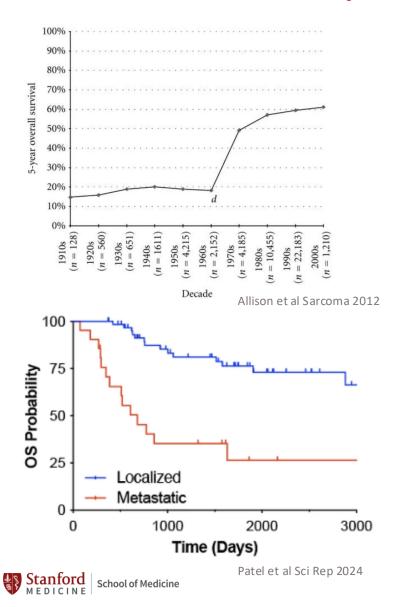


Evaluating tumor evolution and mechanisms of resistance in osteosarcoma

Chelsey M Burke, MD
Clinical Assistant Professor
Stanford University Children's Health

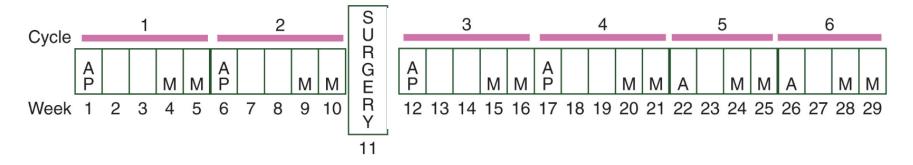
Genomic Instability and Heterogeneity in Osteosarcoma

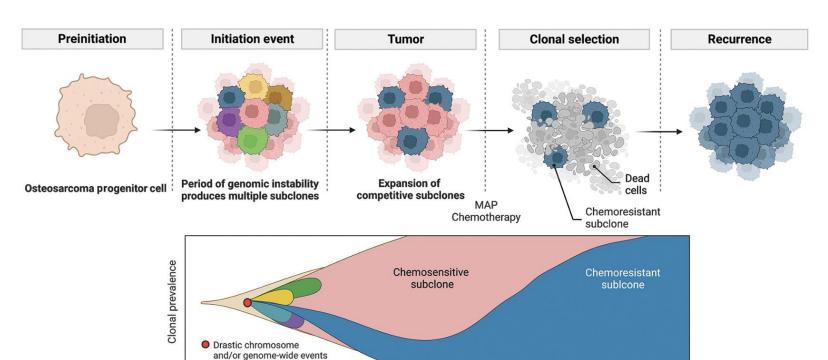




Clonal evolution in resistant osteosarcoma

A – Doxorubicin 75 mg/m²/course P – Cisplatin 120 mg/m²/course M – Methotrexate 12 g/m²/course

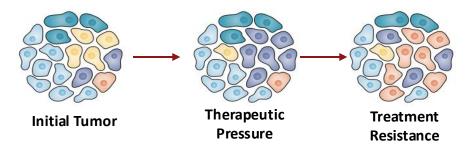


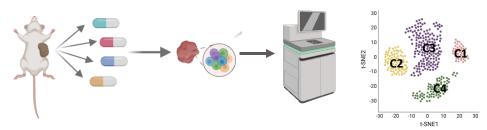




Michael Kinnaman

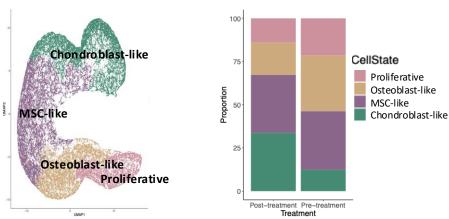
Single-cell RNAseq

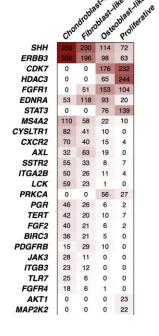




Identify and target Master Regulators of Therapy Resistant States

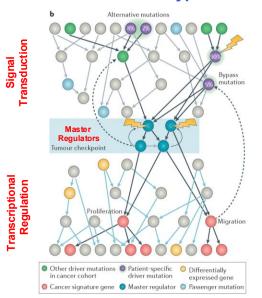
Single cell RNA-seq of pre- vs. post-treatment tumors identifies cell state-specific depletion

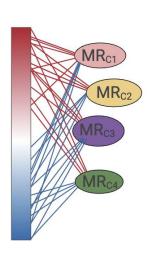




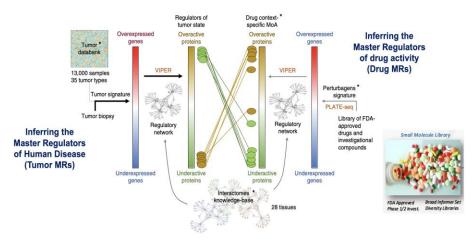
'Bottle-neck' analysis

Tumor Bottleneck Hypothesis

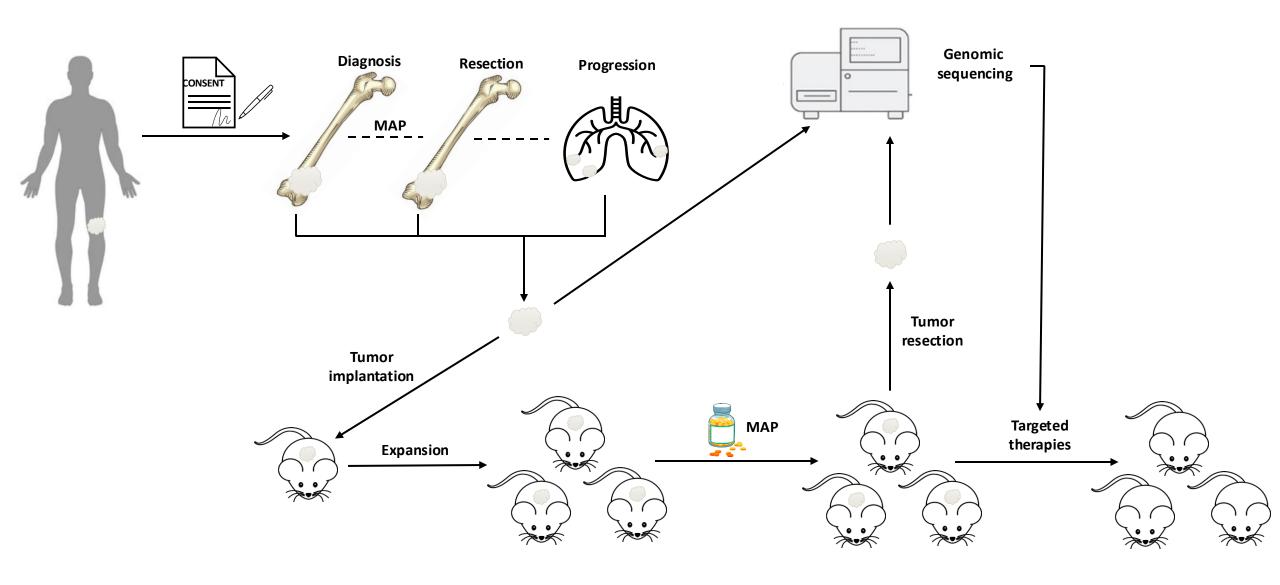




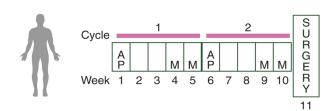
OncoTarget[™] and OncoTreat[™]

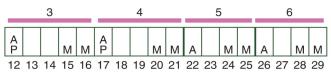


Evaluating tumor evolution in osteosarcoma PDX models

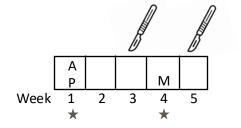


Replicating MAP therapy in PDX models





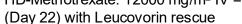


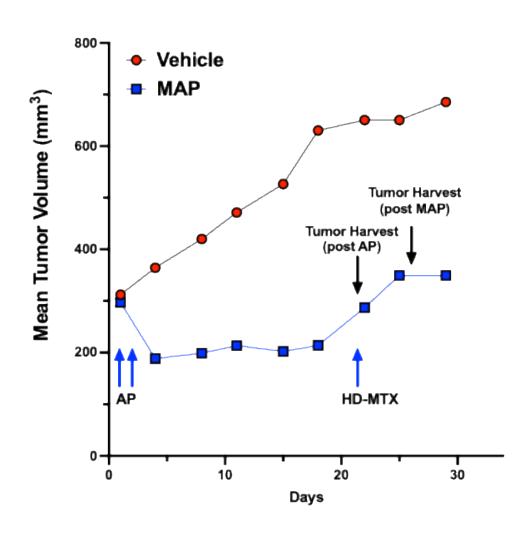


★ Subcutaneous fluid support Leucovorin rescue

Mouse-equivalent dosing of MAP

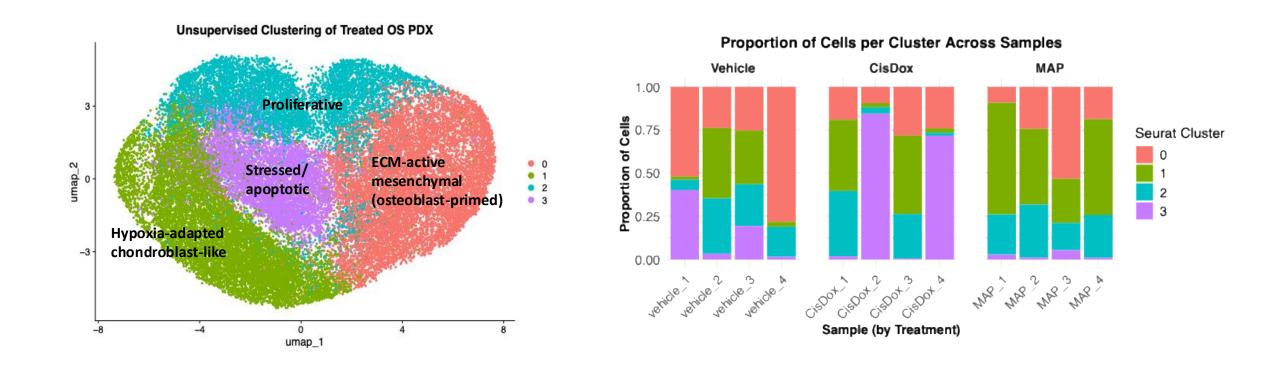
Doxorubicin: $37.5 \text{ mg/m}^2 \text{ IV} = 6 \text{ mg/kg IP (Day 1, 2)}$ Cisplatin: $60 \text{ mg/m}^2 \text{ IV} = 3 \text{ mg/kg IP (Day 1,2)}$ HD-Methotrexate: $12000 \text{ mg/m}^2 \text{ IV} = 225 \text{ mg/kg IP}$





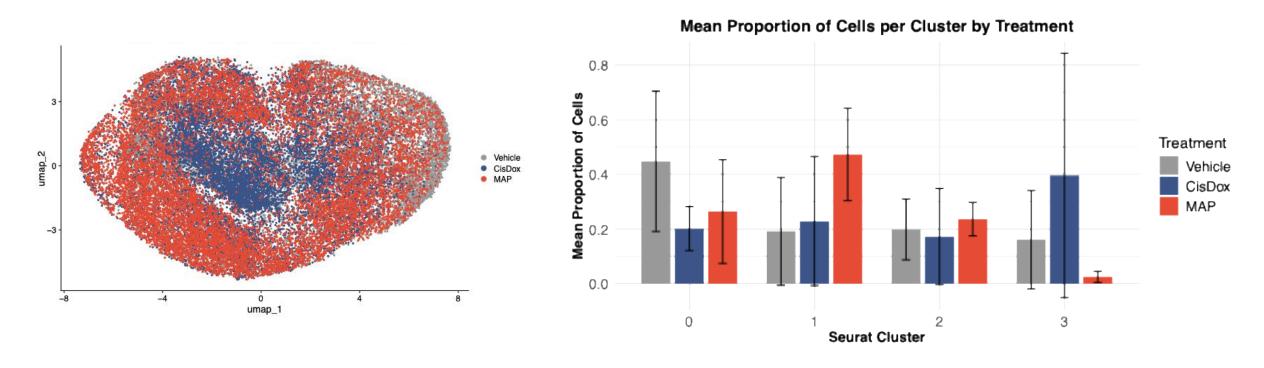
Gene expression analysis of treated OS PDX snRNA-seq

snRNA-seq for 264,401 high-quality tumor nuclei across 12 samples (n = 4 / treatment arm)



 Subpopulation proportions vary between replicates, emphasizing the need for multiple biological replicates to capture true treatment effects

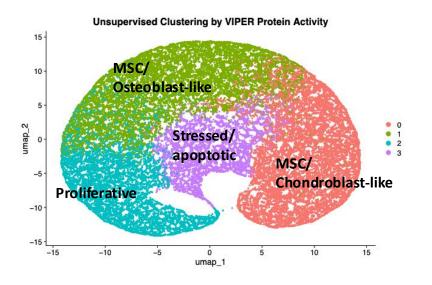
Gene expression analysis of treated OS PDX snRNA-seq



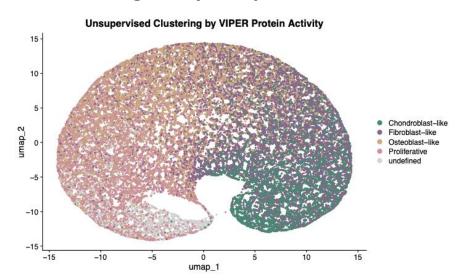
- Chemotherapy treatment alters cell state composition
- Depletion of ECM-active mesenchymal (osteoblast-primed) C0 cells and expansion of Hypoxiaadapted chondroblast-like C1 cells post MAP chemotherapy
- Stressed/apoptotic cells most enriched after Cisplatin/Doxorubicin, consistent with predominant cell death occurring with these drugs

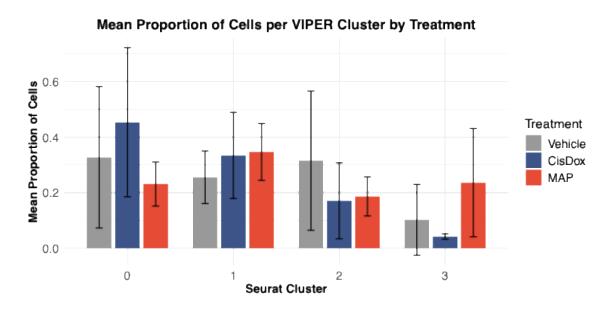
VIPER-inferred protein activity analysis of treated OS PDX snRNA-seq

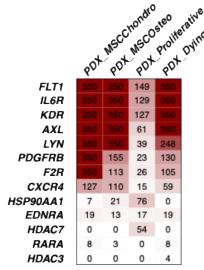
Transform gene expression profiles to activity profiles for ~3,000 transcriptional regulators



Patient heterogeneity recapitulated in the PDX







OncoTarget of treated versus vehicle tumor cells can identify cell state-specific therapeutic vulnerabilities activated post chemotherapy for therapeutic translation

Ongoing research and future directions

- Complete MAP treatment of PDX models (n=5 discrete models)
- Analyze single cell data to characterize cell state-specific evolution in response to chemotherapy treatment
- Utilize regulatory network analysis to identify and target MRs of chemotherapy-resistant disease
- Perform in vivo validation of MR predictions



A special thank you to #BecauseOfAva, the Levin family, and all of the OsteoWarriors and OsteoAngels!

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Raven Rose

Xinyi Wang

MSKCC

Jovana Pavisic Damon Reed **Emily Slotkin** Julia Glade Bender Asmin Tulpule

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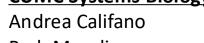


Jovana Pavisic



The Dela Cruz/Kung Lab











Thank You!

