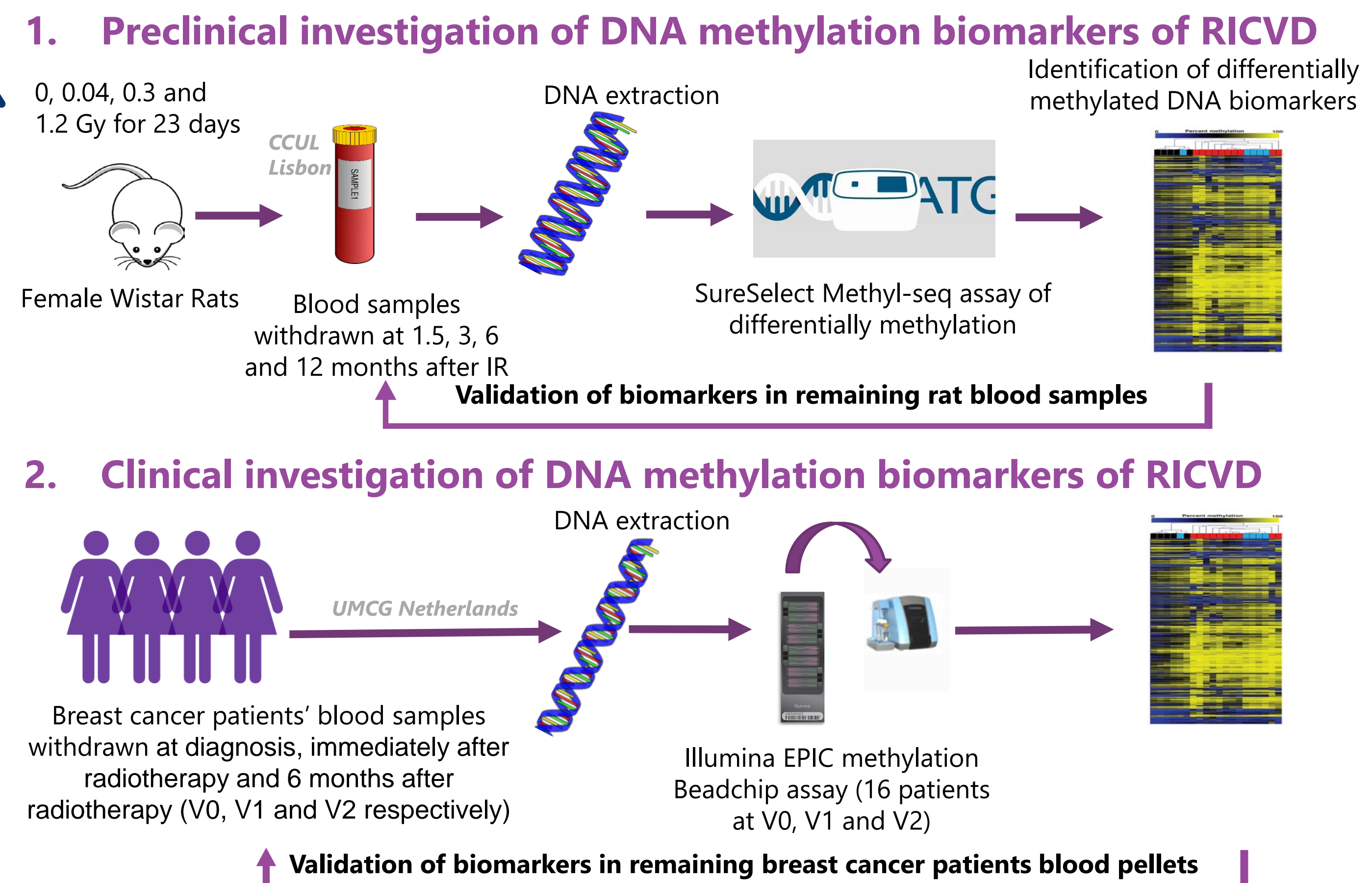
## Radiation... the good, the bad and the epigenetics



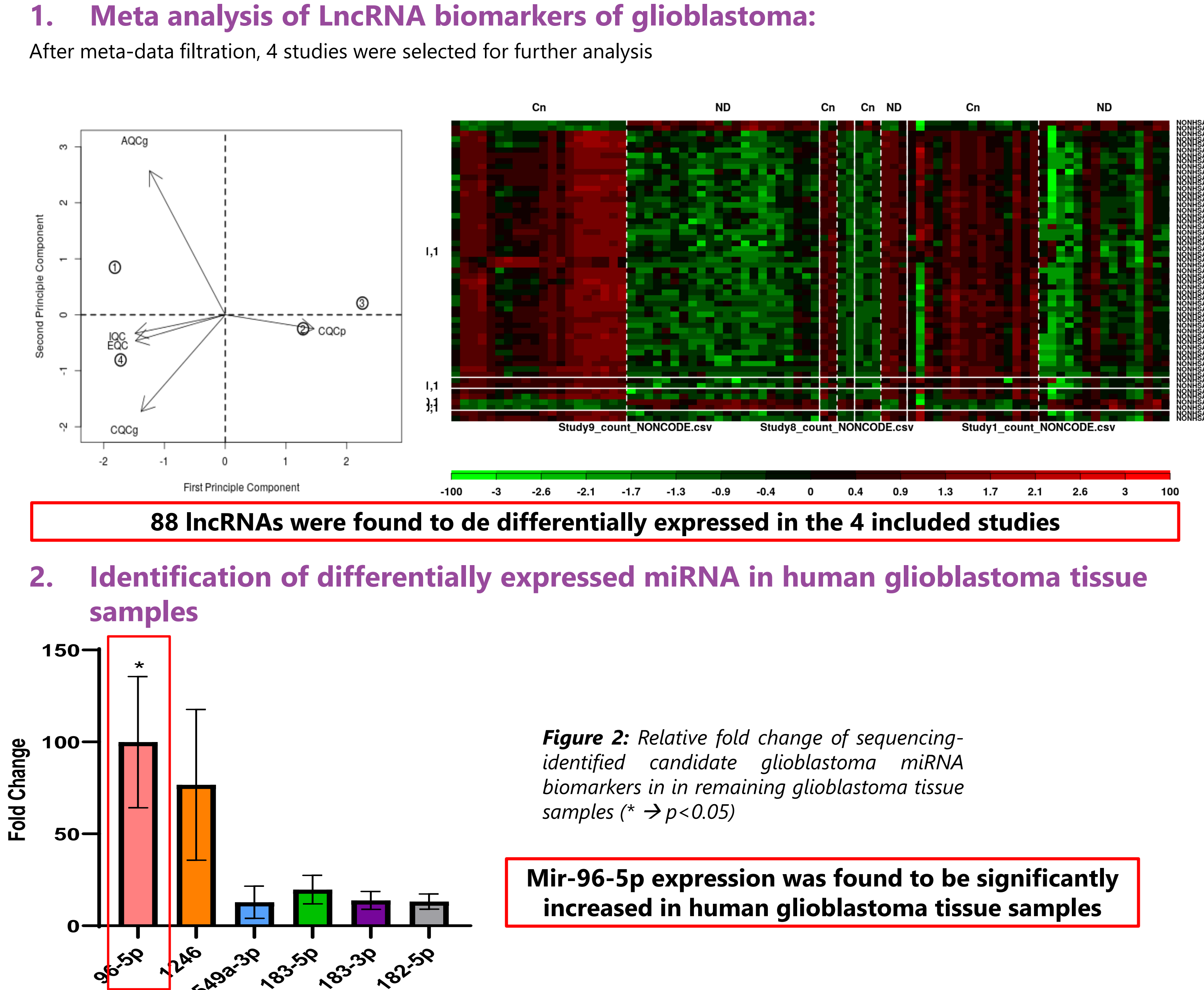
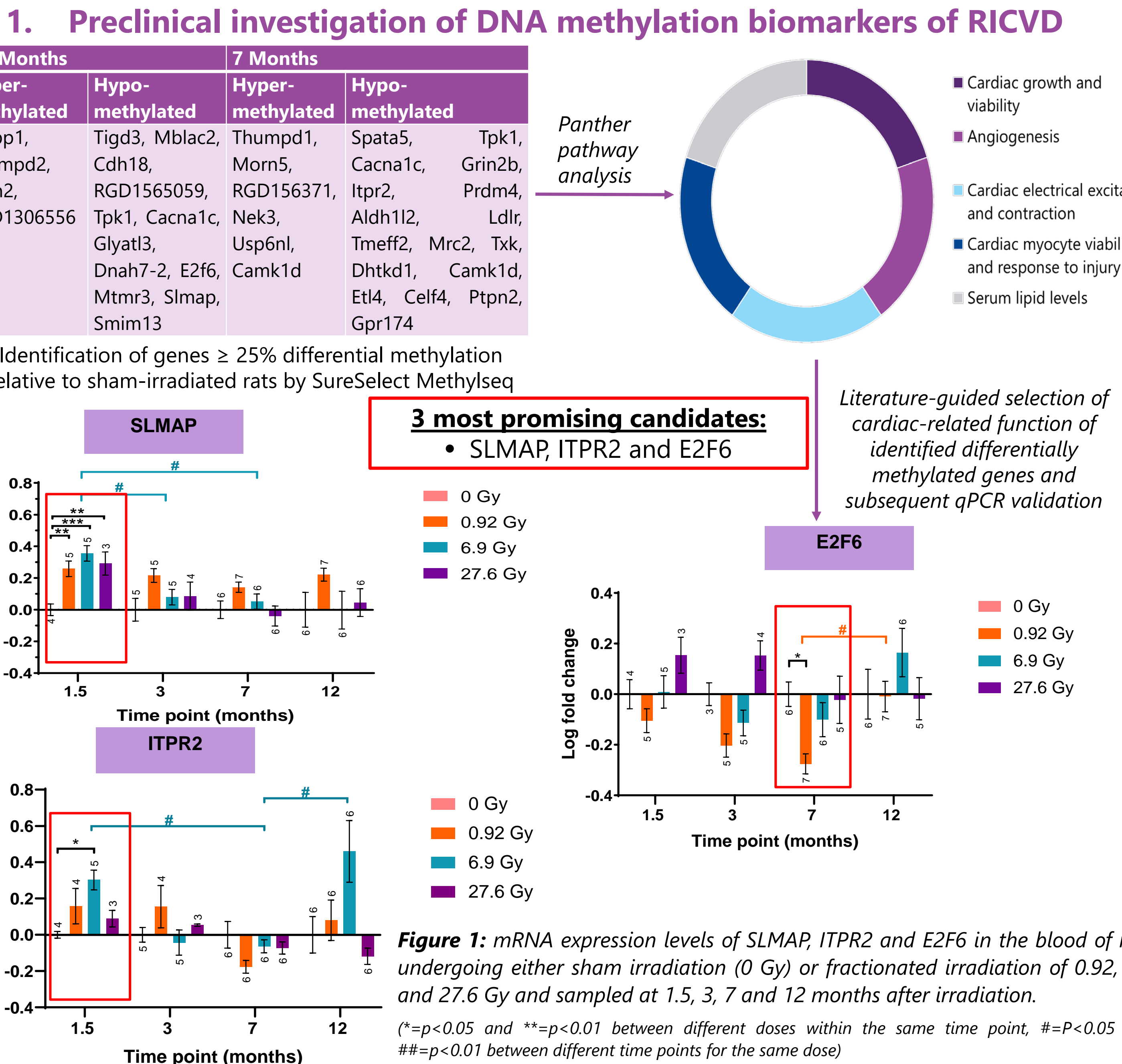
## Aims

1. Finding DNA methylation biomarkers to estimate the risk of early and late radiation-induced cardiovascular events after breast cancer radiotherapy.
2. Finding microRNA (miRNA)/long non coding RNA (lncRNA) biomarkers for glioblastoma risk assessment.

## Methods



## Results



## Conclusions

- Rat irradiation with 1.2 Gy induced **DNA methylation alterations** that were detectable in blood samples until 7 months after irradiation relative to sham irradiated rats.
- **3 promising** differentially methylated genes were identified in irradiated rat (SLMAP, ITPR2 and E2F6), which have been associated previously with **cardiac function** in literature.
- **DNA methylation alterations** were observed in breast cancer patients after radiotherapy and a number of differentially methylated genes were identified (validation is ongoing)
- Meta analysis of publicly available glioblastoma RNAseq data identified **88 lncRNAs** that were found to be differentially expressed in all included studies.
- **miR-96-5p** was found to be differentially expressed in **glioblastoma tissue** samples relative to normal brain tissue.

## Acknowledgements

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