

Human blood  
plasma stored  
at -80° C  
≥ 0.5 mL



extra-cellular  
vesicle  
isolation



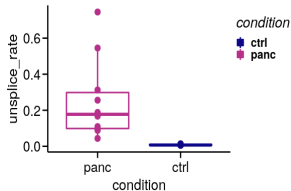
60 pg - 0.01 ug  
RNA

- polyA+ RNA isolation
- 24 cycles, 1 ug cDNA
- NGS sequencing
- ≥ 5 million PE reads
- Sequenced read QC
  - Library depth: ✓
  - GC content: ✓
  - Duplicated reads: ✓

multi-reference transcript quantification  
custom annotations cover majority of genomic space

- Canonical + -Coding & lncRNA
  - 61,114 annotated mRNA
  - 243,577 RNA transcripts
- Repeat Elements
  - 5x10<sup>6</sup> TE insertions
  - + -Transposable Elements -15,441 TE elements
- Process/Intron Aware
  - 38,100 potentially un-spliced genes
  - + -Unspliced transcripts -393,345 intronic transcripts

Intron-aware analysis  
creates novel features  
with diagnostic potential



TE -aware feature sets  
w/ expanded diagnostic  
capabilities

Feature Engineering



AI/ML classification

whole-transcriptome sequencing will enable generalizable  
diagnosis of various diseases

Training Regularize Expression | Sequence | Splice-rate

Validation Cross-validated sensitivity at 90-99% sensitivity

Test model generalizability to patient population

incoming patient data + **model** → clinical diagnosis