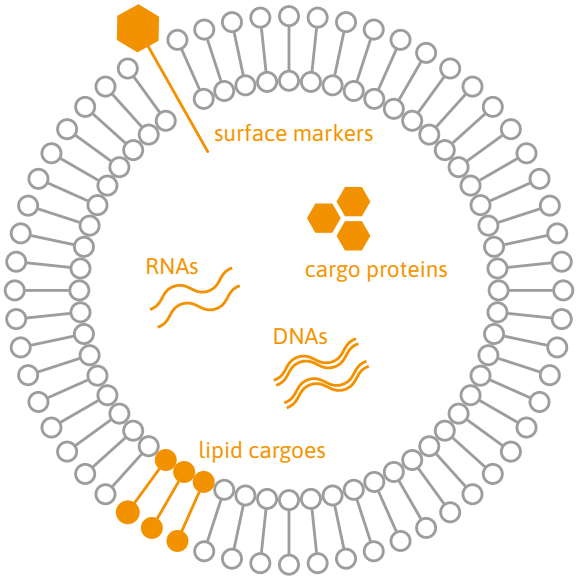


Unlocking Extracellular Vesicle Secrets

TAmiRNA
stability for life.

Therapeutic applications of EVs: transcriptomic & proteomic characterization

EV Therapeutics

EVs are promising therapeutic modalities for regenerative medicine and beyond. **TAmiRNA has supported top academic and industrial partners** with the molecular (omics) characterization of therapeutic EVs to:

1. **Unveil the molecular composition:** comprehensive analysis of RNAs, proteins and lipids in/on EVs to confirm EV identity, cellular origin, and abundant cargo.
2. **Ensure consistency between manufacturing runs:** by establishing reference RNA, DNA, protein, or lipid profiles the reproducibility across batches can be monitored and used to identify process parameters that impact on EV composition.
3. **Explore modes-of-action:** cargo-activity-relations can be identified by linking molecular EV composition to observed biological activity in cell-based assays or in-vivo models.

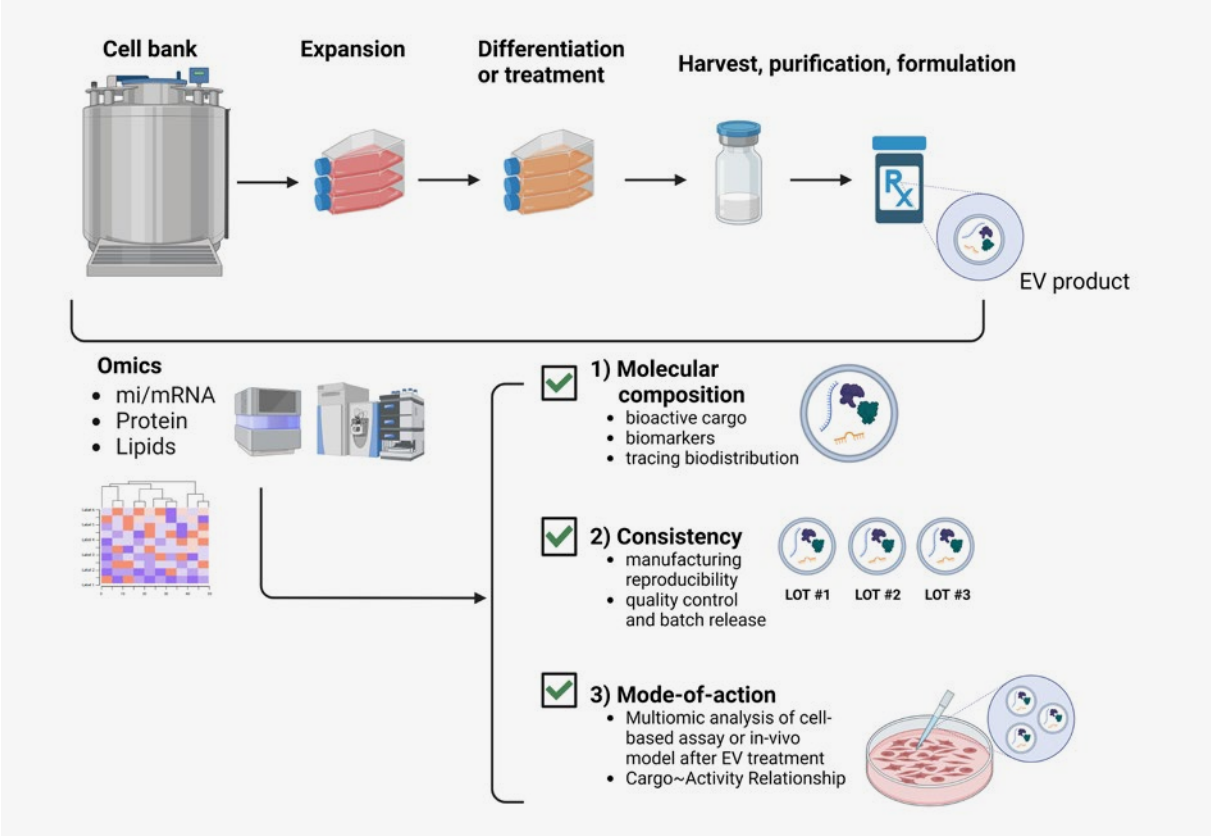


Figure 1: Simplified illustration of an EV therapeutic production process and how EV omics data can support the drug development process.

Unleashing the potential of EV RNA cargo as biomarker candidates

EV biomarkers

Small RNA-sequencing enables microRNA biomarker discovery in EVs from various sample sources

microRNA-seq of EVs: sample source & miRNA detection

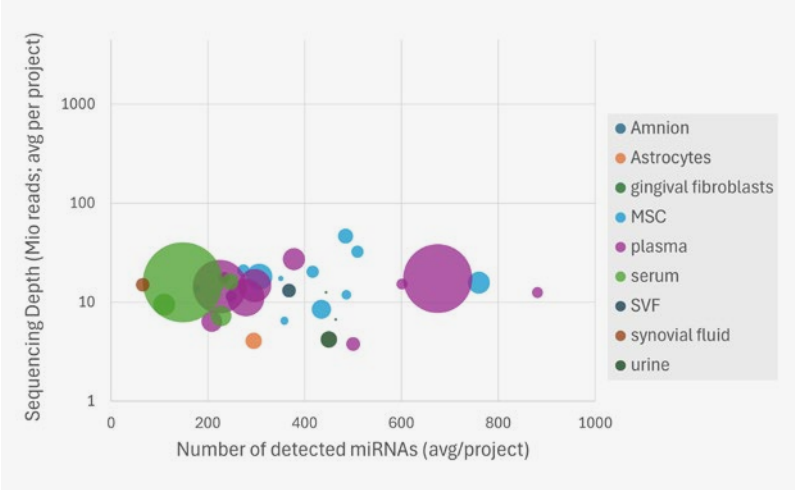


Figure 2: Dot plot summarizing experience from >35 completed EV projects with 500+ samples: sensitivity (detected miRNAs) vs sequencing depth is shown. Dot size corresponds to the number of samples per project.

Whole-transcriptome sequencing by TAmiRNA enables mRNA, lncRNA, and circRNA analysis

Reproducibility of transcriptomic analysis

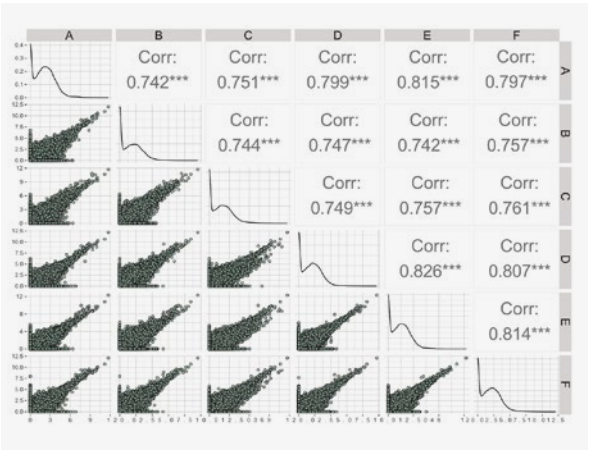


Figure 3: Correlation matrix illustrating the reproducibility based on of replicate analyses from mouse plasma EV preparations.

Sensitivity of transcriptomic analysis

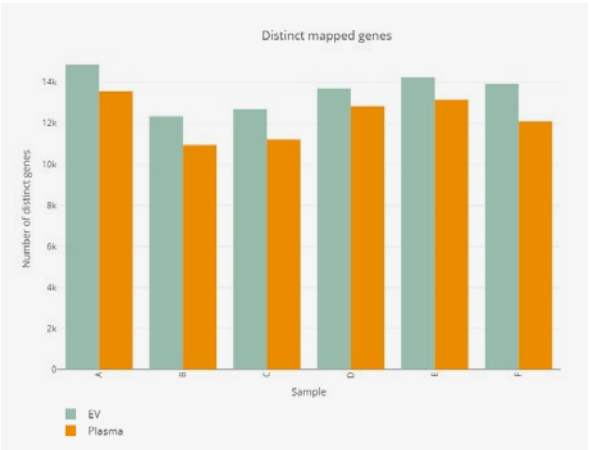
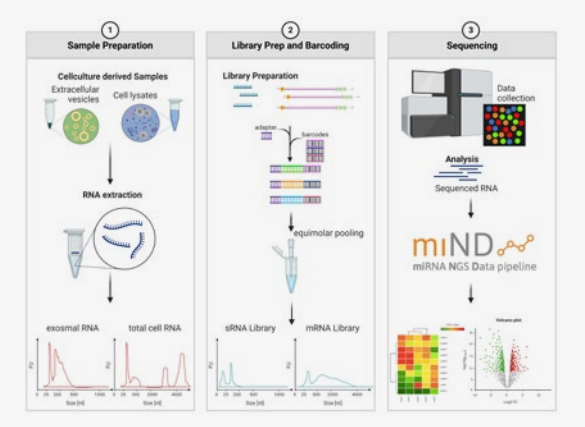


Figure 4: Bar chart showing the number of transcripts (mRNAs and pseudogenes) detected in total plasma and plasma EVs.

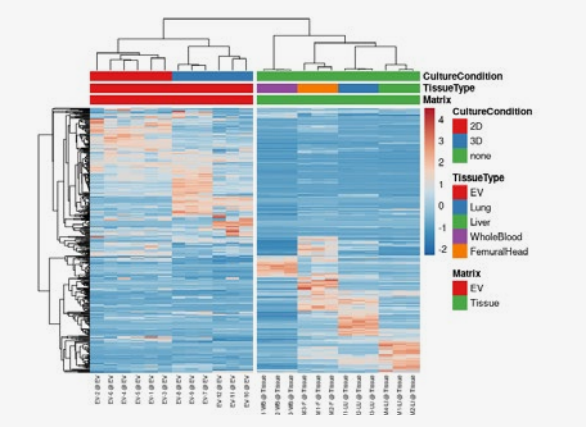
Multi-omics analysis to understand EV mechanisms and biodistribution

Multiomics

Ⓐ Workflow at TAmiRNA



Ⓑ Unsupervised analysis



Ⓒ Multi-omic data integration

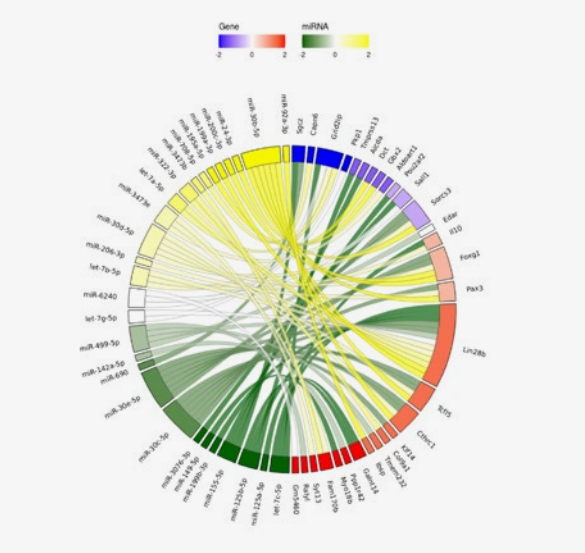


Figure 4: multi-omic EV analysis

Ⓐ: parallel processing of EV samples and cells/ tissues from in-vitro/in-vivo efficacy models including univariate analysis.

Ⓑ: unsupervised (and supervised, not shown) analysis to map transcriptional landscapes of EVs and target cells/tissues.

Ⓒ: microRNA/mRNA data integration for functional analysis.

Key publications

1 Analysis of extracellular vesicle microRNA profiles reveals distinct blood and lymphatic endothelial cell origins. Pultar M, Oesterreicher J, Hartmann J et al. Journal of Extracellular Biology. https://doi.org/10.1002/jex2.134

2 Independent human mesenchymal stromal cell-derived extracellular vesicle preparations differentially attenuate symptoms in an advanced murine graft-versus-host disease model. Madel RJ, Börger V, Dittrich R et al. Cytotherapy. doi: 10.1016/j.jcyt.2023.03.008.

3 Circulating endothelial extracellular vesicle signatures correspond with ICU requirement: an exploratory study in COVID-19 patients. Zipperle J, Oesterreicher J, Hackl M et al. Intensive Care Med Exp. doi: 10.1186/s40635-023-00567-7

4 Small non-coding RNA landscape of extracellular vesicles from a post-traumatic model of equine osteoarthritis Anderson JR., Jacobsen S., Walters M. et al. Frontiers Veterinary Science. doi: 10.3389/fvets.2022.901269

5 SVF-derived extracellular vesicles carry characteristic miRNAs in lipedema. Priglinger E., Strohmeier K., Weigl M et al. Scientific Reports. doi: 10.1038/s41598-020-64215-w.

Stay up-to-date:

Overview of EV cargo analyses at TAmiRNA

Target molecule	workflow	cells	tissue	Liquid biopsy*	EVs
Required Input		> 50 cells	> 10,000 µm²	> 25 µL	> 10^9 particles
microRNAs, tRNAs, other small RNAs	miND®: small RNA-seq	✓	✓	✓	✓
mRNA, lncRNA, circular RNAs	SMARTer®: Whole transcriptome-seq	✓	✓	✓	✓
Proteins & lipids	Mass Spectrometry	✓	✓	✓	✓
RNA/DNA (any sequence)	RT-qPCR	✓	✓	✓	✓
EV size, concentration, & surface markers	NTA, NanoFCM, and CryoEM				✓

*serum, plasma, urine, CSF, synovial fluid, tear fluid, inner ear fluid

"We strive to assist our customers in quickly transforming their ideas into tangible results through our one-stop EV services!"

Matthias Hackl, CEO TAmiRNA

Why work with TAmiRNA?

- **Expert Team:** Experienced professionals with extensive expertise in EV research (>500 sequenced EV preparations). Consultation & interpretation support included in the service.
- **Cutting-Edge Technology:** Access to the latest tools and methodologies in the field such as absolute quantification by NGS.
- **End-to-End Solutions:** From initial EV isolation and characterization to bioinformatic data analysis, we cover every step.
- **Customization:** we adapt and tailor our workflows to meet your specific research & input sample needs.
- **Quality Assurance:** ISO 13485 accredited with rigorous protocols to ensure the highest standards of data quality and reliability.

TAmiRNA's EV characterization services at a glance

① **Isolation:** High-purity isolation of extracellular vesicles from a variety of biological samples. We use state-of-the-art techniques including ultracentrifugation, UF/TFF, SEC, or trapping methods to optimize isolation methods based on sample type.

② **Size, concentration, and surface markers:** Precise nanoparticle tracking analysis (NTA) for size distribution and concentration. Advanced instrumentation such as NanoFCM or CryoEM for additional characterization.

③ **Single- or Multi-omics analysis:** In-depth analysis of EV cargo with next-generation sequencing (NGS) and mass spectrometry coupled to bioinformatic analysis provide the answers to scientific questions about EV cargo, biomarkers, and mode-of-action.

Contact us for a free consultation and quotation to discuss your project

Get a Quote!

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