In this talk, I will present the development of our transcriptome deconvolution model, DeMixT, and the subsequent development of transcriptional activity score (TAS) and our biological findings using the consortial datasets from The Cancer Genome Atlas and from the International Cancer Genome Consortium. We have developed a new summary metric using sequencing data from patient tumor samples, to compute, in vivo and using deconvolution, the relative global gene expression level of tumor cells. TAS may serve as a tractable phenotype to help elucidate the biology that underlies metastasis, prognosis and response to treatment in cancer.