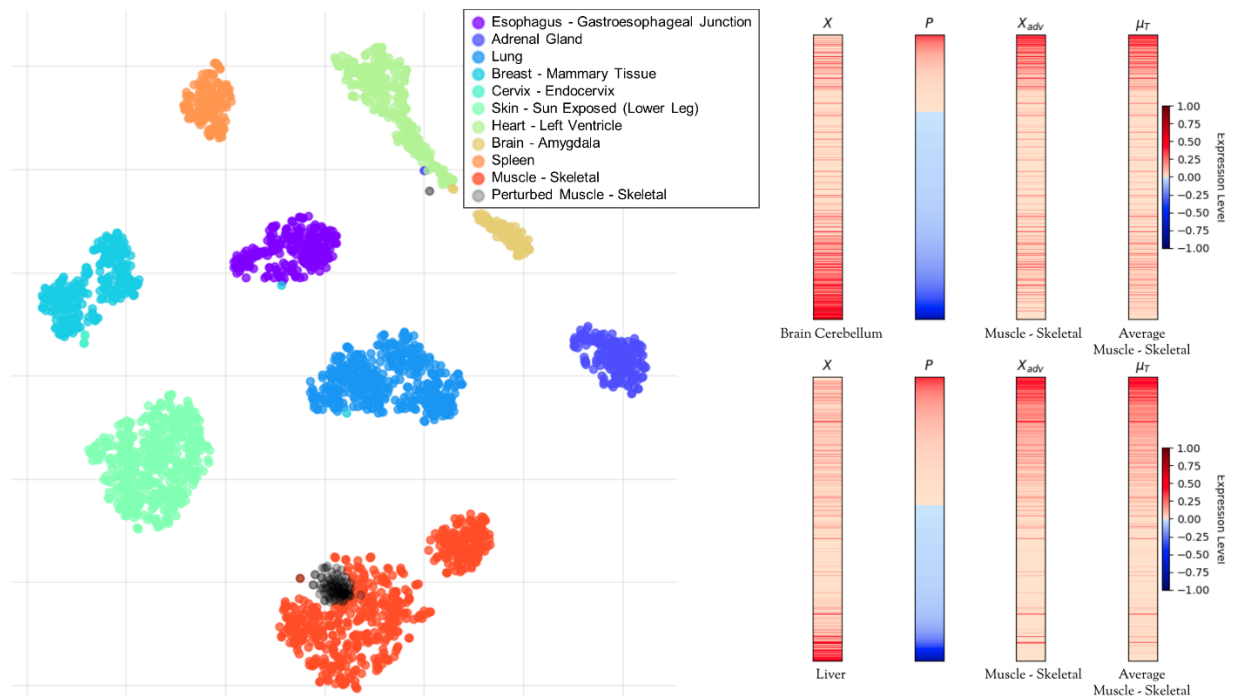


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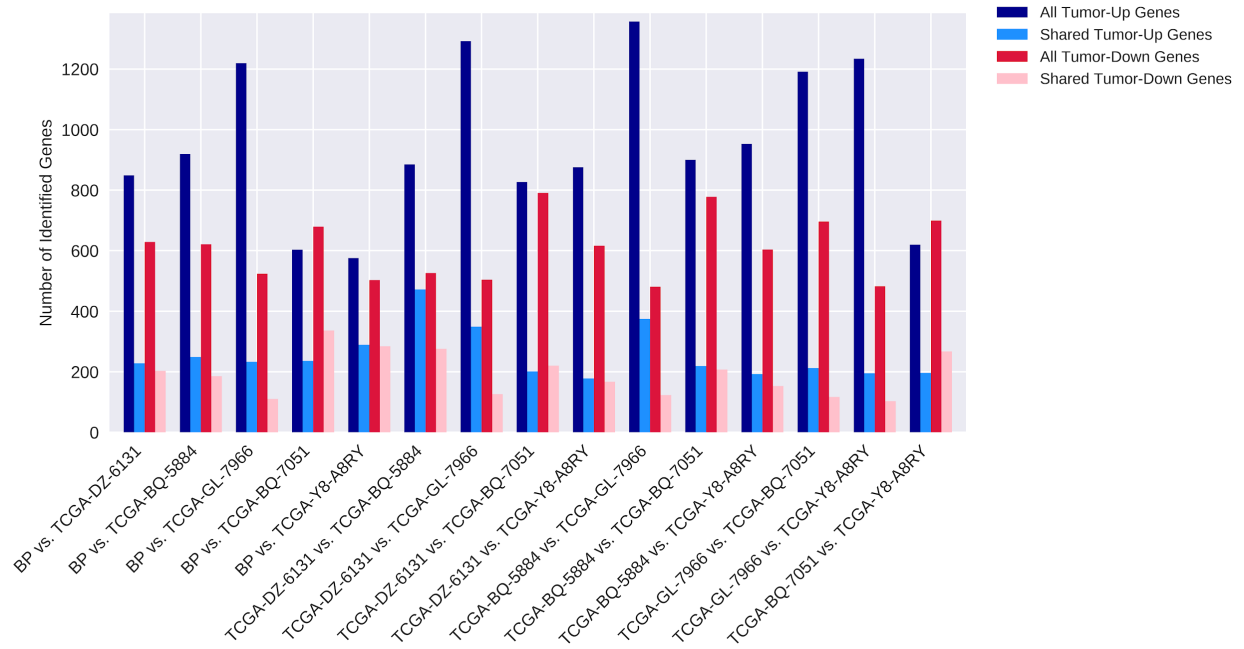
Supplemental Information

**Cellular State Transformations Using Deep
Learning for Precision Medicine Applications**

**Colin Targonski, M. Reed Bender, Benjamin T. Shealy, Benafsh Husain, Bill
Paseman, Melissa C. Smith, and F. Alex Feltus**



Supplemental Figure S1. Adversarial Generation for Muscle-Skeletal Target Using all Hallmark Genes as the Input Gene Set. t-SNE plot of original and perturbed samples using the all Hallmark genes (left). Heatmap of cellular transformations from Brain-Cerebellum and Liver to Muscle-Skeletal (right). Perturbations (P) range from $[-1, 1]$, which is added to original sample (x), then adversarial sample (x_{adv}) is clipped to $[0, 1]$. The mean expression vector (μ_T) of the target class (Muscle-Skeletal) is shown.



Supplemental Figure S2. Uniquely Perturbed Genes in Kidney Tumors.

Comparison of TSPG results between patients shows a pattern of more unique *tumor-upregulated* genes being identified than *tumor-downregulated* genes.