

Acrivon
Therapeutics

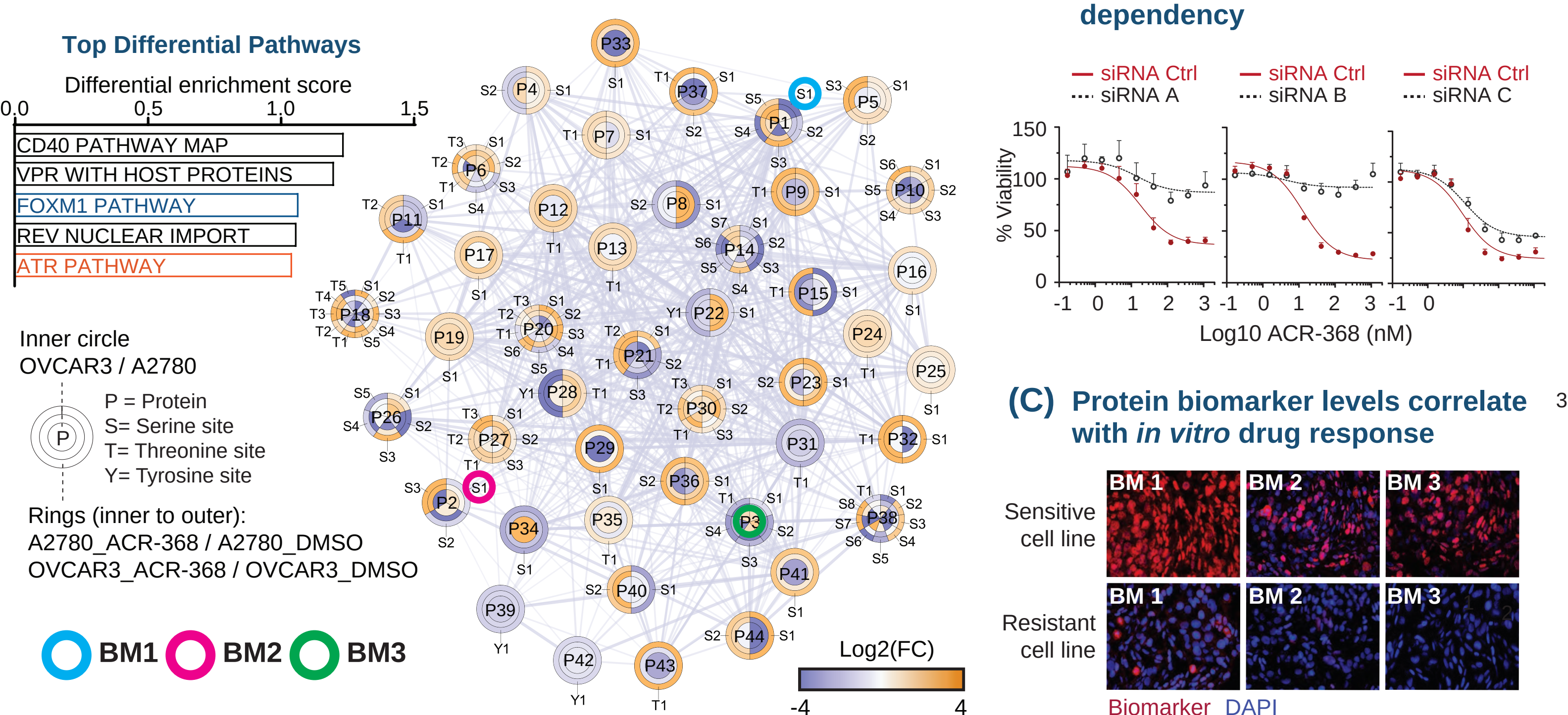
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Acrivon Predictive Precision Proteomics (AP3)

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- MS-based phosphoproteomic drug profiling and biomarker ID**
- Biological sample**
- Cells FFPE Fluid Tumor
- Protein extraction and proteolysis**
- Protein Peptides
- PTM enrichment and mass spectrometry**
- Quantification of drug-regulated phosphosites and biological analysis**
- >100,000 phosphosites
- Technical and functional biomarker validation in human tissue and *in vivo* models**
- OncoSignature**
- OncoSignature Negative**
Predicted Non-responder
- OncoSignature Positive**
Predicted Responder
- Prospective response prediction on pretreatment tumor biopsy**
- Dose**
- | | |
|-----|-----|
| --- | BM |
| --- | Ref |
- Tumor growth**
- Vehicle Drug
- Time

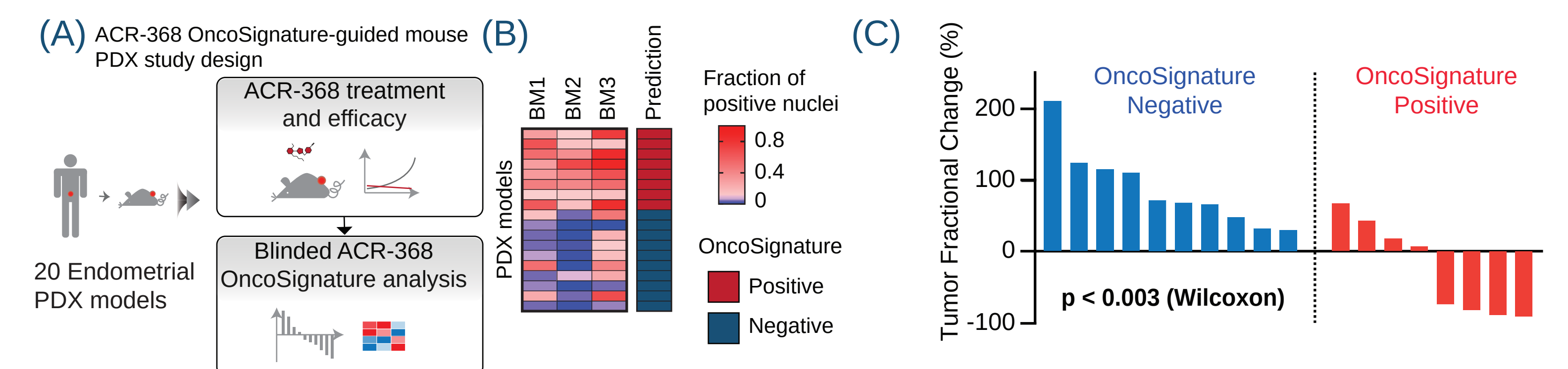
AP3 Approach Identifies Predictive Functionally Validated Biomarkers for ACR-368

(B) Validating functional biomarker dependency



(A) Top differentially ACR-368 regulated pathways were compared in sensitive OVCAR3 and resistant A2780 cells and a quantitative STRING-based network representing the drug-regulated phosphosites was used for candidate biomarker identification. **(B)** siRNA mediated knockdown of candidate predictive biomarkers abrogates sensitivity to ACR-368 in OVCAR3 cells. **(C)** Example of nuclear biomarker levels in sensitive and resistant cell lines.

ACR-368 OncoSignature-Based Response Prediction in Endometrial PDX model



(A) Outline for ACR-368 efficacy study in Endometrial PDX models. (B) Heatmap of ACR-368 OncoSignature biomarker scores and prediction in PDX models. (C) Positive ACR-368 OncoSignature enriches ACR-368 responding Endometrial PDX tumors. The bar graph shows tumor response by tumor size change with ACR-368 treatment relative to vehicle control.

Conclusions and Future Directions

