

Identification of a Minimal, Generalizable Gene Expression Signature for Breast Cancer Molecular Subtype Classification

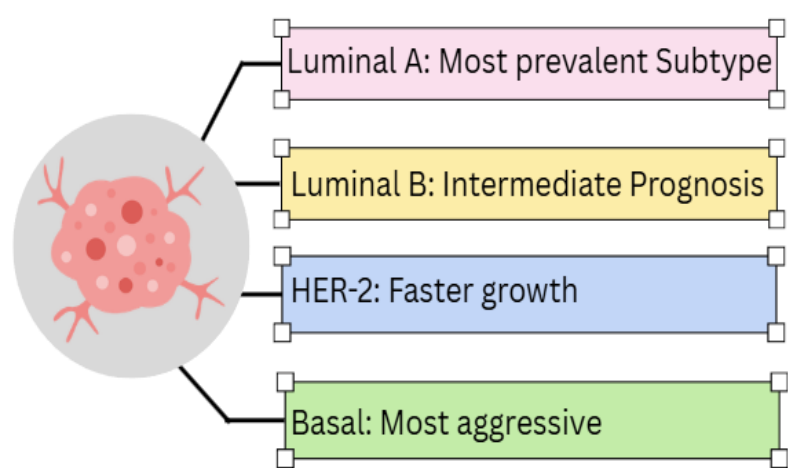
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INTRODUCTION

Breast Cancer is a disease where abnormal breast cells grow uncontrollably and can spread to other parts of the body

- By 2040, cases are predicted to exceed 3M a year (**40% increase**) (2)
- Annual deaths are expected to **rise by 50%** (2)

Breast Cancer is a heterogenous disease



Each tumor has a unique gene expression pattern across thousands of genes, enabling classification into molecular subtypes

OBJECTIVES

Can a minimal gene expression signature be developed that accurately classifies breast cancer subtypes and remains stable across independent cohorts and sequencing technologies?

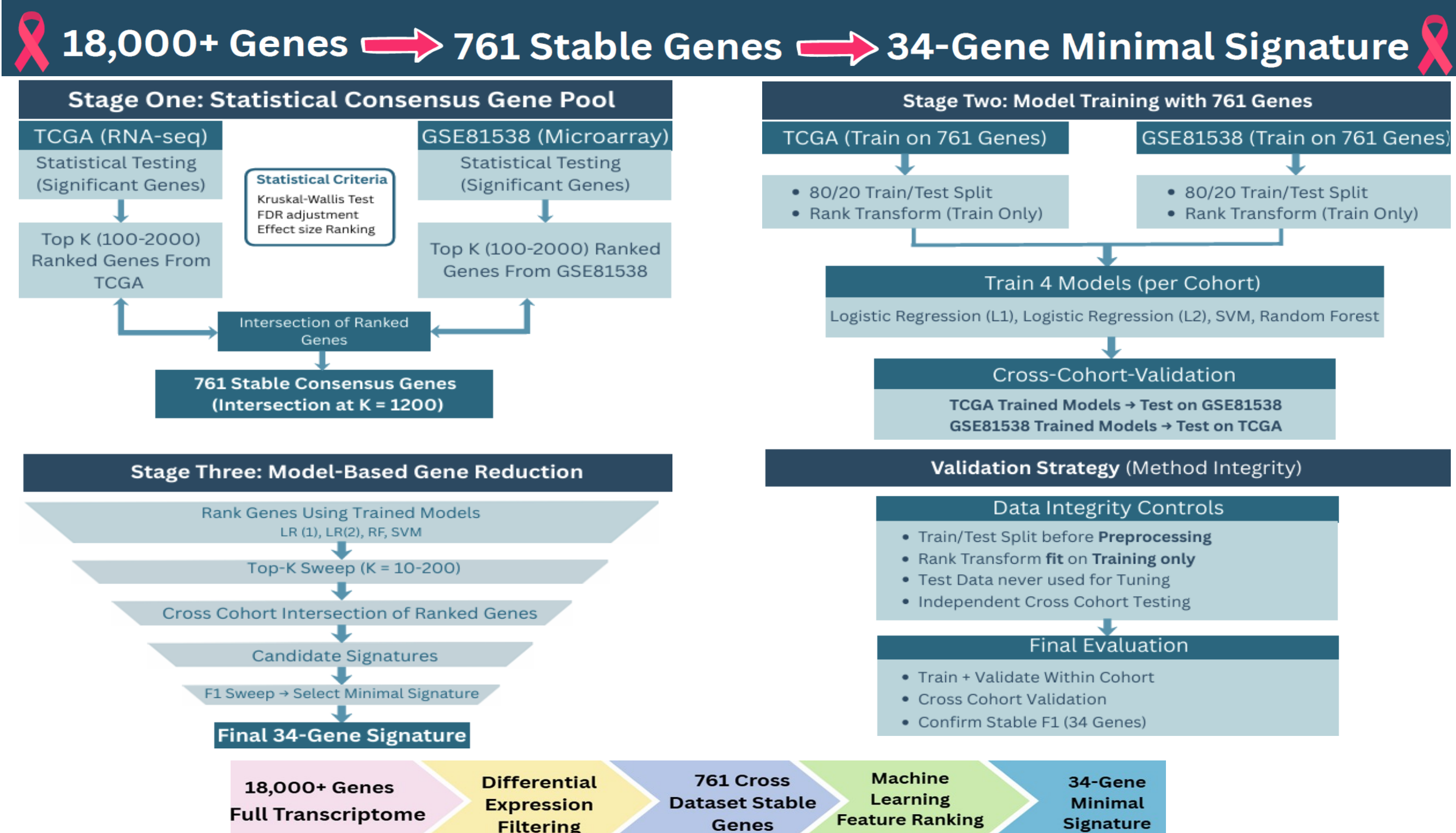
Reproducibility: Do gene expression-based subtype classifiers maintain consistent performance across independent datasets?

Cross Platform Stability: Are subtype associated gene patterns preserved between RNA-seq and microarray technologies?

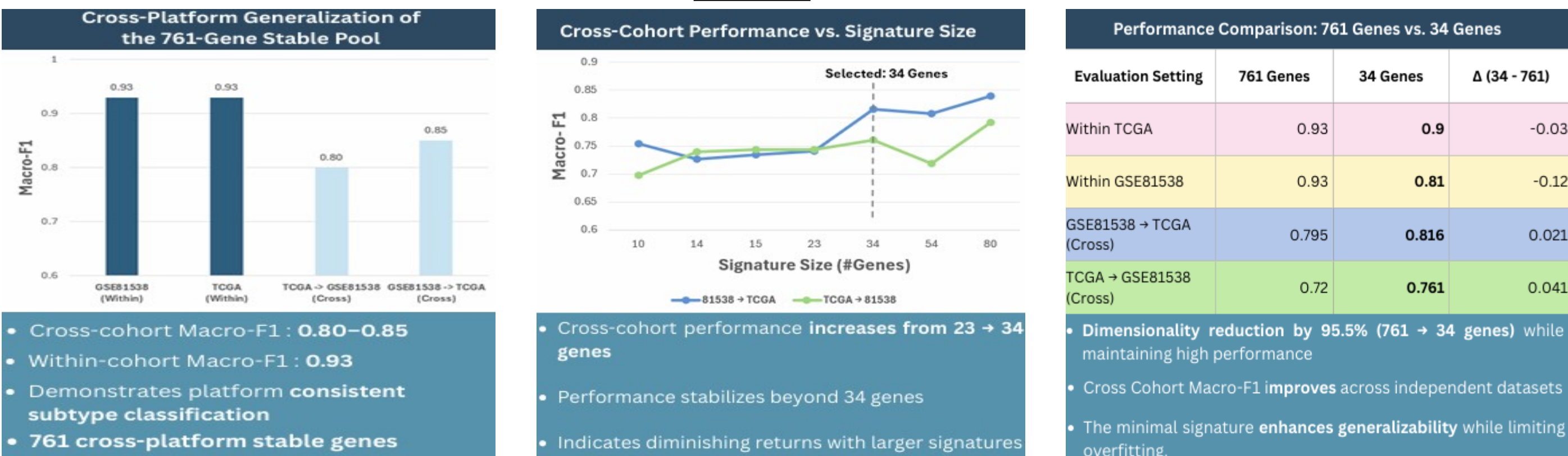
Signature Size vs. Performance: How small can a gene signature become while still maintaining strong classification accuracy?

Biological Relevance: Do the most stable subtype associated genes reflect known biological pathways in breast cancer?

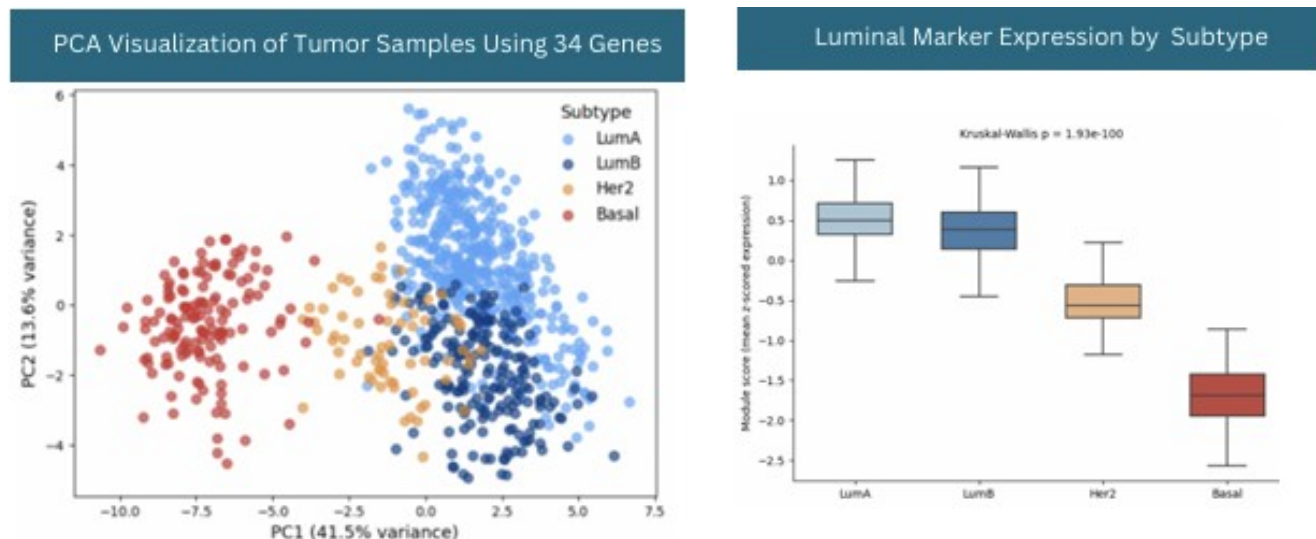
METHODOLOGY



RESULTS



CONCLUSIONS



- 34 Gene Signature clusters tumors by subtype
- Luminal Markers show expected subtype specific expression
- Validation of independent METABRIC dataset supports generalizability

CLINICAL IMPACT

- Minimal 34-gene signature could enable simpler, more affordable molecular diagnostics.
- Cross-dataset performance supports potential clinical applicability.

FUTURE WORK

- Validated in additional independent cohorts and annotated samples

REFERENCES

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