

Mouse I/O RNA-Seq Panel

NGS-based murine targeted panel for I/O and TME studies

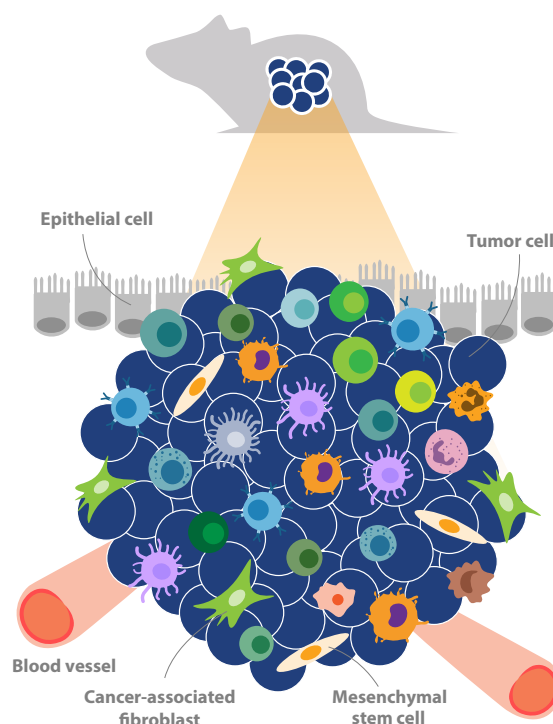
Rapidly gain in-depth genomic insight into immune cell populations and I/O pathways and processes of your murine immunity pharmacology study samples.

Gain a comprehensive profile of genes associated with tumor immunity by measuring 1080 mouse transcripts from a single sample. Deeply profile the immunogenomics of murine tumor-immune interactions to:



















- Elucidate the drug mechanism of action
- Develop biomarker signatures of response
- Understand drug resistance
- Inform the next decision in your drug development process

Apply the Mouse I/O RNA-Seq Panel to:

- Interrogate 1080 genes covering immune cell signatures, surface markers, transcriptomic immune cell-specific biomarkers, and key pathways at the interface of the tumor, TME, and immune response
- Streamline your preclinical workflow by analyzing your existing syngeneic or **MuPrime™** *in vivo* study samples
- Reduce background noise enabled by the high dynamic range of next-generation sequencing
- Detect upregulated and downregulated genes within key immune cell populations
- Make timely decisions with a turnaround of 3 weeks from sample receipt to a comprehensive analysis report including:
 - data QC
 - mRNA quantification
 - cluster analysis
 - differential expression analysis on requested comparisons
 - gene ontology enrichment analysis on differentially expressed genes



Panel Includes Key Immune Cell Signatures

 B cells*	 CD4 T cells*
 Dendritic cells*	 CD8 T cell*
 Tolerogenic DCs	 Naïve T cells
 Macrophages	 Memory T cells*
 Tumor-associated macrophages	 Th1 cells
 G-MDSCs*	 Th2 cells
 M-MDSCs*	 Th17 cells
 Neutrophils	 T _{reg} cells
 Natural killer cells*	 iT _{reg} cells

*Strain specific gene signatures available for C57BL/6 and BALB/c



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Schedule Scientific Consultation

Request a consultation to discuss your project.
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Explore Scientific Data

Log into **MuBase®** to review murine immunity model data
mubase.crownbio.com