

P2.2268: Large-Scale Plasma Proteomic Profiling Reveals Treatment-Stratified Landscapes and Prognostic Biomarkers in Patients with Non-Small Cell Lung Cancer (NSCLC)

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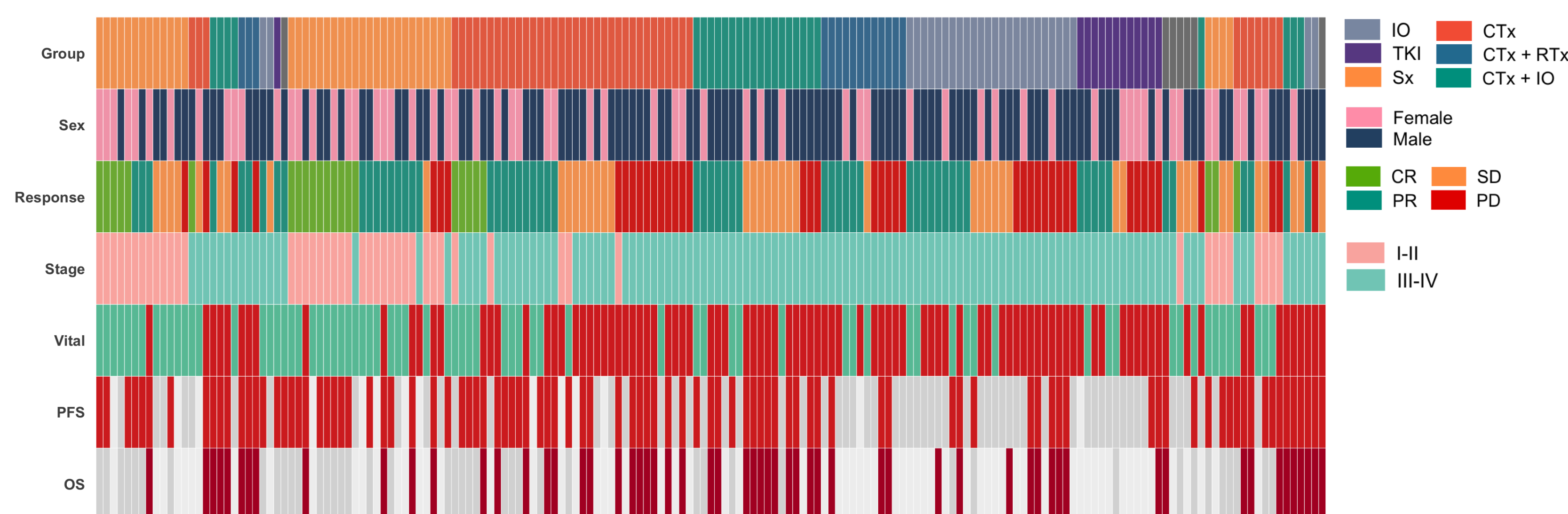
Summary

High-plex plasma proteomic profiling effectively captures the dynamic physiological landscape of NSCLC treatments. These immune-related signatures provide a promising, minimally invasive foundation for real-time patient stratification and long-term prognostic monitoring. Here we report preliminary results from cohort studies profiling the blood proteome of patients with NSCLC patients before and after surgical tumour resection and for patients undergoing Immune Checkpoint Inhibitor therapy +/- chemotherapy or chemotherapy alone as first-line treatments. The proteome profile was obtained using the Nomic Bio 1000-plex nELISA platform, achieving scalable and low-cost proteome profiles of immune pathways, inflammatory factors, and disease-specific markers in various cancers. Many of our detected markers have been reported in the literature as potential cancer prognosis biomarkers, providing motivation for expanded studies utilizing these plasma profiles and statistically robust methods to accurately stratify patients into their appropriate treatment types, with this scalable platform having significant translational potential.

Methods

Nomic Bio nELISA Panel: Plasma proteome profiles were obtained from patients pre- and post-surgery and post-immunotherapy treatment.

Standard of Care		ICI/TKI Cohort Samples	
Pre Treatment	139	Pre Treatment	54
Post Treatment	18	Post Treatment	11



Risk Predictions from Pre-Treatment Plasma

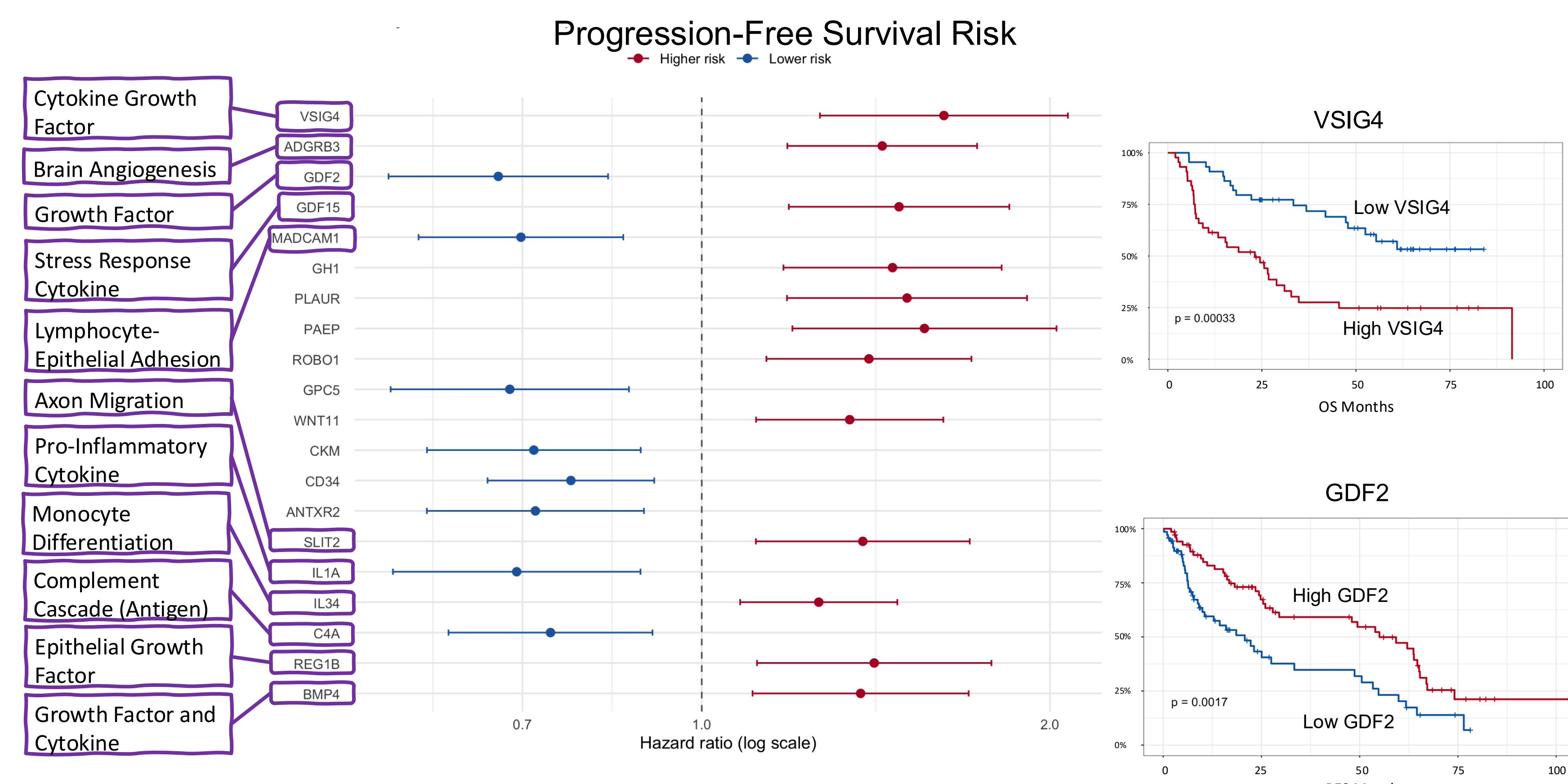
Pre-treatment blood proteome provide indicators of risk for cancer progression/recurrence

 $HR < 1$

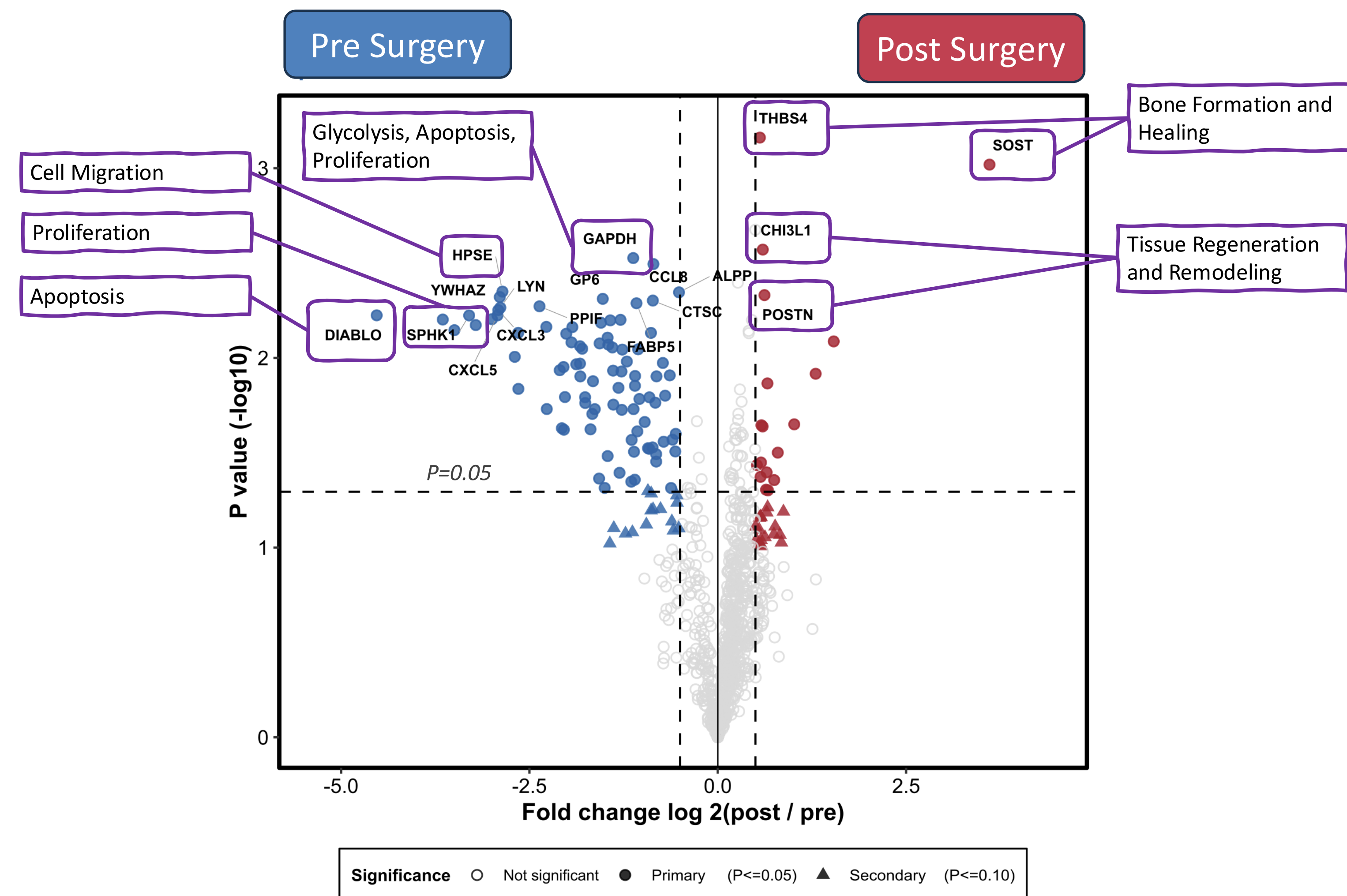
Growth factors, lymphocyte adhesion molecules, cell signaling, metabolism, hematopoietic stem cells, monocyte differentiation, antigen complement

 $HR > 1$

Markers for cytokines, angiogenesis, growth factors, cell adhesion, immunomodulators, axon development, interleukin signaling, and migration



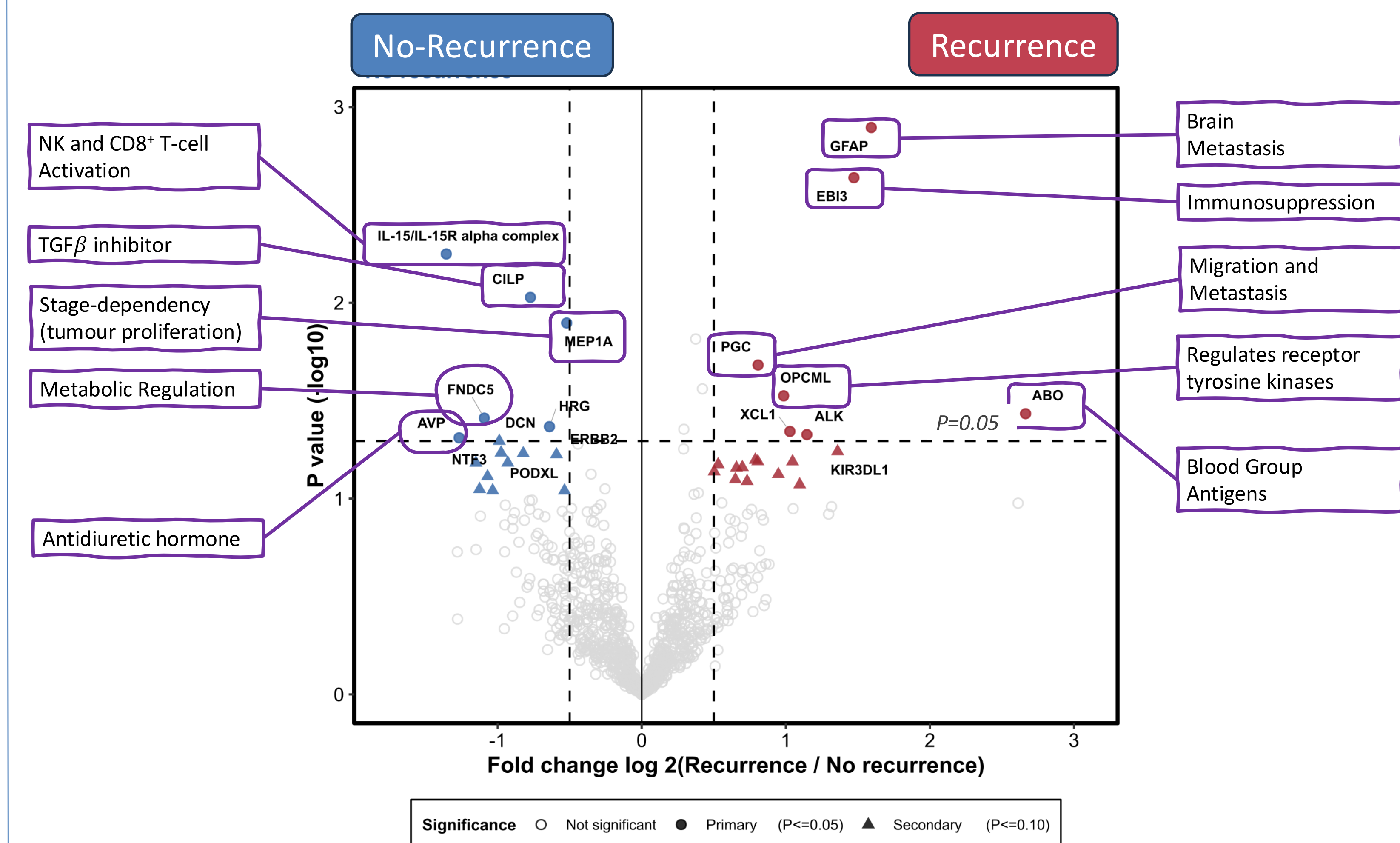
Longitudinal Surgery-Induced Changes



Pre- and Post- Lobectomy Associated Changes (n=13 patients)

Differences attributable to tissue re-modelling and wound healing increased compared to tumour proliferation, apoptosis, and metabolic markers which decreased post-surgery.

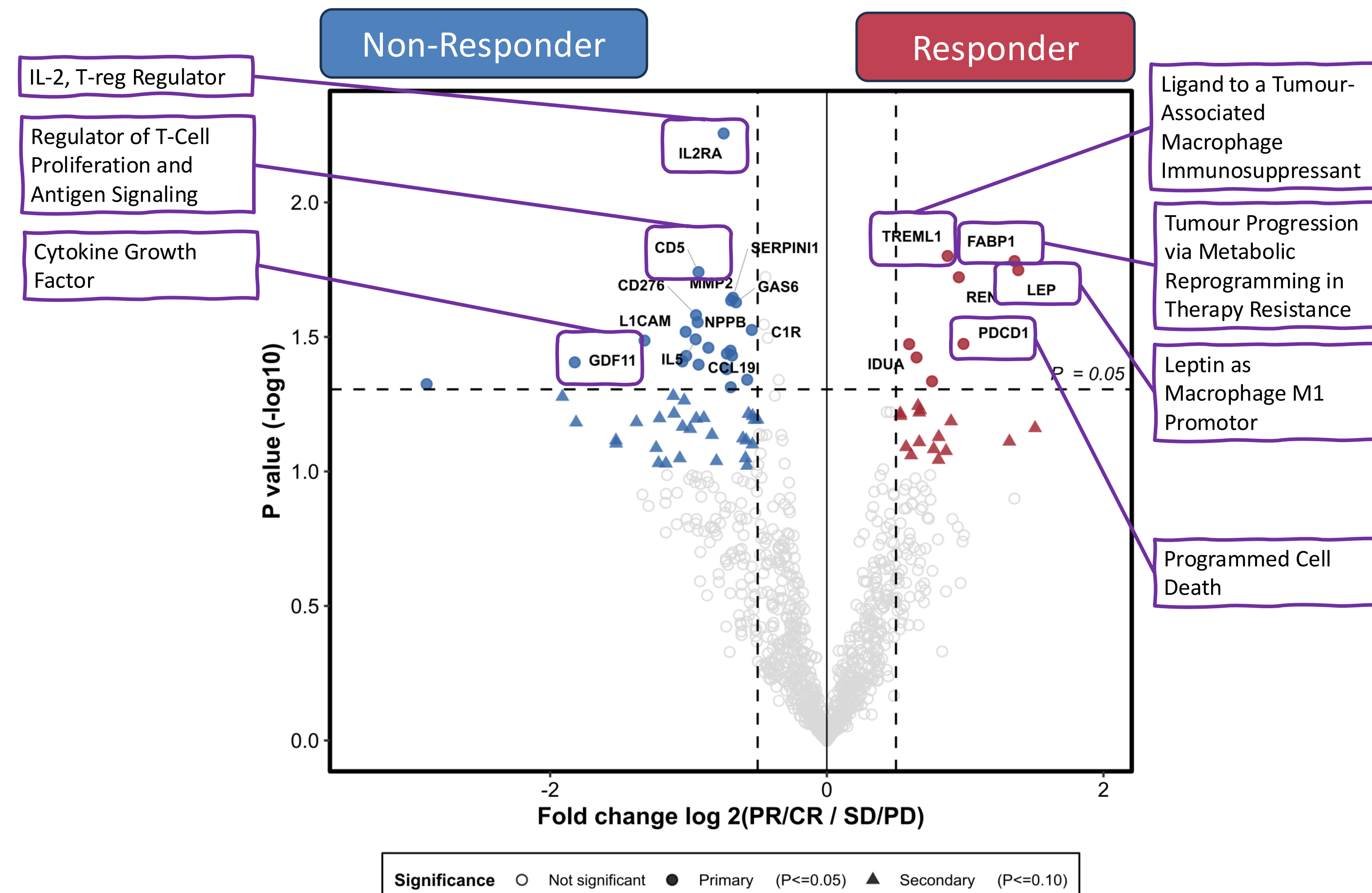
Cancer Recurrence Post-Surgery Profile



Post Surgery Recurrence Profile (n=16 Recurrent Patients, n=20 Non-Recurrent Patients)

Patients with cancer recurrence post-surgery showed elevated markers for potential brain metastasis and immunosuppression. High risk (HR > 1) was also associated with cytokines, angiogenesis, and blood group markers.

Immunotherapy Response

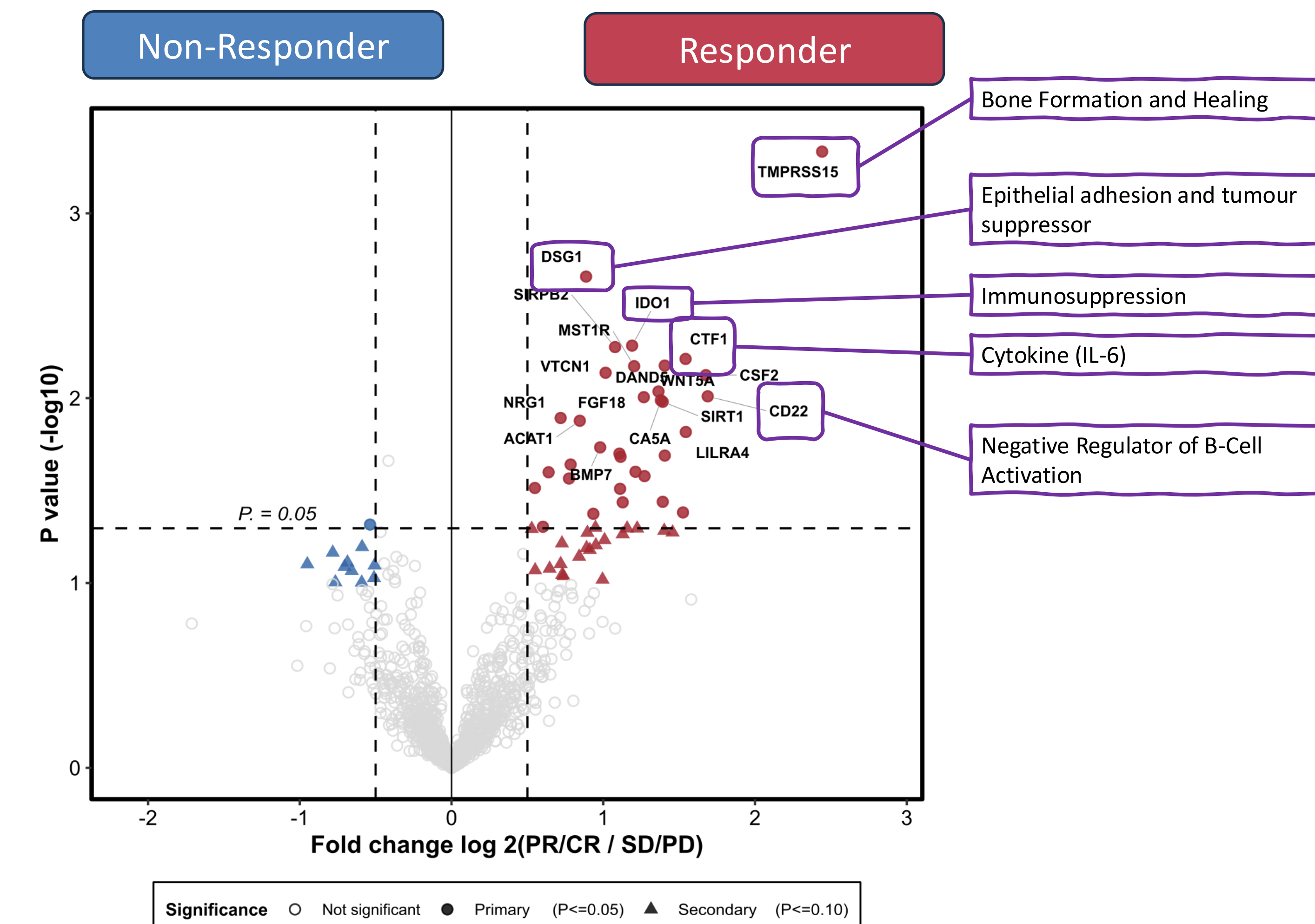


Immunotherapy (+ SOC) Response Difference (n=21 Responders, n=31 Non-Responders)

HR > 1 differentially expressed proteins attributable to macrophage immunosuppression, metabolic reprogramming, and cell death factors.

HR < 1 differentially expressed proteins attributable to IL-2 regulation of T-regs, regulation of T-cell proliferation, growth factors, neuron adhesion, and interleukin signaling.

Response to Chemotherapy



Chemotherapy (+ Additional Therapies) Response Profile (n=24 Responders, n=30 Non-Responders)

Differentially expressed proteins were low risk (HR < 1) and attributable to wound healing, epithelial adhesion, immunosuppression (tryptophan scavenging by IDO1), interleukin signaling, and regulation of B-cell activation