

Human patient-derived models for translational immuno-oncology and inflammation drug discovery

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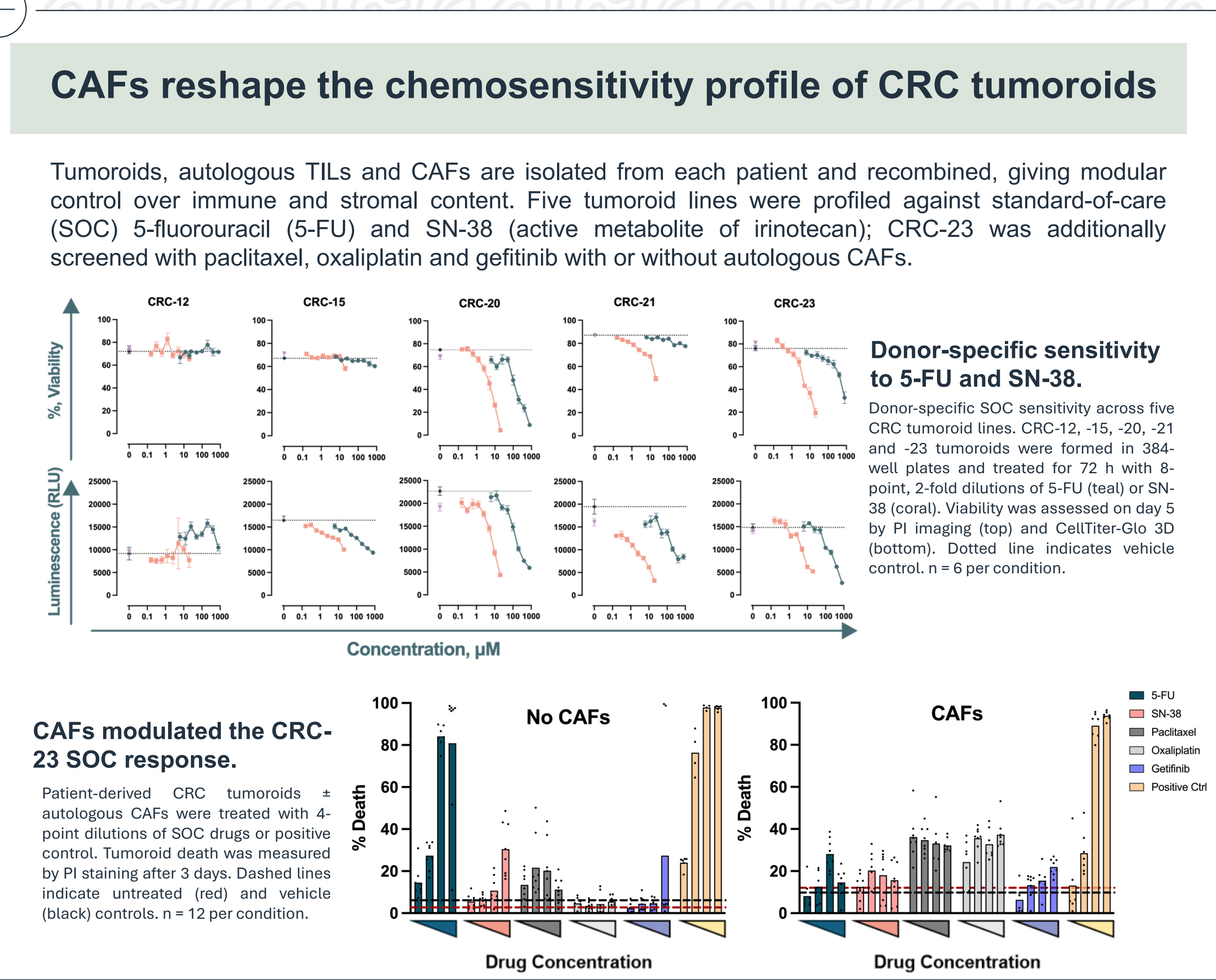
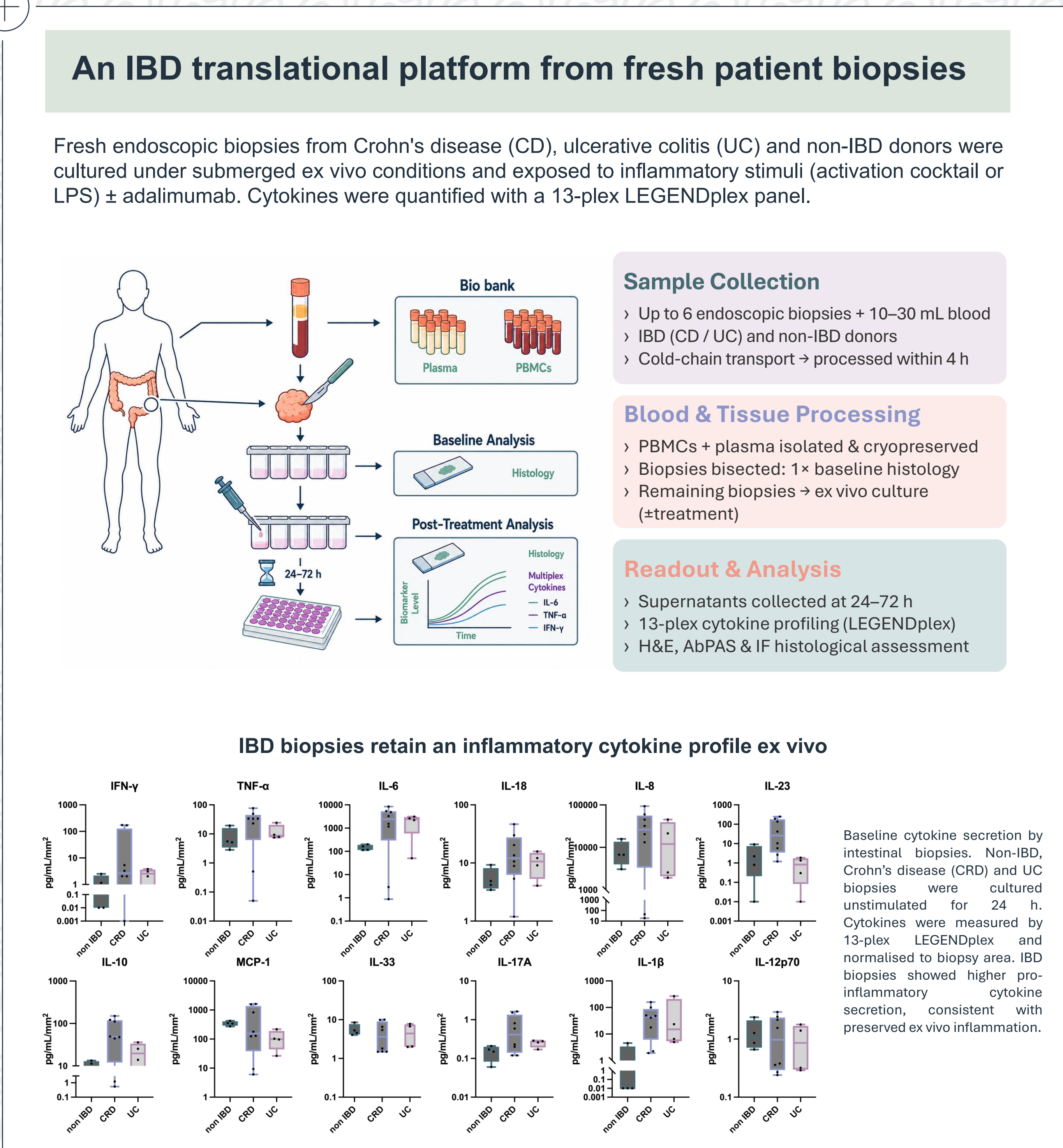
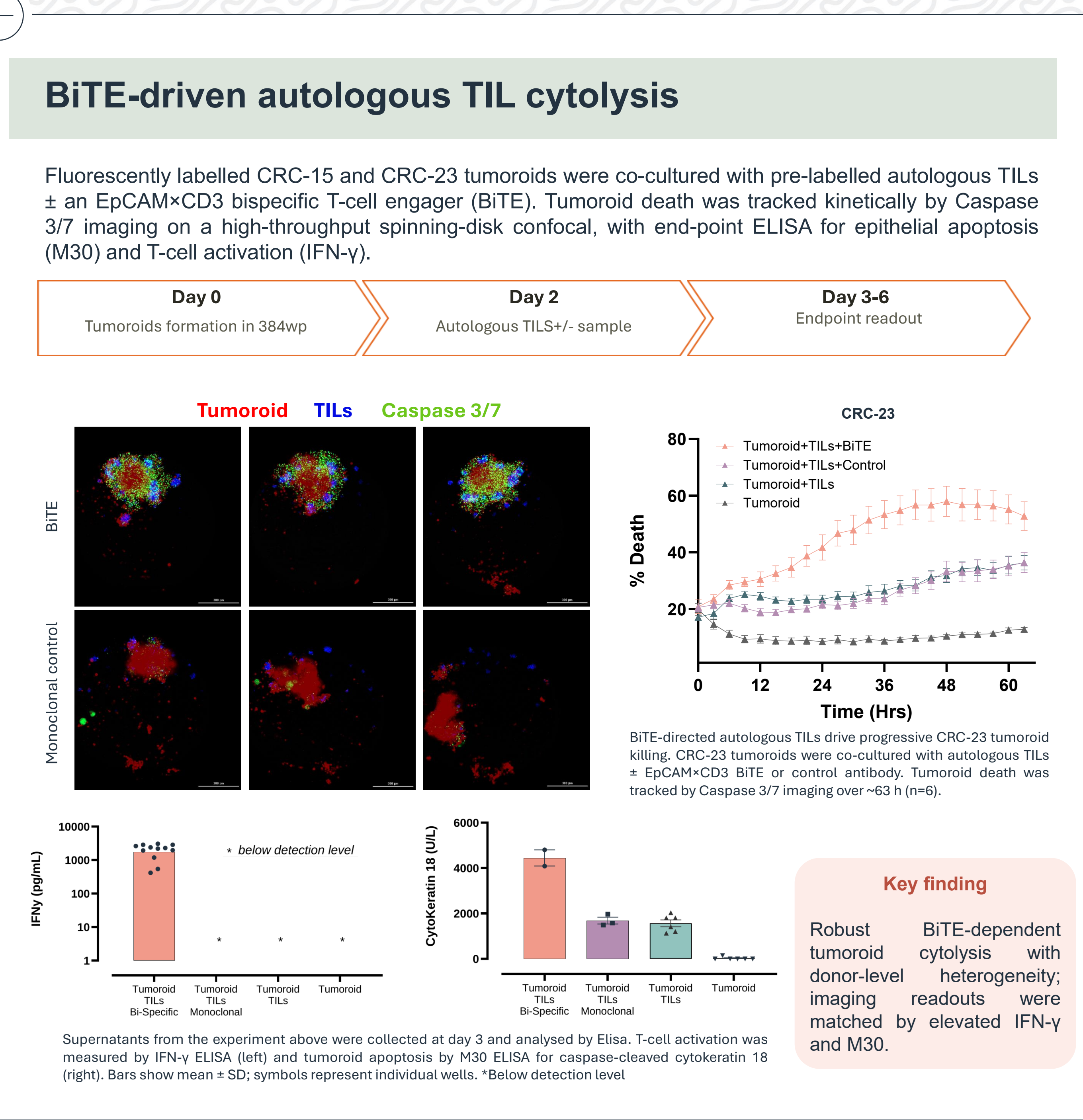
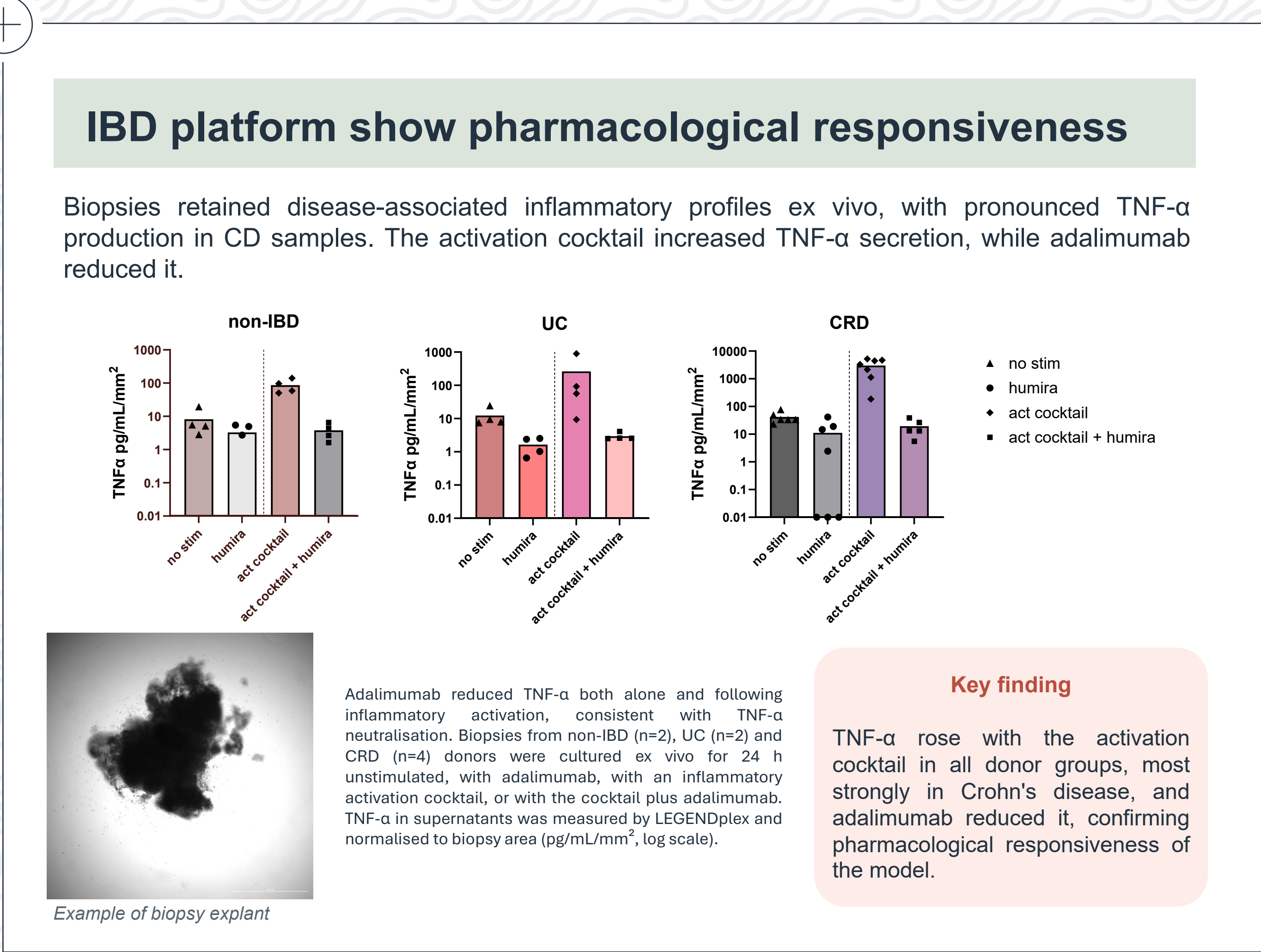
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Background

Translation of preclinical findings into effective therapies remains limited by conventional models that fail to capture the complex immune, stromal and inflammatory interactions present in human disease. To address this, we developed two complementary patient-derived ex vivo platforms spanning immuno-oncology and inflammatory disease: a colorectal cancer (CRC) tumoroid system assembled bottom-up with autologous tumour-infiltrating lymphocytes (TILs) and cancer-associated fibroblasts (CAFs), and an intact human intestinal biopsy platform for inflammatory bowel disease (IBD). Both generate functional readouts to therapeutic intervention while capturing donor-to-donor heterogeneity.

IMMUNO-ONCOLOGY
CRC tumoroids
+ TILs + CAFs
Bottom-up assembled:
modular control of immune and stromal content and dose

INFLAMMATION
IBD intestinal biopsies
Top-down intact:
native cellular architecture and spatial organisation



Conclusions

- Reconstituted (CRC) and native (IBD) patient-derived ex vivo systems both generate clinically relevant functional readouts across distinct disease areas.
- The bottom-up CRC model offers modular control over immune–stromal composition and dose, resolving donor-specific SOC and BiTE responses.
- The top-down IBD biopsy model preserves intact tissue biology and responds pharmacologically to anti-TNF-α therapy.
- By capturing inter-patient heterogeneity, both support predictive biomarker identification across immuno-oncology and inflammation drug discovery pipelines.

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