

# LKCM23015- Evaluating the Prognostic Power of Signature NP Genes in Breast Cancer Outcomes

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## Introduction

### Breast Cancer Biomarkers

Biomarkers are critical in early cancer detection and risk assessment. However, meta-analyses used to create gene signatures can inadvertently favor genes unrelated to cancer processes, thus diminishing the potential effectiveness of these signatures.

### Current Biomarkers

Venet and Dumont's 2011 study revealed that even random gene expression profiles are often significantly correlated with breast cancer outcomes. This phenomenon primarily stems from the inadvertent emphasis on proliferation genes, which, despite their relevance, may overshadow other informative non-proliferation (NP) genes in predictive models.

### Non-Proliferation Genes

If non-proliferation (NP) genes are given a fair chance of selection, would that improve the existing gene signature set? Non-Proliferation Genes  
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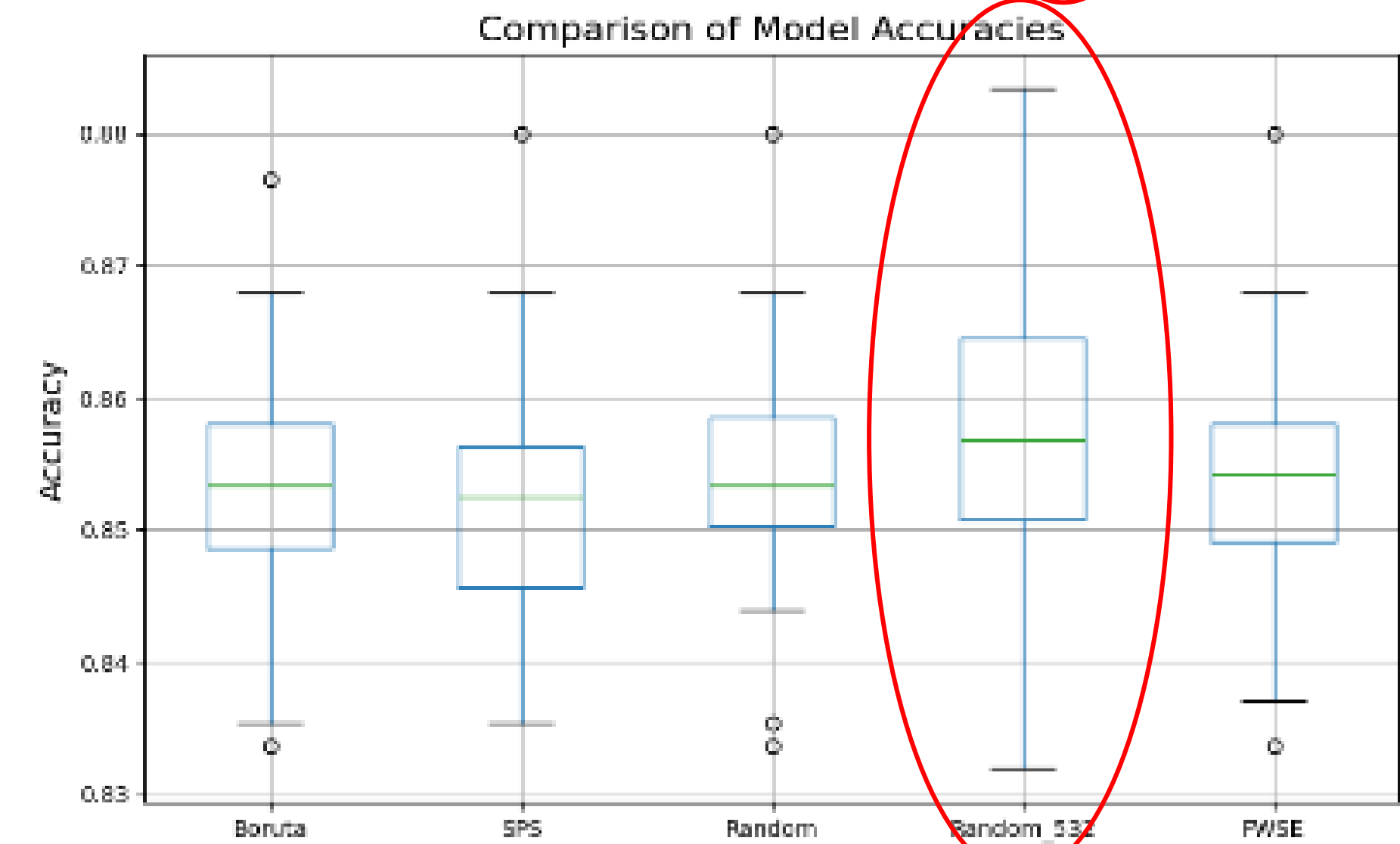
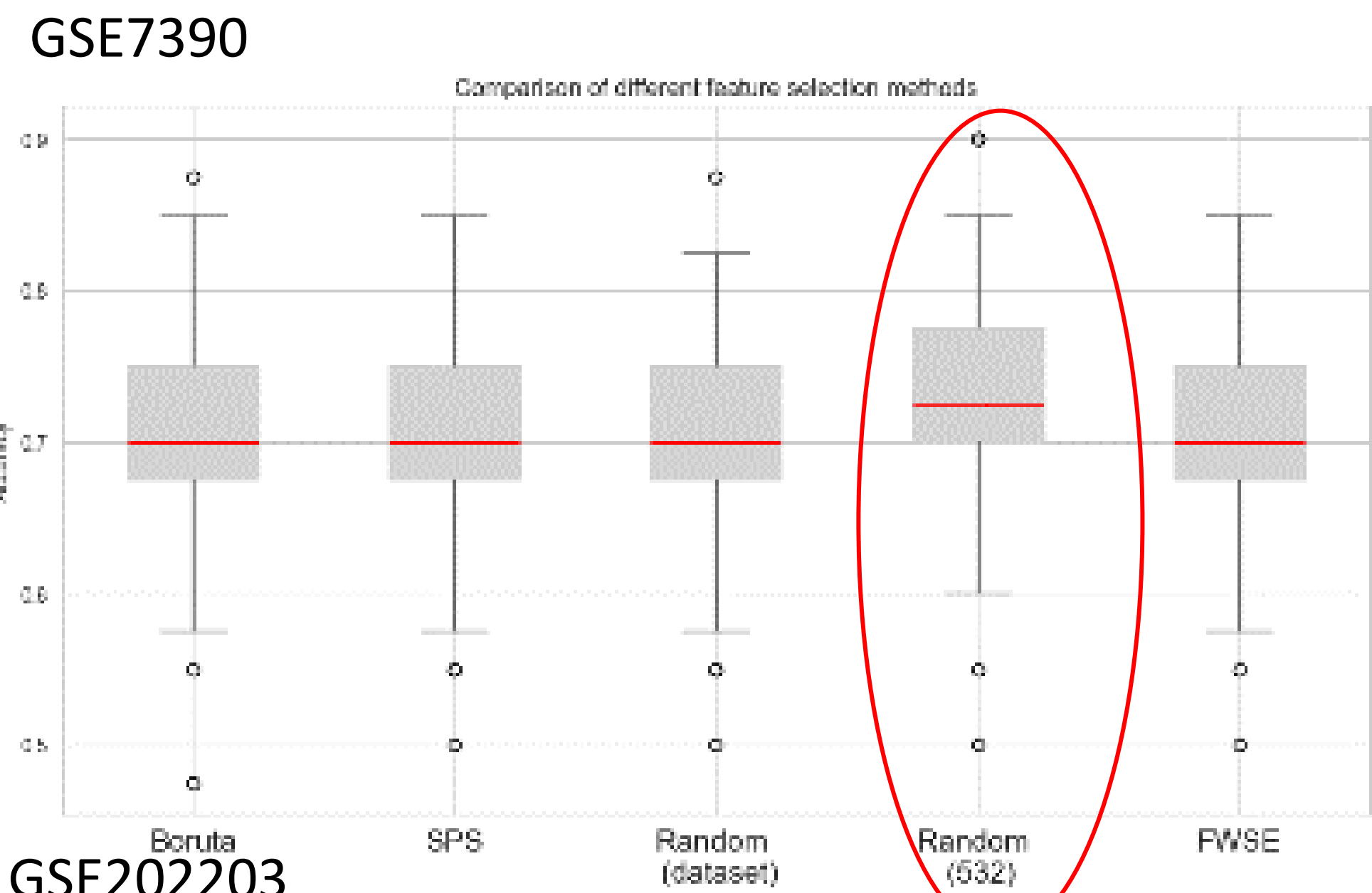
## Methodology

Aim: Give NP genes chance to be selected

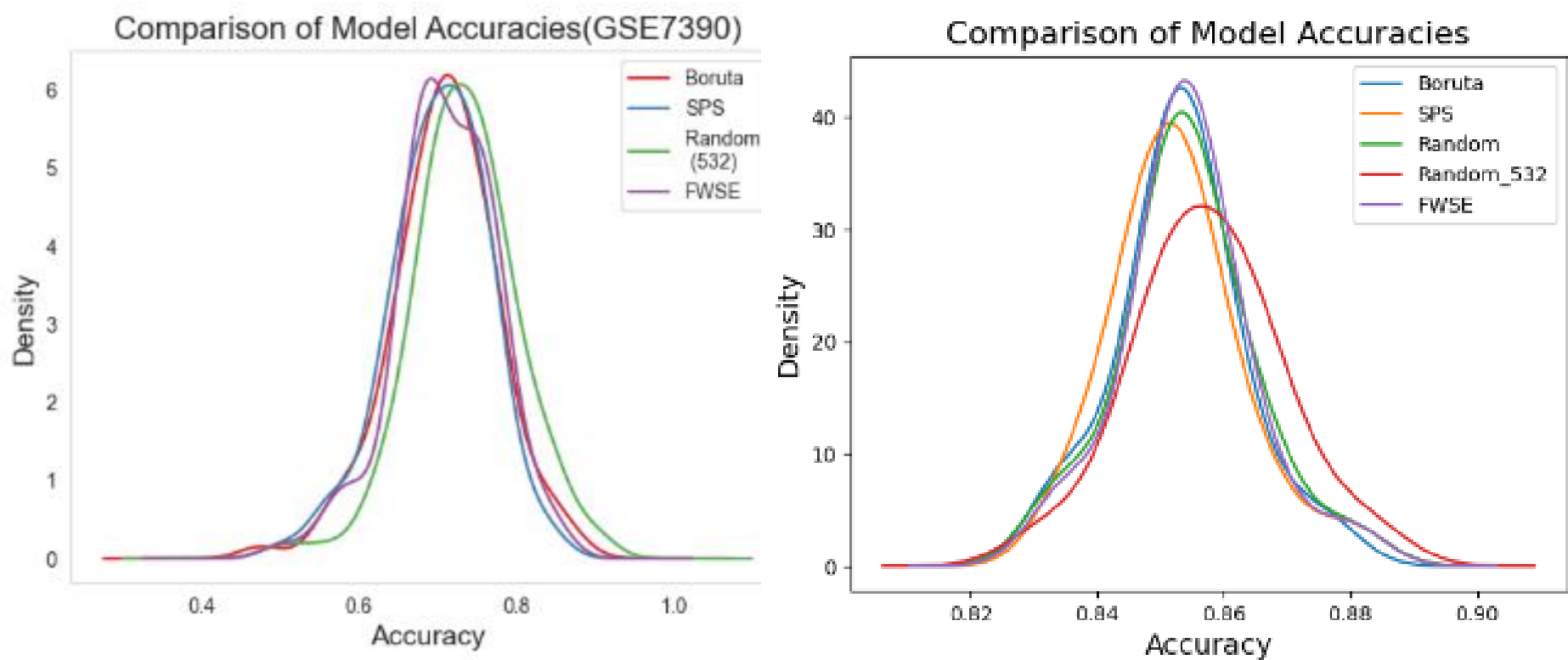
- Balance proliferation and non-proliferation genes.

Type	Subtype	Selection Method	
		p(P) < 0.05	p(NP) < 0.05
Signatures only has NP genes		NIL	Union
p(NP) ~= p(P)	num(P) > num(NP)	Intersection	Union
	num(NP) > num(P)	Union	Intersection
p(P) >> p(NP)	num(P) > num(NP)	Intersection	NIL
p(NP) >> p(P)	num(NP) > num(P)	NIL	Intersection

## Results



Random genes from superset outperform those chosen from feature selection



Similar density for all except random (which makes sense)

### Conclusion

- Random selection from p-value-based superset outperforms FWSE/Boruta.
- Indicates p-value criteria's effectiveness in candidate selection.
- Necessitates advanced feature selection for precise biomarker identification.