# Experimental Plan

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## Contents

roject 1: A20 Modelling the BL Tumour Microenviroment
Overview
Background
Experimental Plan
E1: NSG vs BALB/C A20 injection
E2: Trial BL Therapies
Loncastuximab tesirine
E3: Immune focused CRISPR Screen
roject 2: Spatial Transciptomics of BL
Paper Plan
Thesis ID
Publically Available RNAseq
leas
Ferritin as a drug delivery system

## Project 1: A20 Modelling the BL Tumour Microenviroment

#### Overview

- Using A20 to model BL immune TME
  - Look specifically at T-cell infiltration
  - Immune evasion mechanisms deployed by BL
- Compare results to patient data
- Apply findings to humanised mouse models of BL PDX

#### Background

- The impact of immune TME in BL is unclear
- BL

#### Experimental Plan

#### E1: NSG vs BALB/C A20 injection

#### E1 Overview

- Compare between immunocompetent and immunocomprimised mice
- Basic actors to compare
  - Tumour growth rate
  - Tumour size

#### Injection Plan

Group	Strain	Location	Cell Injection
1	BALB/c	Sub-cut	A20
2	BALB/c	$\operatorname{IP}$	A20
3	NSG	IP	A20
4	NSG	Sub-cut	A20

#### **IHC Panel**

- Compare markers between tumour types
- Burkitt IHC indentification:
  - CD10+ (B-Cell Germinal Centre)
  - Bcl-2-
  - Ki-67%hi (proliferation index)

Potential IHC Panel Markers

Cell Type	Marker
Proliferation marker	Ki67
B cell	CD20
T cells (all)	CD3
T Cells (cytotoxic)	CD8
T cells (helper)	CD 4
Dendritic Cells	CD11c
Macrophage	F4/80

#### Flow Panel

- Options are:
  - Standard T Cell
  - TRegs
  - B-cells
  - DC Mono CD11c
  - Th17
  - TfH
- Check what Swetha ordered
- Box 7 antibody sheet dropbox

#### Standard T Cell

Cell Type	Marker
T Memory	CXCR3
Naive Immune Cells	CCR7
Naive T Cells	CD45RA
$\mathrm{Th}17$	CCR6
GC B-Cells	CD38
TRegs (Helper)	CD4
Macrophage	HLA-DR
T Cells (all)	CD3
T Cells (Cytoxic)	CD8

#### E2: Trial BL Therapies

- Balb/c drug vs no drug vs WS-A20 drug vs WS-A20 no drug
  - Want to compare effect of GFP on immune cell infiltration
  - Look at clonal dynamics of rituximab treatment
- Glo-BNHL Trial
  - Odronextamab
    - \* CD20xCD3 Bispecific antibody

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#### Loncastuximab tesirine

- Rituximab
- CAR treatments?
- Bi-Specific antibodies (check that they can be applied to mice)
- Rituximab comparison
  - Clonal dynamics of Rituximab treatment
    - \* WILDseq

#### E3: Immune focused CRISPR Screen

- $\bullet\,$  Immune compromised vs Immune competent
  - Think very carefully about specific mouse models (some still have macrophages, NK cells, ect.)
  - JAX Lab Article

## Project 2: Spatial Transciptomics of BL

- 11 Samples of BL acquired from VIVO BioBank
- Want to do stuff similar to these studies:

- \* PDAC Spatial Transcriptomics
- \* Genomic/Transcriptomic analysis of Clinical BL Samples

### Paper Plan

Based on PDAC ST paper

- Panel 1:
  - Patient Data
    - a. Correlation survival studies between immune cell infiltration and survival
- Panel 1:
  - Patient sample characterisation
    - a. Work Flow (sample backgrounds, collection from sources)
    - b. Overview of all cell types profiled in the scRNA-seq cohort.
    - c. Overview of spatial transcriptomics cohort
- Panel 2
  - Characterize the tumour (Tumor vs stroma vs immune cells)
    - a. Differential pathway enrichment case-level tumor subpopulations
    - b. Tumor cluster pathway enrichment for specific case
    - c. Tumor cluster pathway enrichment for another specific case
    - d. UMAP of tumor subclusters for specific case
    - e. UMAP of tumor subclusters for specific case
- Panel 3
  - Genomic Landscape and oncogenic driver heterogeneity (??)
- Panel 4
  - Tumour cell heterogeneity in ST data(?)
- Panel 5
  - Immune Populations in TME
- Panel 6
  - Mibiscope

#### Thesis ID

Looking at characterizing the Human BL TME

- Publically available BL Data
- VISIUM internal samples
- Mibiscope Internal Samples

Publically available datasets analysis

- Talk to Jamie again
  - 10x Visium transcriptomics
    - T Cell Dynamics
      - \* Infiltration
      - \* Exhaustion
    - NK cell dynamics
    - Places to get it done:
      - \* CI (no)
      - \* Source Bioscience
      - \* Wellcome Sanger Institute
        - · Teichmann Lab used 10x Visium
  - MIBIScope Comparison
    - Does Protein expression map onto spatial gene expression?
    - Collaborate with Nina in Germany

### Publically Available RNAseq

- 1. The iDEP or TACITuS pipeline for transcriptomic profiling and GSEA/pathway analysis.
- 2. The CIBERSORT immune-cell deconvolution algorithm to obtain cell-fractions and gene expression/enrichment scores of tumor-infiltrating lymphocytes.
- 3. The GEPIA2 database for survival analysis correlating to immune infiltration and/or differential gene expression.

## Ideas

### Ferritin as a drug delivery system

• Does BL have increased Tfr1 expression relative to normal cells/B cells?