

# Convergence of Divergent Tumors: A Systems Biology Approach of Tumor-specific Signaling

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## Purpose & Objectives

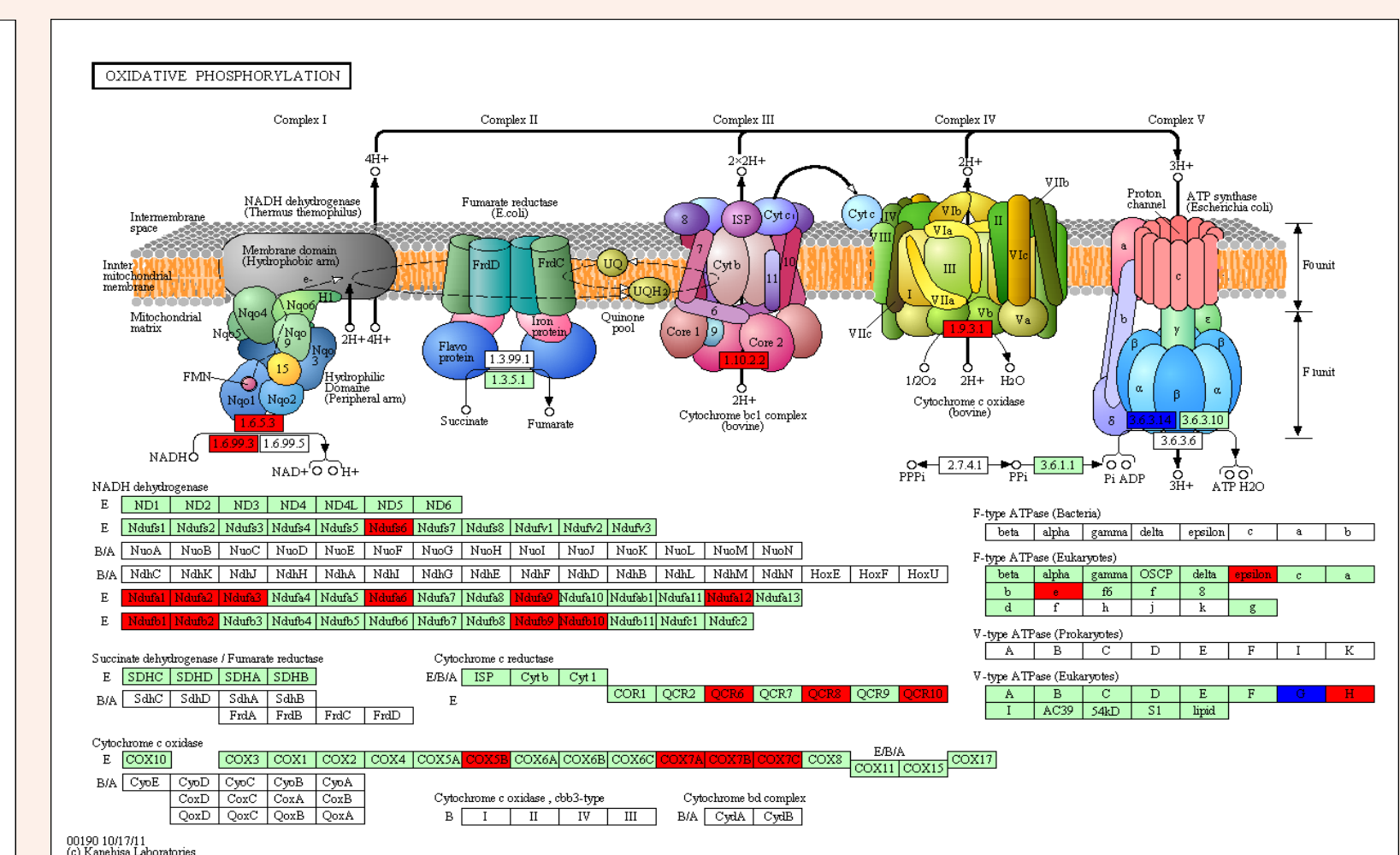
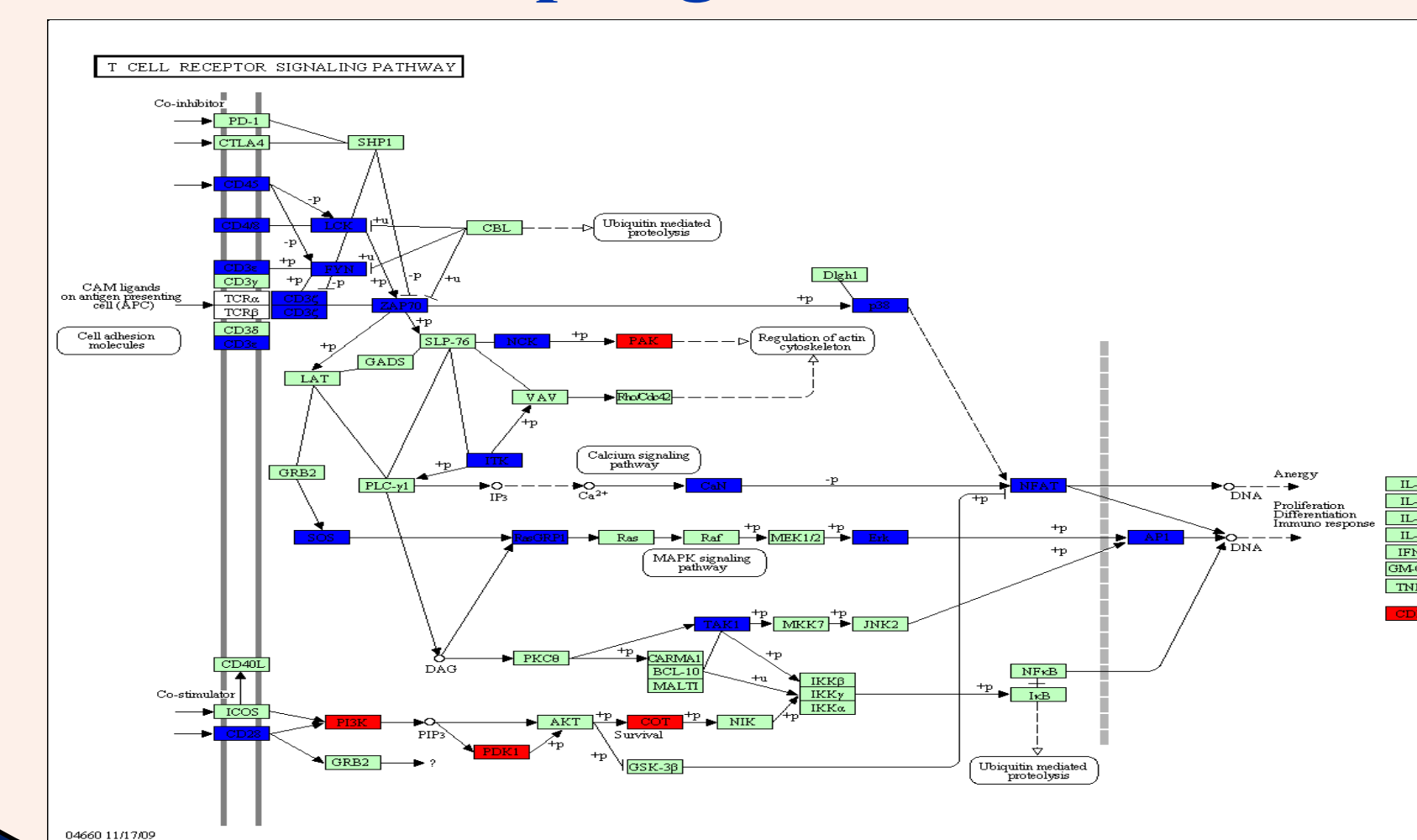
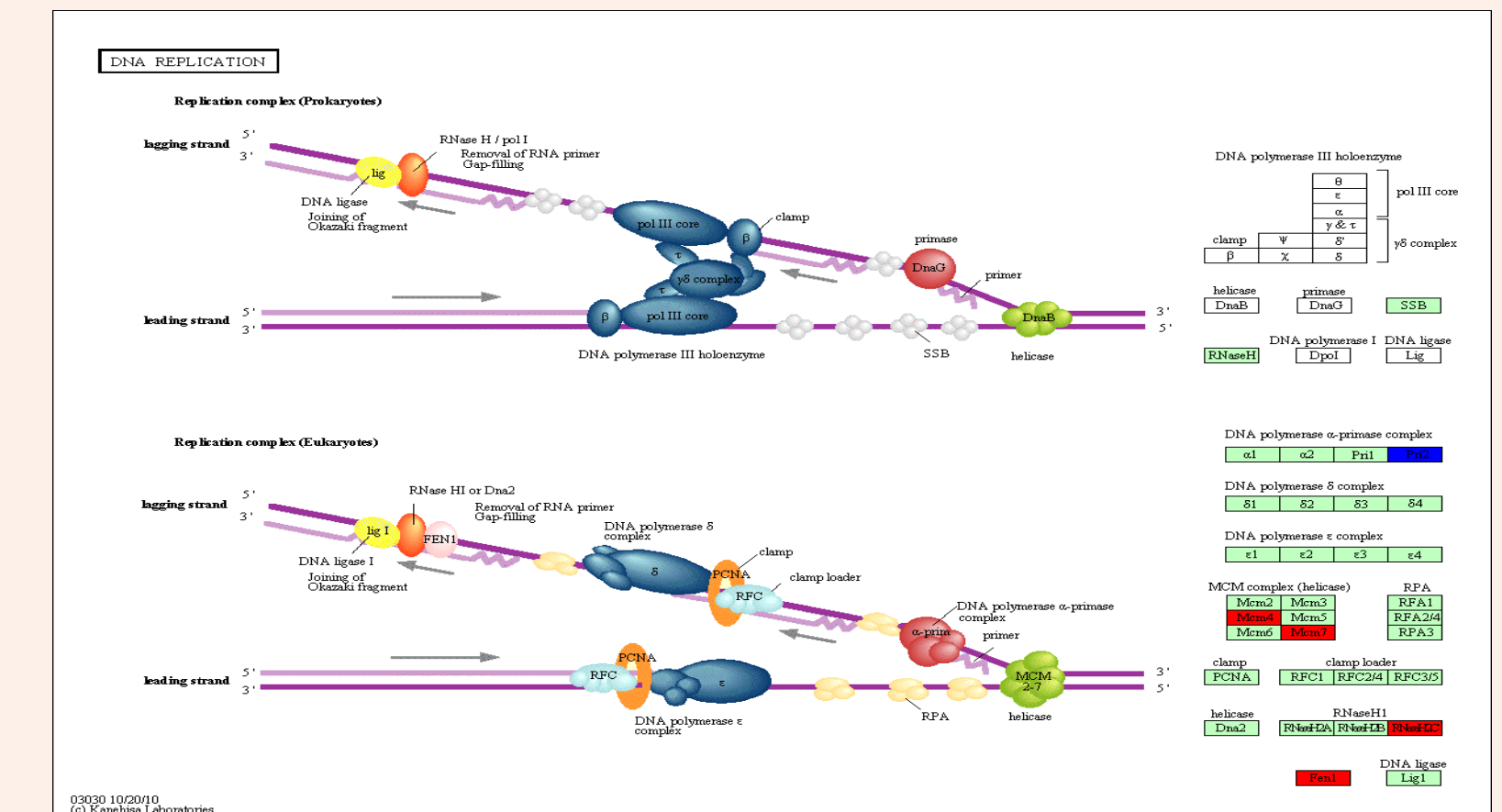
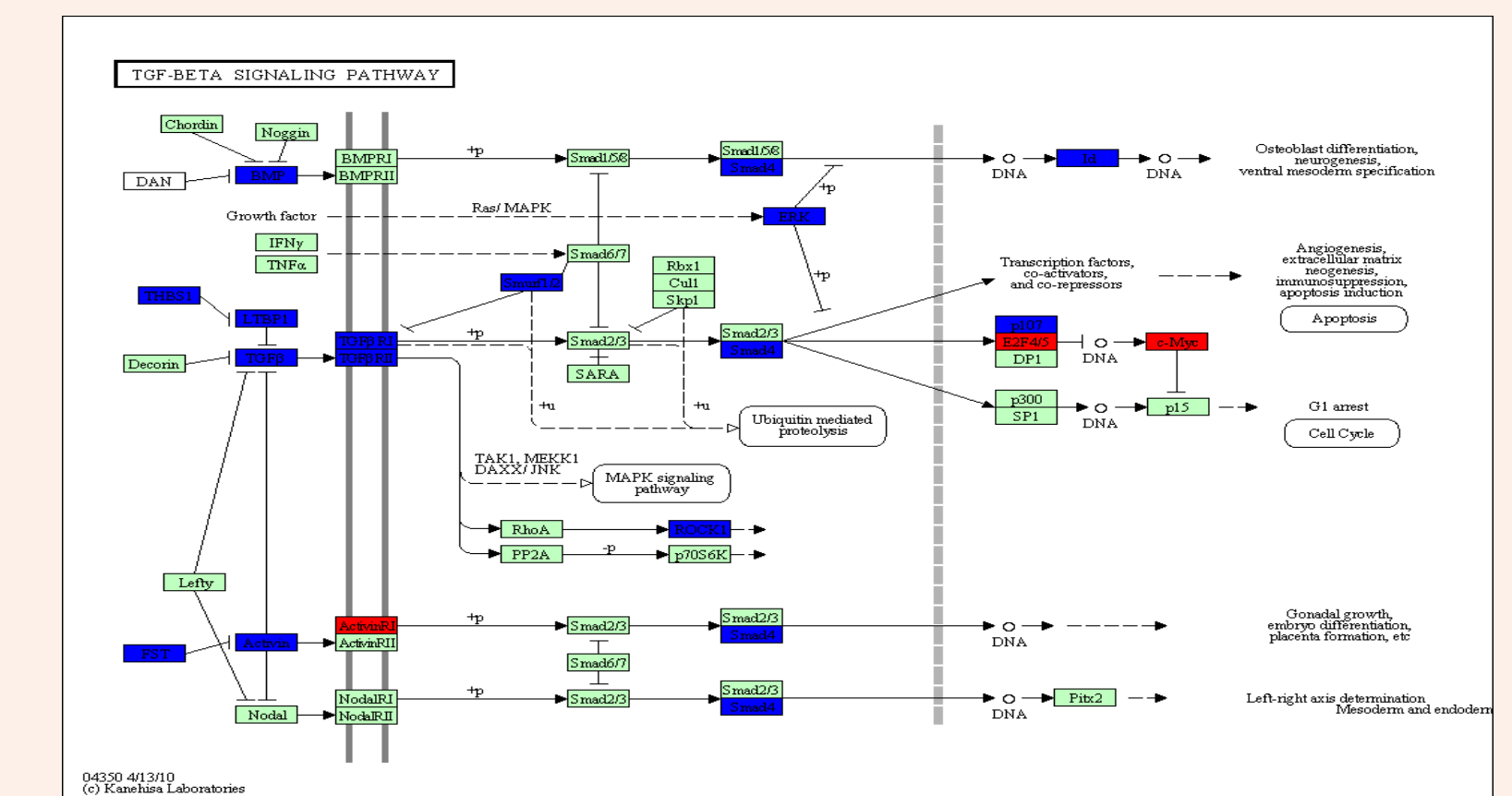
We **hypothesized** that divergent tumor types share common components inherent to oncogenesis. The **specific aim** of this study is to identify convergent gene expression among divergent cancer types. We performed a systematic analytical approach to probe Gene Expression Ominibus (GEO), a public database, using bioinformatics tools.

## Methods

- ❖ Created a subset of the GEO database containing 23 tumor datasets, including blood, breast, soft, squamous, colon, ovarian, prostate, renal, soft tumor.
- ❖ Applied Bioconductor programming language to conduct bioinformative analysis. Each dataset were:
  - Filtered
  - Normalized
  - ArrayQualityMetrics applied
  - Linear model fit and Bayes function applied
  - KEGG pathways applied

## Results

- ❖ 2000 intersection genes differentially expressed
- ❖ 240 KEGG Signaling Pathways impacted [shown in figures: Up-regulated (red); down-regulated (blue)]
- ❖ The most dramatic signaling pathways impacted are:
  - TGF $\beta$  signaling pathway completely shutdown .
  - Immune response signaling pathways are down-regulated.
  - Mini Chromosome Maintenance (MCM) complex are up-regulated.
  - Four of five components of oxidative phosphorylation electron transport chain are up-regulated.



## Conclusions

We conclude that divergent tumors share certain common components inherent to oncogenesis and that some of these impact unique or previously unappreciated signaling pathways. This leads us to hypothesize that targeting converged tumor core processes can be a potential and potent therapeutic tool.

### Acknowledgement

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