

## Background

- Endometriosis is a chronic inflammatory condition
- Characterized by:
  - Inflammation
  - Chronic pelvic pain
  - Infertility
- Current diagnostic methods relying on symptom evaluation and imaging can be misleading, and surgery is invasive.

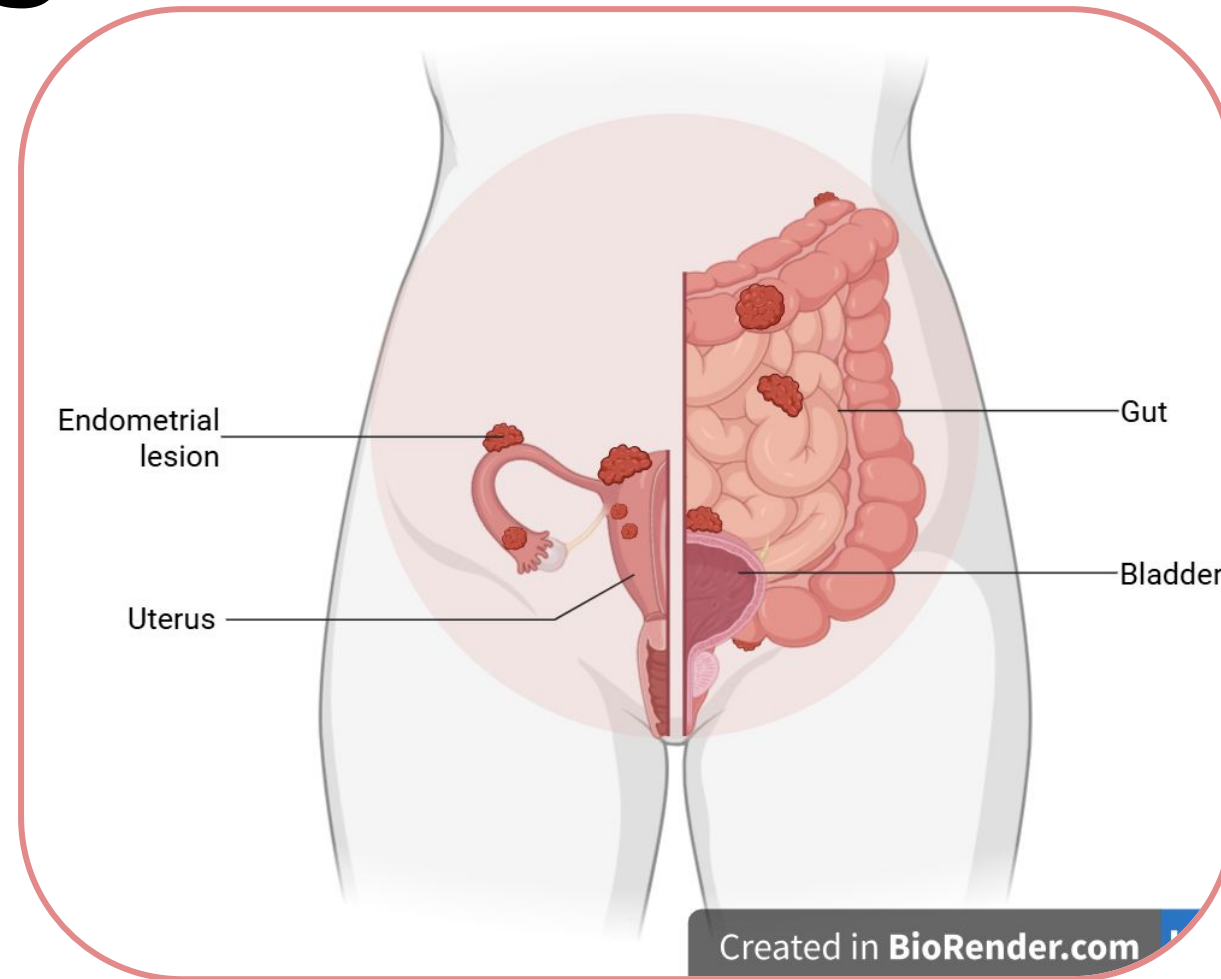


Figure 1: Diagram illustrating the effects of endometriosis on the body.

- Exosomes are extracellular vesicles (EVs) secreted by cells
- Contain molecular cargo such as:
  - proteins
  - mRNA
  - nucleic acids
 which can act as biomarkers!
- Exosomal biomarkers derived from menstrual effluent may provide insight into endometriosis-associated cellular activity.

### Structure of extracellular vesicles (Exosomes and microvesicles)

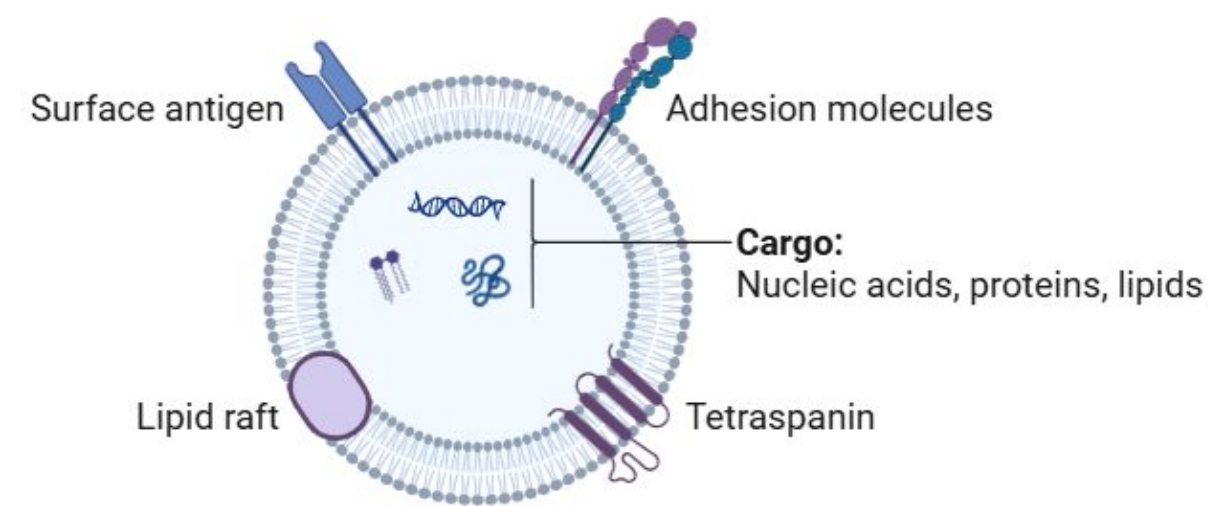


Figure 2: Structure of extracellular vesicles (EVs)

## Objectives

- Reproducibility: Allows for higher biomarker detection
- Effective Isolation: Allows for higher purity and detection
- Compatibility with Downstream Analysis: Allows for accessibility

## Problem Statement

Given the want for less invasive diagnostic methods; A reproducible, standardized ME purification pipeline is needed to minimize variability.

## Experimental Design

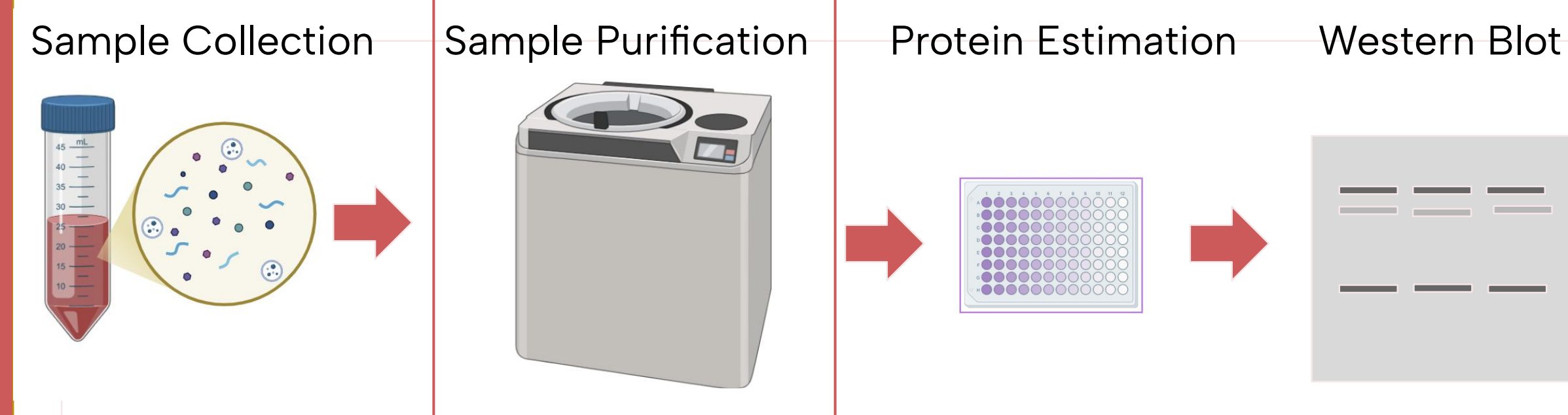


Figure 3: Overview of the menstrual effluent purification pipeline.

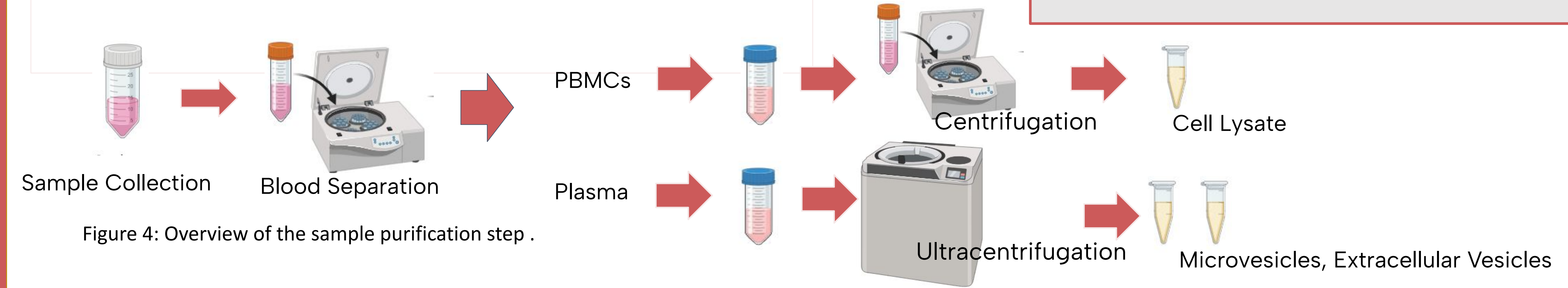


Figure 4: Overview of the sample purification step.

METHOD 1:	METHOD 2:	METHOD 3:
1 Spin x Fraction	Plasma → 4°C	2 Spins for 100k
3 Hour Spin (10k)	Overnight Storage of Plasma in 4°C	3 Hour Spin 10k
↓	↓	↓
1.5 Hour Spin (100k)	Continue Processing Next Day	1.5 Hour Spin
		↓
		1.5 Hour Spin (100k)

## Expected Outcomes

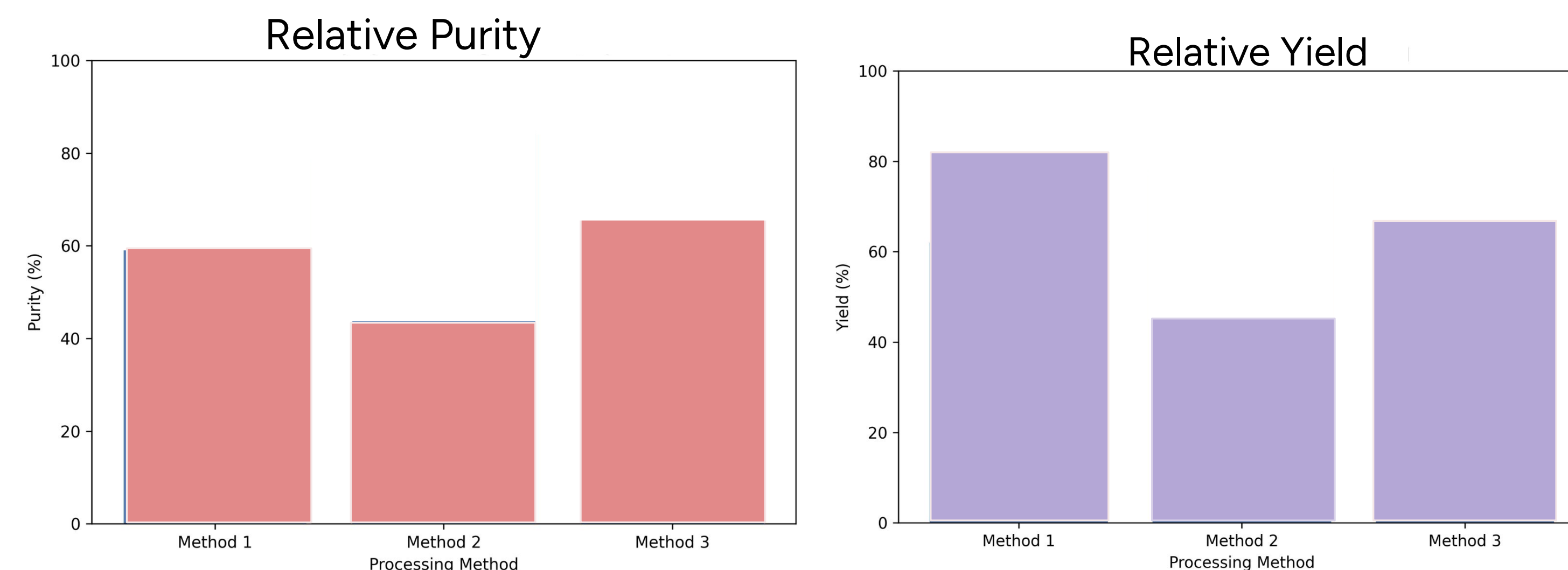


Figure 5: Relative purity and normalized yield of exosome samples processed using different purification methods. Method 1 demonstrated the highest relative yield, while Method 3 showed higher relative purity.

### Data Distribution By Method

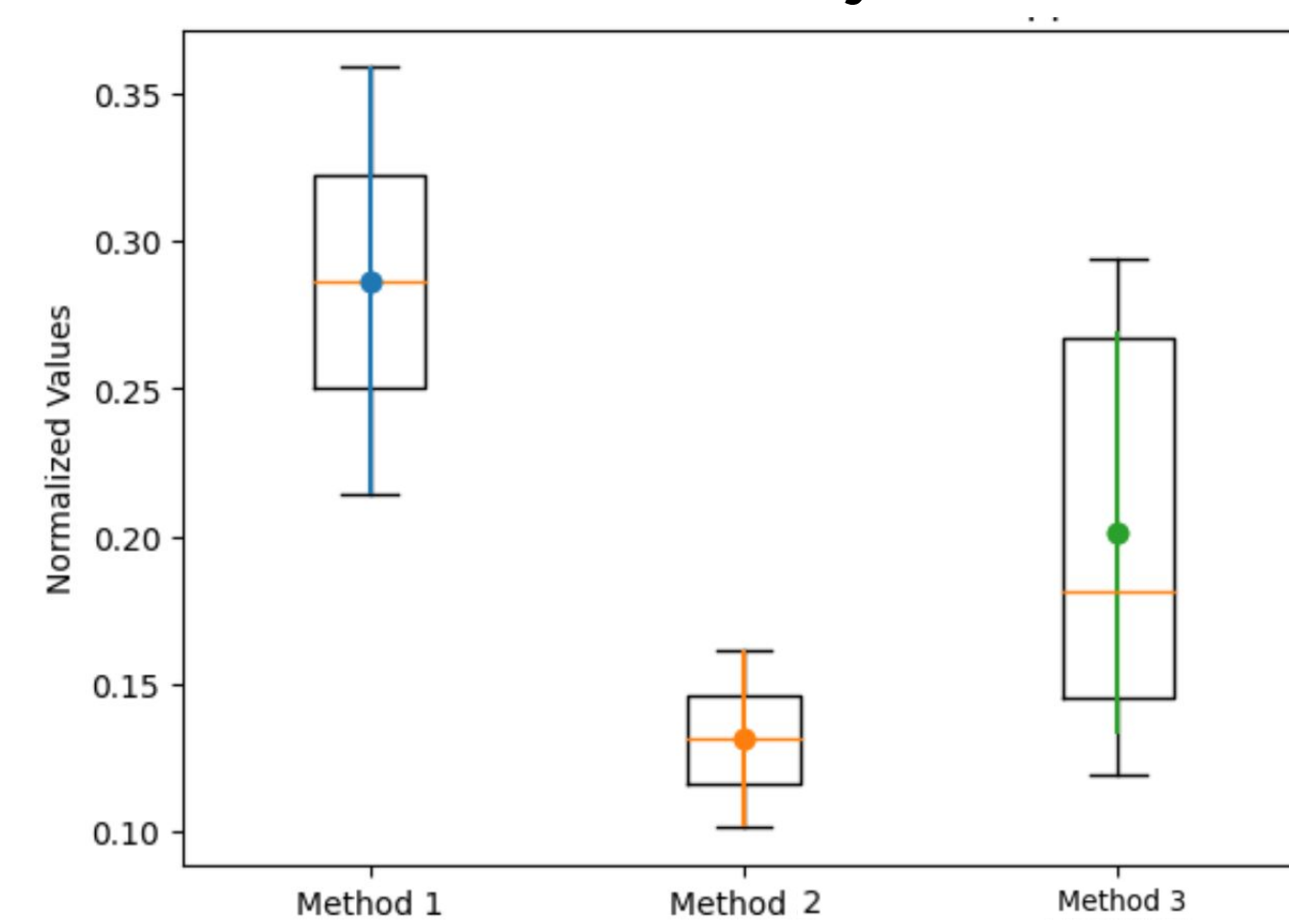


Figure 6: Normalized values protein counts of samples grouped by method, where Method 1 was found to have the most.

### Western Blot Analysis

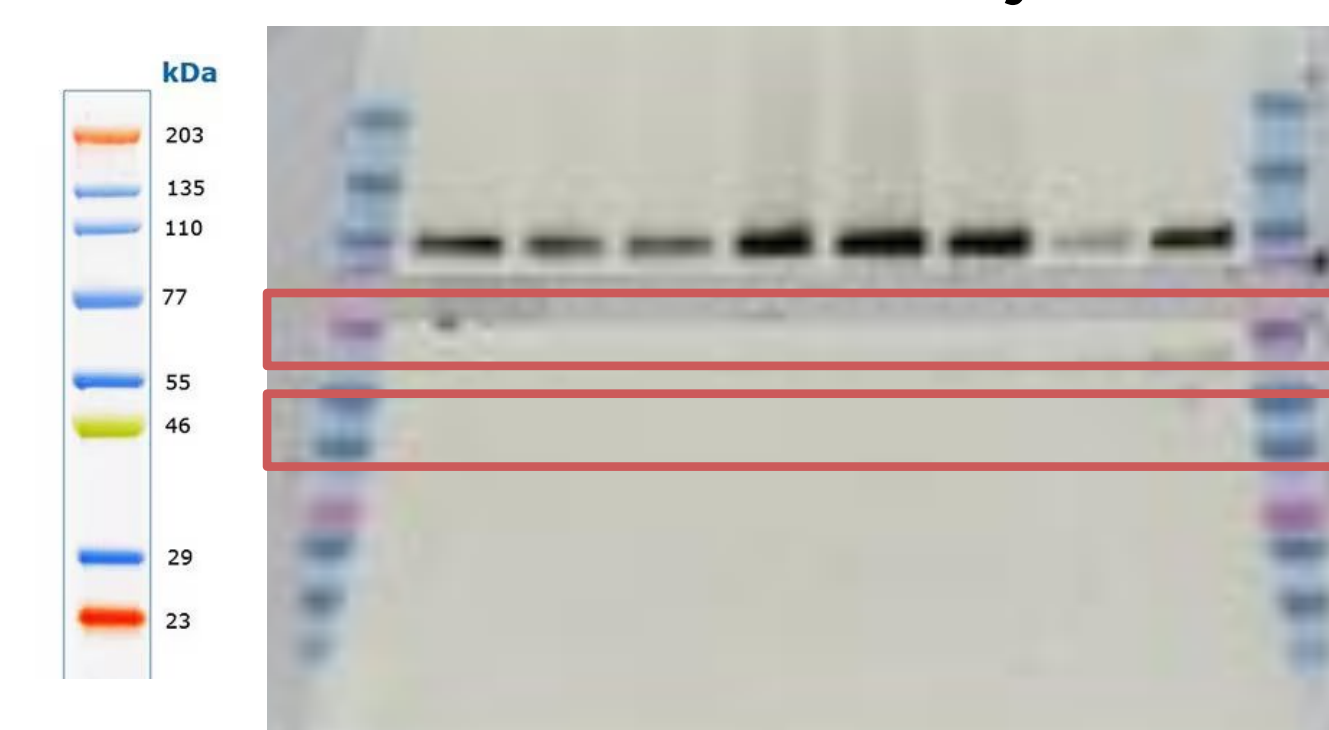


Figure 7: Normalized values protein counts of samples grouped by method, where Method 1 was found to have the most.

## Conclusions

- Overall, Method 3 was selected as the optimal purification approach because it demonstrated the highest relative purity while maintaining a comparatively high normalized yield.
- Although Method 1 produced higher overall yield, it showed lower purity and greater potential contamination.
- These findings suggest that the additional ultracentrifugation step in Method 3 improved contaminant removal while preserving sufficient exosomal material for downstream analysis.
- **Limitations** : Sample heterogeneity, contamination risk, freeze-thaw degradation, and limited sample size may have affected reproducibility.
- **Future work**: improving sterilization, quality control, and sample-processing flexibility while maintaining high purity and yield.

## Acknowledgements & References

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