

## Article

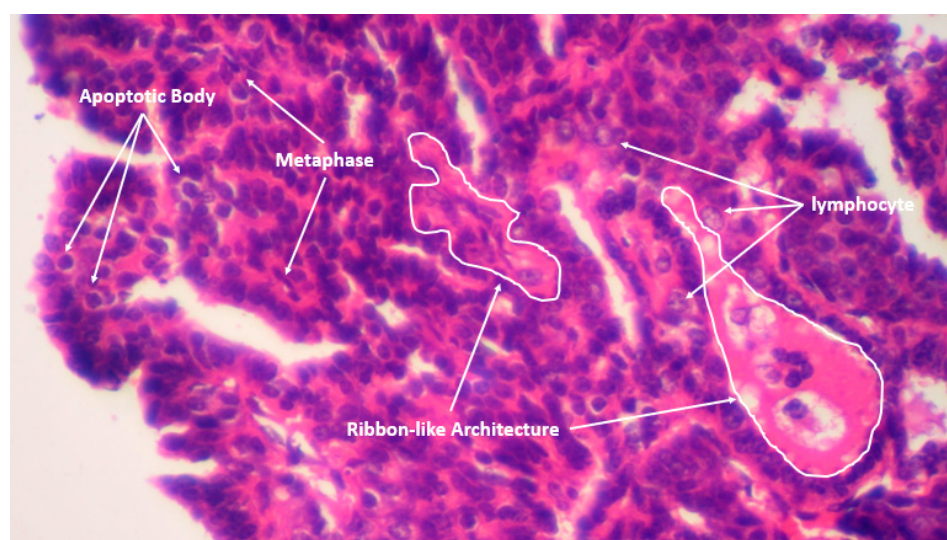
# Comparative Gene Signature of (–)-Oleocanthal Formulation Treatments in Heterogeneous Triple Negative Breast Tumor Models: Oncological Therapeutic Target Insights

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## Supplementary Materials:



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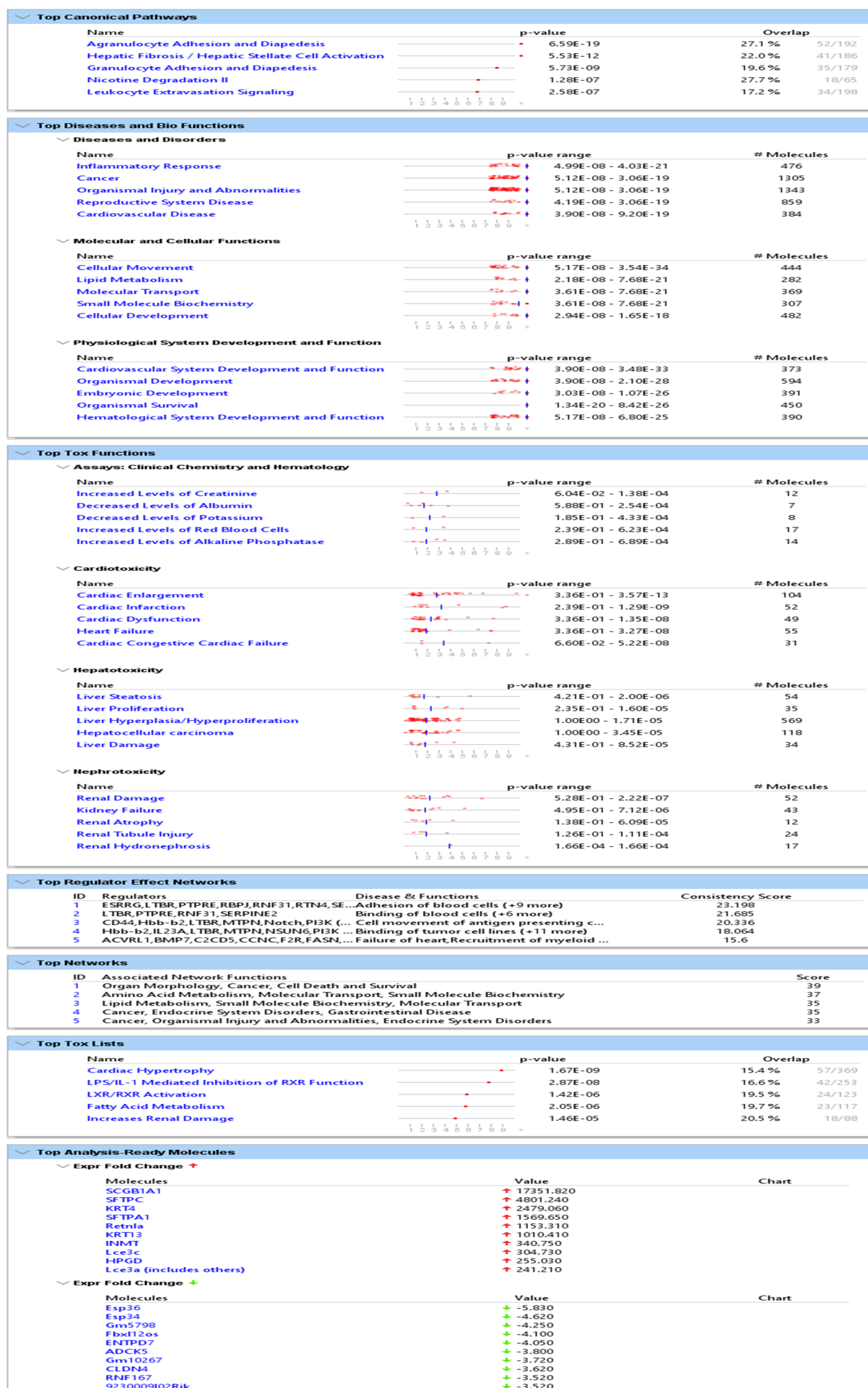


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**Supplementary Figure S1:** Expansion of the H&E stained tumor micromorphology changes in MMTV-PyVT control tumor.

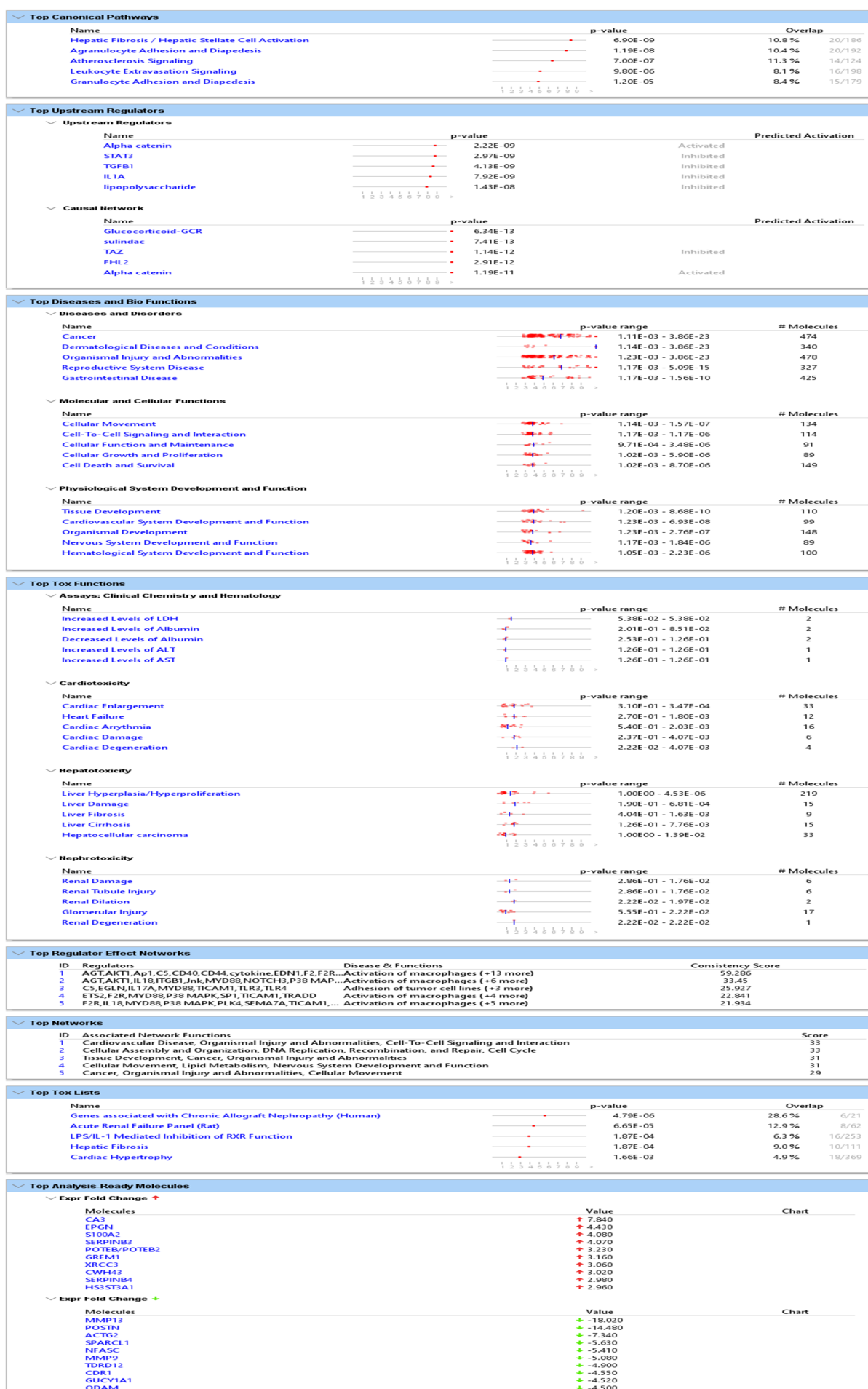
A

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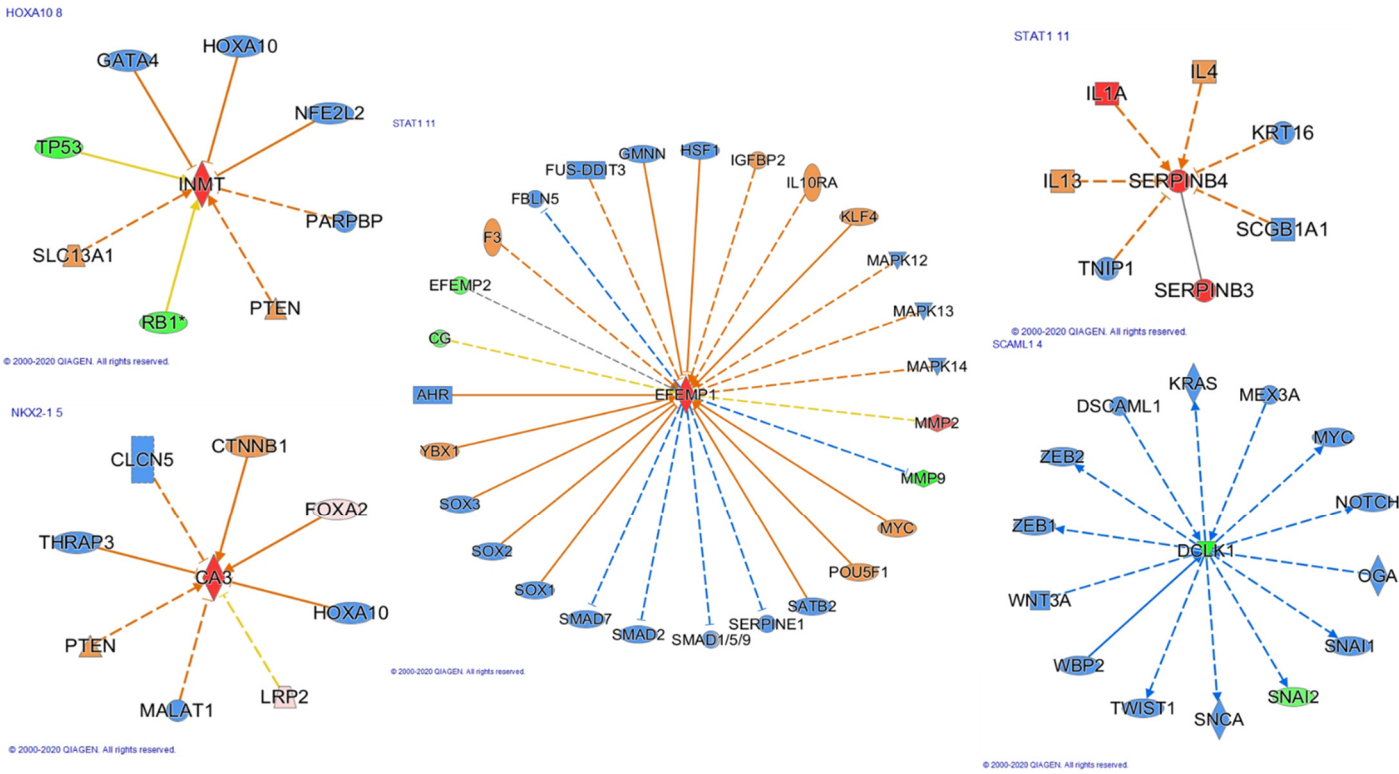


B

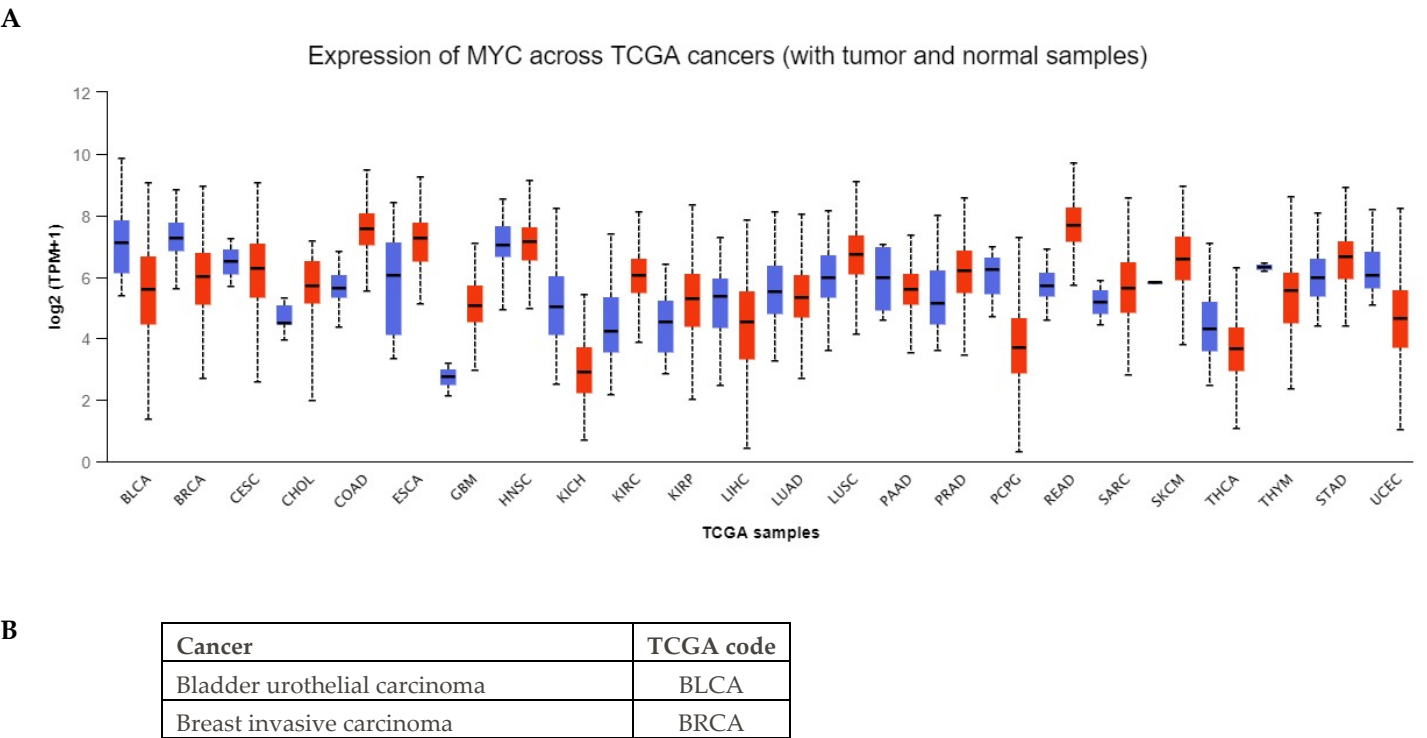
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**Supplementary Figure S2:** Ingenuity Pathway Analysis (IPA)-derived summary reports for MMTV-PyVT transgenic (A) and PDX mouse tumors (B) microarray data.



**Supplementary Figure S3:** IPA-Predicted mapping of the top affected genes by OC-X treatments overlapped in MMTV-PyVT and PDX mice tumor datasets.



Cervical squamous cell carcinoma	CESC
Cholangiocarcinoma	CHOL
Colon adenocarcinoma	COAD
Esophageal carcinoma	ESCA
Glioblastoma multiforme	GBM
Head and neck squamous cell carcinoma	HNSC
Kidney chromophobe	KICH
Kidney renal clear cell carcinoma	KIRC
Kidney renal papillary cell carcinoma	KIRP
Liver hepatocellular carcinoma	LIHC
Lung adenocarcinoma	LUAD
Lung squamous cell carcinoma	LUSC
Pancreatic adenocarcinoma	PAAD
Prostate adenocarcinoma	PRAD
Pheochromocytoma and paraganglioma	PCPG
Rectum adenocarcinoma	READ
Sarcoma	SARC
Skin cutaneous melanoma	SKCM
Thyroid carcinoma	THCA
Thymoma	THYM
Stomach adenocarcinoma	STAD
Uterine corpus endometrial carcinoma	UCEC

**Supplementary Figure S4:** Expression of MYC in different human samples. **(A)** The UALCAN for Cancer Genomics database analysis (<http://ualcan.path.uab.edu/cgi-bin/Pan-cancer.pl?genenam=MYC>) indicates the predominance of the expression of the mRNAs for MYC within the tumor and normal samples across The Cancer Genome Atlas (TCGA) database. **(B)** Key legend for the TCGA tumor samples.