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Supplementary Materials for

Transcriptional census of epithelial-mesenchymal plasticity in cancer

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Table S3
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Other Supplementary Material for this manuscript includes the following:

Tables S1 and S2

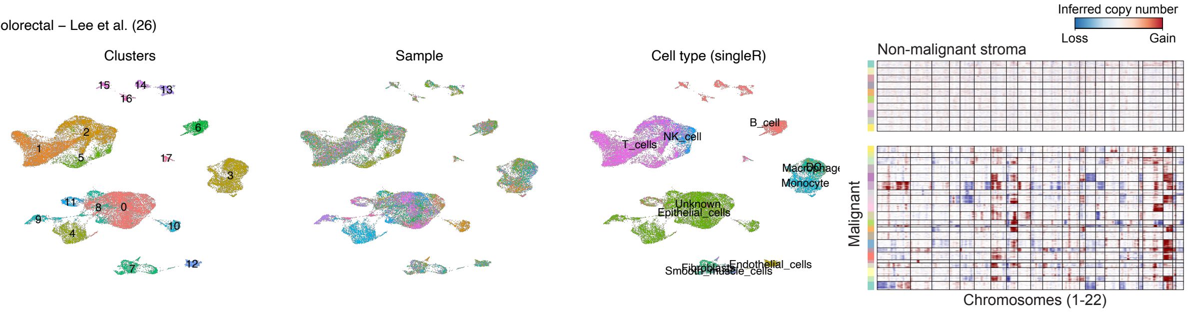
Table S1. A list of the most conserved genes associated with EMP among the 266 tumors analyzed.

Table S2. A refined list of conserved EMP genes, only including those from the signature whose expression is highly specific to malignant cells.

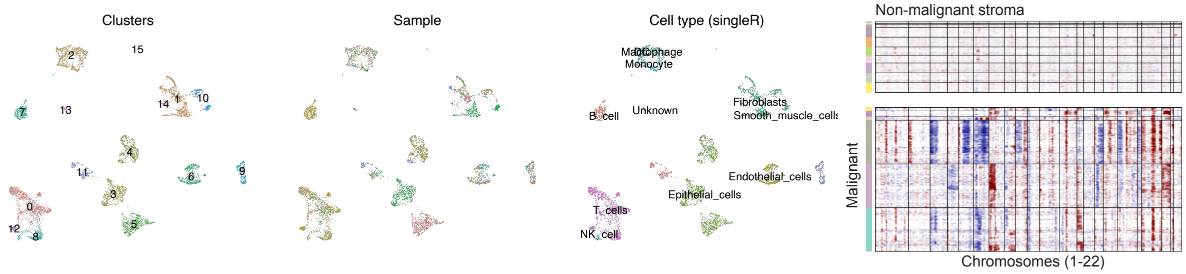
Cancer	Source	Accession	Platform	Sorted?	Patient # (>100 malignant cells)	Total cancer cell #	% mito threshold
Breast	Wu *et al.* (36)	ENA accession PRJEB35405	10x Genomics Chromium (3’ v2)	NA	4	4452	20%
Breast	Qian *et al.* (28)	http://blueprint.lambrechtslab.org	10x Genomics Chromium (3’)	NA	10	8766	20%
Breast	Bassez *et al.* (37)	http://biokey.lambrechtslab.org/	10x Genomics Chromium (5’)	NA	62	38,765	15%
Colorectal	Lee *et al.* (26)	GEO Accession GSE144735 & GSE132465	10x Genomics Chromium (3’ v2)	NA	25	18,058	20%
Colorectal	Uhlitz *et al.* (27)	Direct from authors	10x Genomics Chromium (3’ v3)	NA	8	2659	20%
Colorectal	Qian *et al.* (28)	http://blueprint.lambrechtslab.org	10x Genomics Chromium (3’)	NA	11	8766	25%
Gastric	Sathe *et al.* (29)	https://dna-discovery.stanford.edu	10x Genomics Chromium (3’ v2)	NA	7	6909	20%
Lung	Kim *et al.* (32)	GEO Accession GSE131907	10x Genomics Chromium (3’ v2)	NA	20	15,396	20%
Lung	Lambrechts *et al.* (31)	ArrayExpress Accessions E-MTAB-6149 & E-MTAB-6653	10x Genomics Chromium (3’ v1/v2)	NA	9	8036	20%
Lung	Qian *et al.* (28)	http://blueprint.lambrechtslab.org	10x Genomics Chromium (3’)	NA	24	6794	20%
Lung	Laughney *et al.* (24)	GEO Accession GSE123904	10x Genomics Chromium (3’ v2)	Viability (scatter & DAPI)	8	3097	20%
Lung	Wu *et al.* (32)	GEO Accession GSE148071	GEXSCOPE (Singleron Biotechnologies)	NA	35	54,052	30%
Nasopharyngeal	Chen *et al.* (33)	GEO Accession GSE150430	10x Genomics Chromium (3’ v2)	NA	9	7400	20%
Ovarian	Geistlinger *et al.* (34)	GEO Accession GSE154600	10x Genomics Chromium (3’ v2)	NA	5	7479	20%
Ovarian	Qian *et al.* (28)	http://blueprint.lambrechtslab.org	10x Genomics Chromium (3’)	NA	5	4967	20%
Pancreatic	Steele *et al.* (35)	GEO Accession GSE155698	10x Genomics Chromium (3’)	NA	15	10,495	20%
Pancreatic	Peng *et al.* (53)	GSA: CRA001160	10x Genomics Chromium (3’ v2)		24	41,986 (all cell types)	10%
Squamous cell carcinoma	Ji *et al.* (20)	GEO Accession GSE144236	10x Genomics Chromium (3’ v2)	NA	9	12,154	10%

Table S3. Various metadata for the tumor scRNA-seq data analyzed.

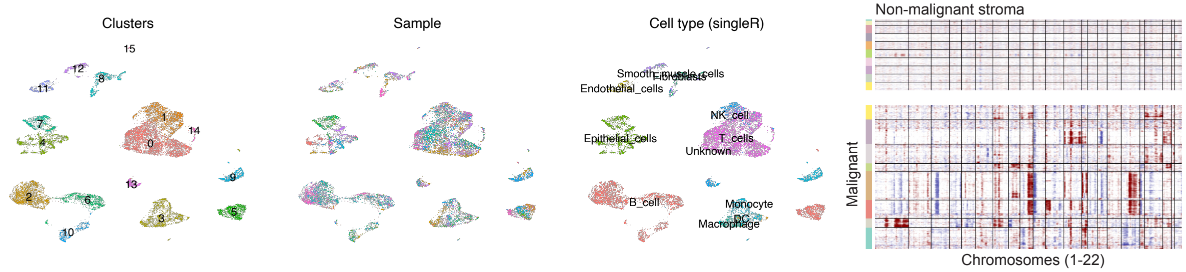
Colorectal – Lee et al. (26)



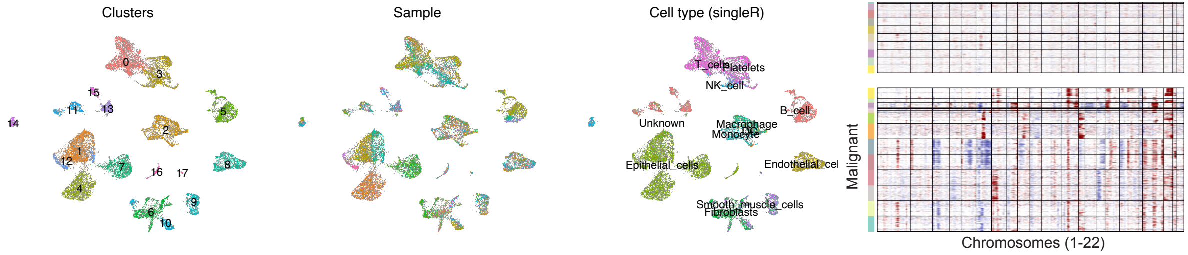
Colorectal – KUL – Lee et al. (26)



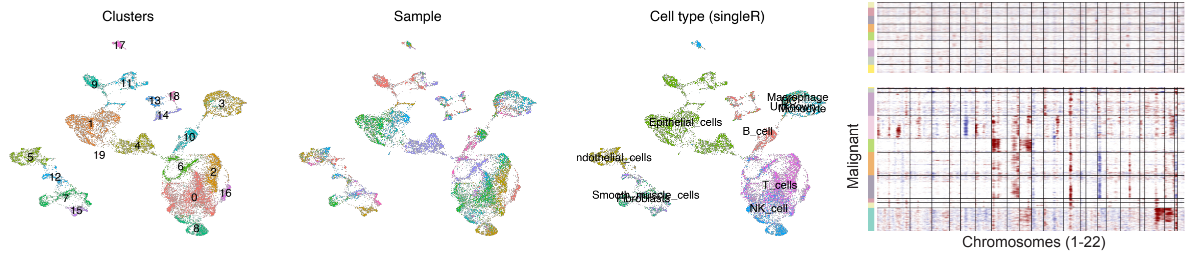
Colorectal – Uhlitz et al. (27)



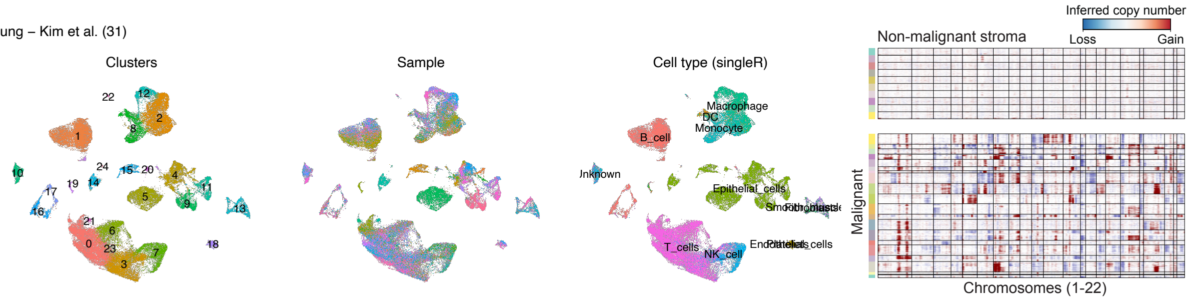
Colorectal – Qian et al. (28)



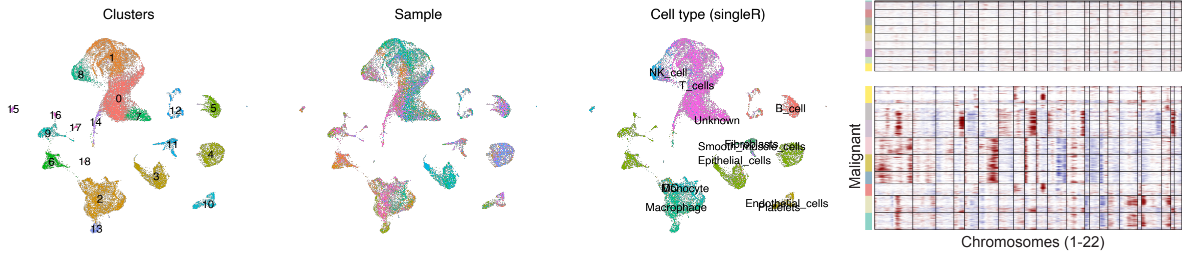
Gastric – Sathe et al. (29)



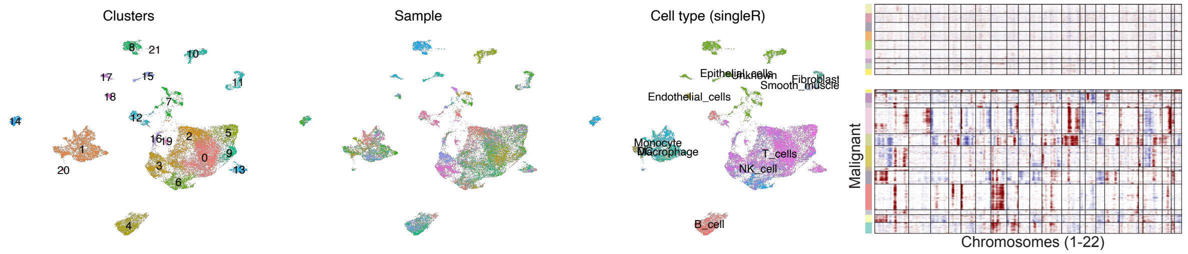
Lung – Kim et al. (31)



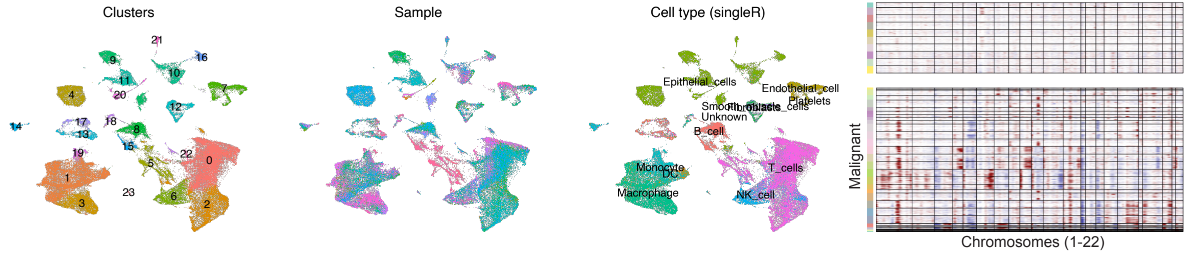
Lung – Lambrechts et al. (30)



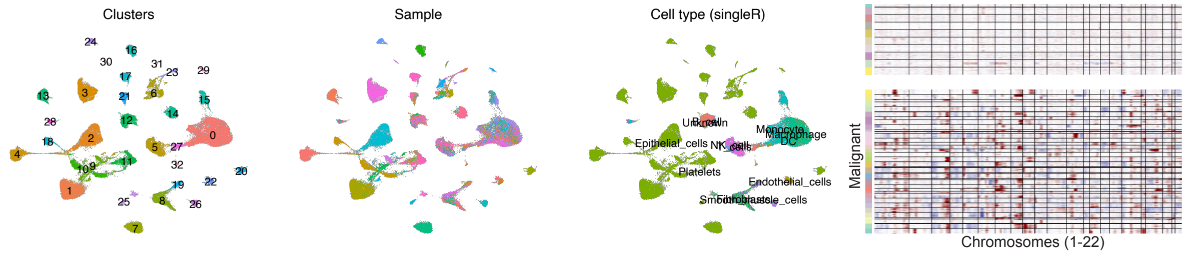
Lung – Laughney et al. (24)



Lung – Qian et al. (28)



Lung – Wu et al. (32)



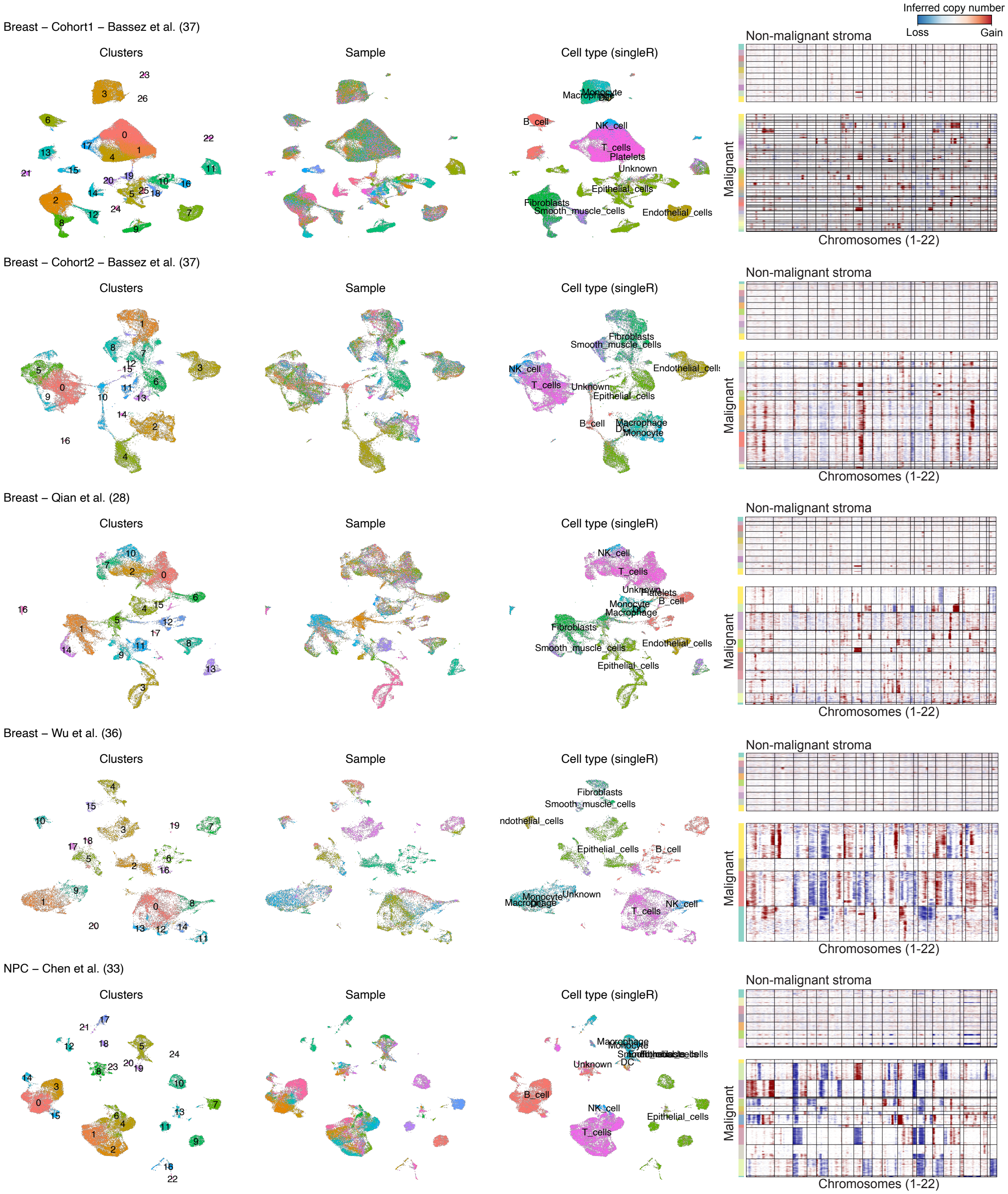
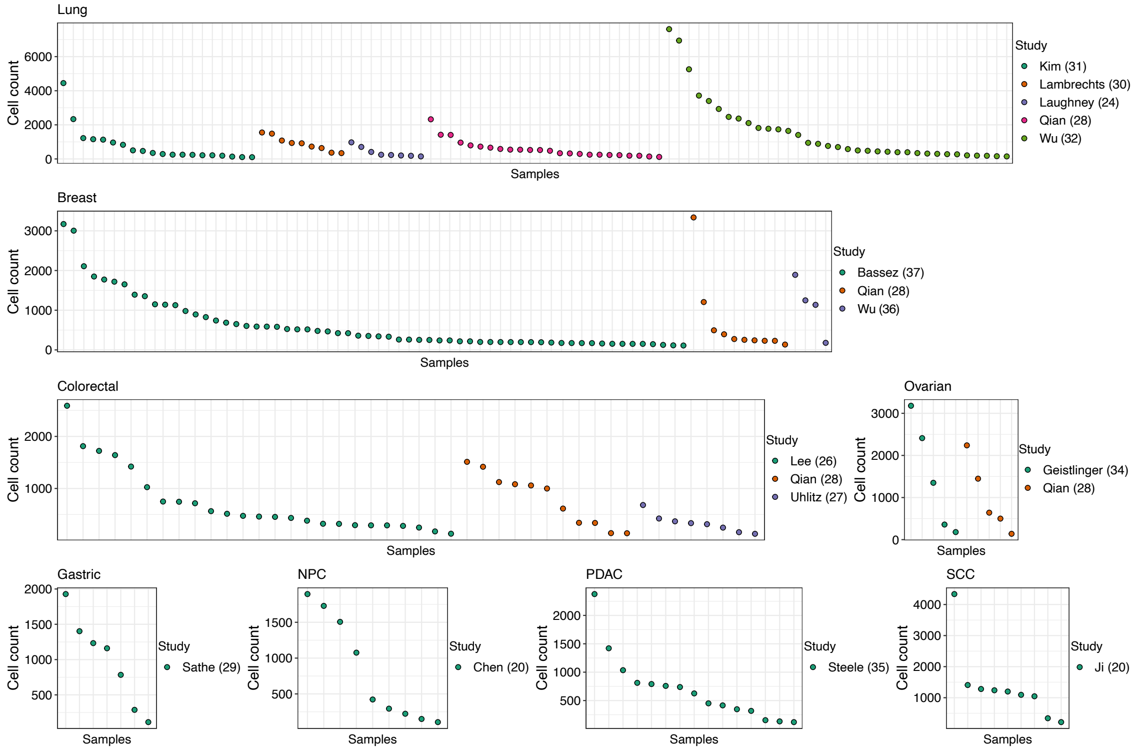
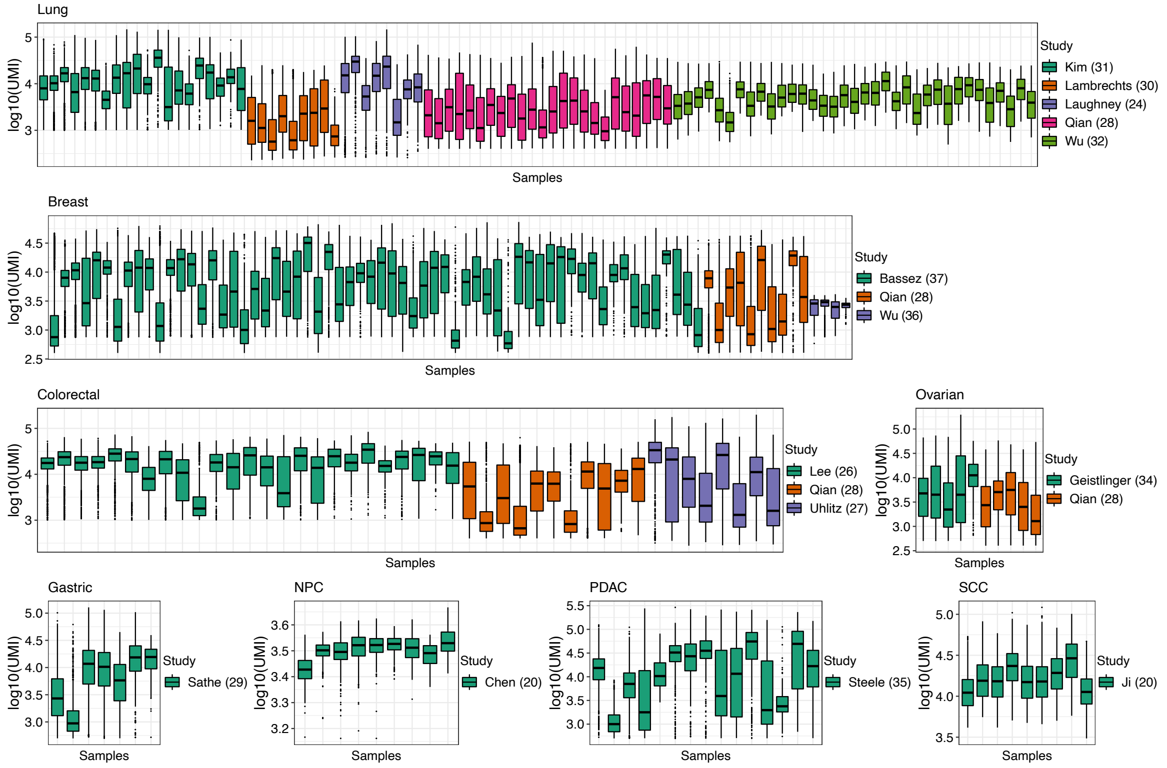


Figure S1. Processing pipeline for all 266 tumours. UMAP embeddings (left) of each data set showing hierarchical cluster, sample identity, and cell type identities of each cell. Cell type annotations were generated by automated annotation with singleR. Copy number alterations were predicted from the gene expression data of all cell types (right) and epithelial populations with genetic aberrations were classified as malignant cells.

Sample cell counts



Sample UMI counts



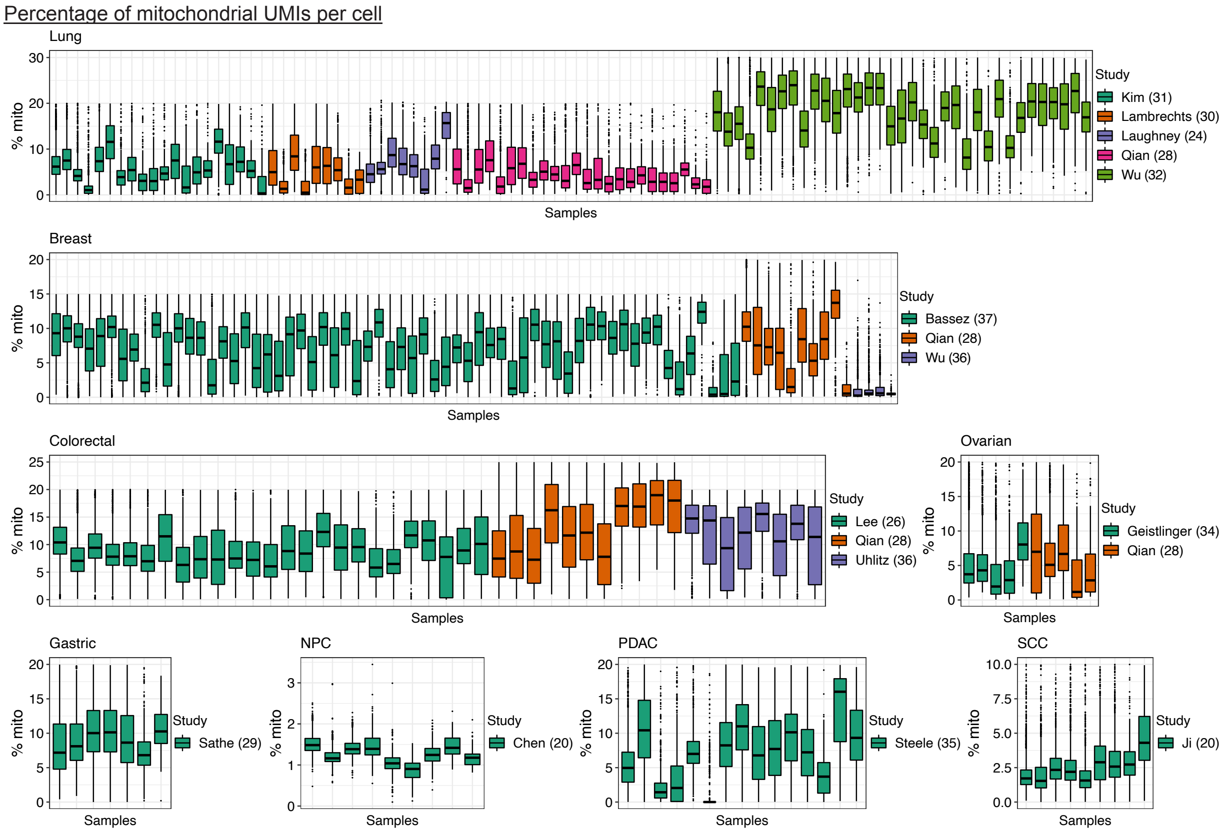


Figure S2. **Quality control metrics of all 266 tumours**. Plots showing the number of malignant cells analyzed for each tumour, separated by study and cancer type. The distribution of total UMI counts and the percentage of mitochondrial UMIs per cell are also shown.

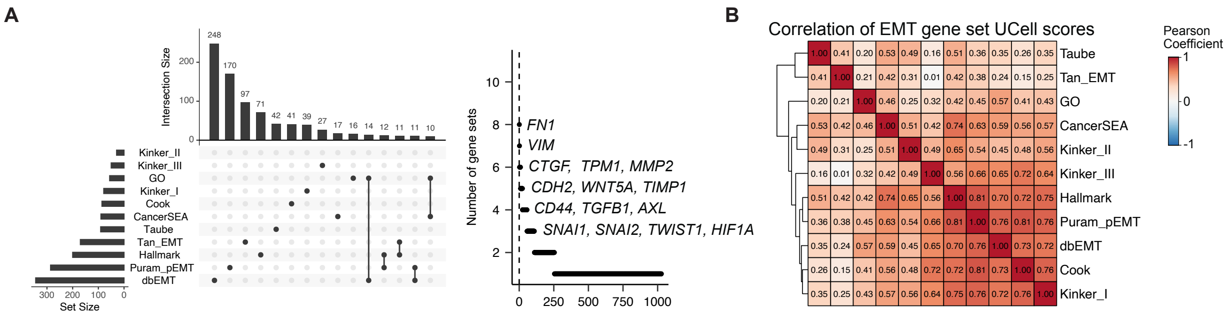


Figure S3. Variability of EMT gene sets. (A) UpSet plot showing the overlap of gene composition for 11 EMT gene sets (left) and plot showing the number of gene sets within which each gene occurs (right). (B) Pearson correlation coefficients of gene set UCell scores for each of the 11 EMT gene sets across the 266 tumours analyzed.

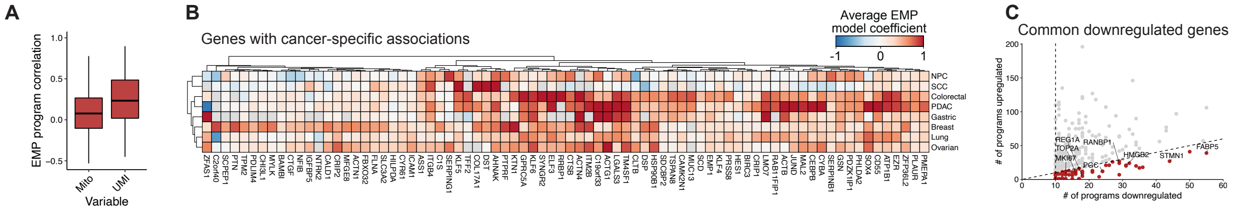


Figure S4. Characteristics of EMP programs. (A) Boxplot showing the distribution of Pearson correlation coefficients of sample-specific EMP program activity with the total number of UMIs and the percentage of mitochondrial UMIs per cell. (B) Clustered heatmap showing 78 genes from the conserved EMP signature whose expression has significant ($p<0.05$, ANOVA) associations with specific cancers. (C) Plot showing genes most commonly downregulated with EMP program activity. Each point represents an individual gene downregulated in >=10 EMP programs and colored points represent those downregulated more frequently than they are upregulated.

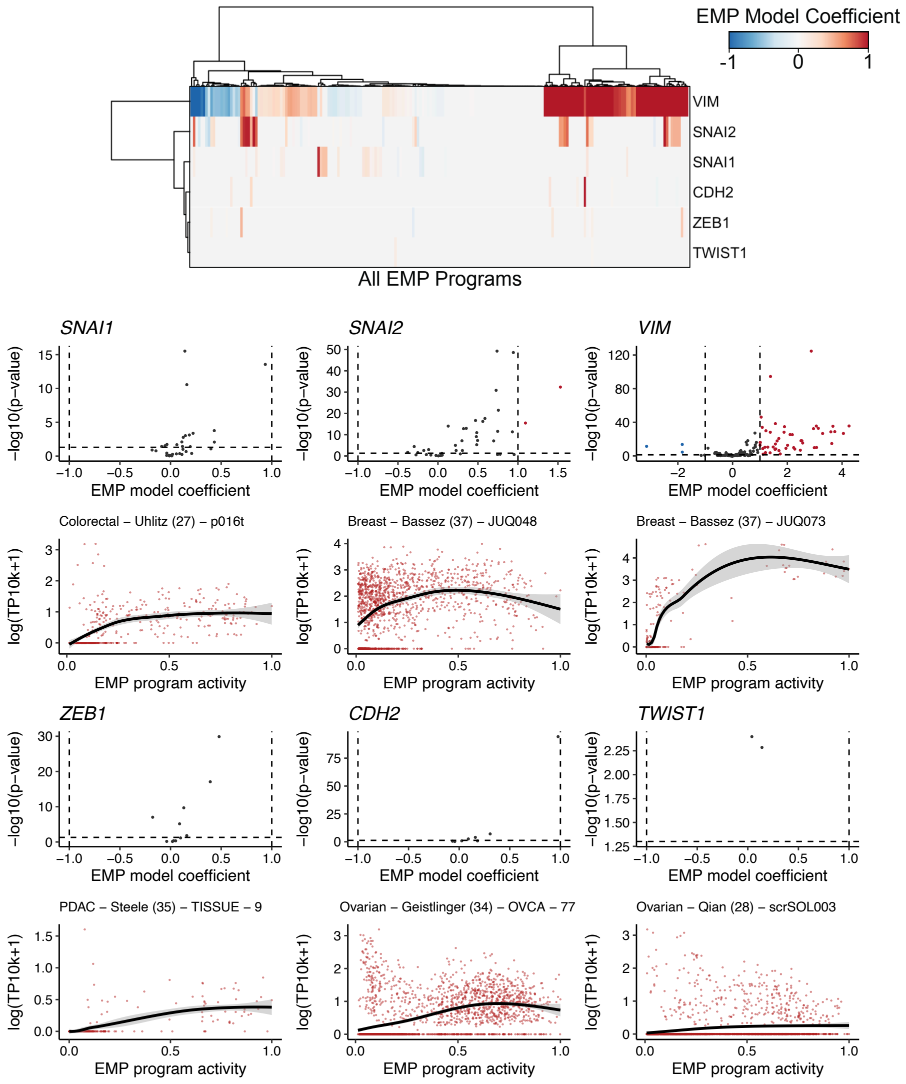


Figure S5. Association of canonical EMT genes with EMP programs. Top: Heatmap of EMP model coefficients for *VIM*, *SNAI1*, *SNAI2*, *ZEB1*, *CDH2*, and *TWIST1*. Bottom: Distribution of EMP model coefficients for each gene and expression values for programs with the highest coefficient for a given gene.

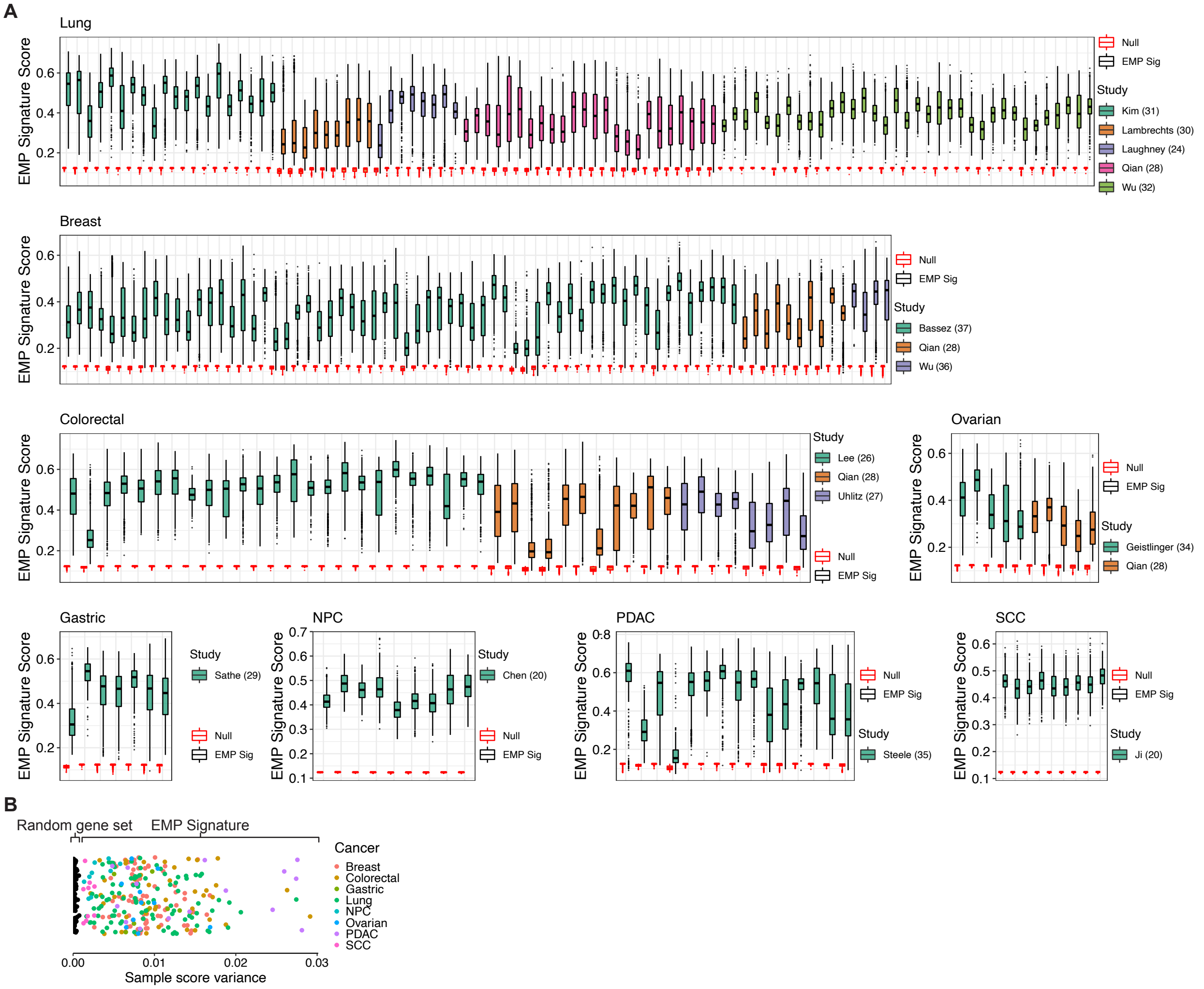


Figure S6. Distribution of EMP signature UCell scores. (A) Boxplots showing the distribution of EMP signature UCell scores within each tumour. Scores of a random gene set of an equivalent set are shown in red. (B) Variance of EMP signature UCell scores within individual tumours. The EMP signature variance in all tumours is greater than the variance from all permutations (n=100) of random gene sets.

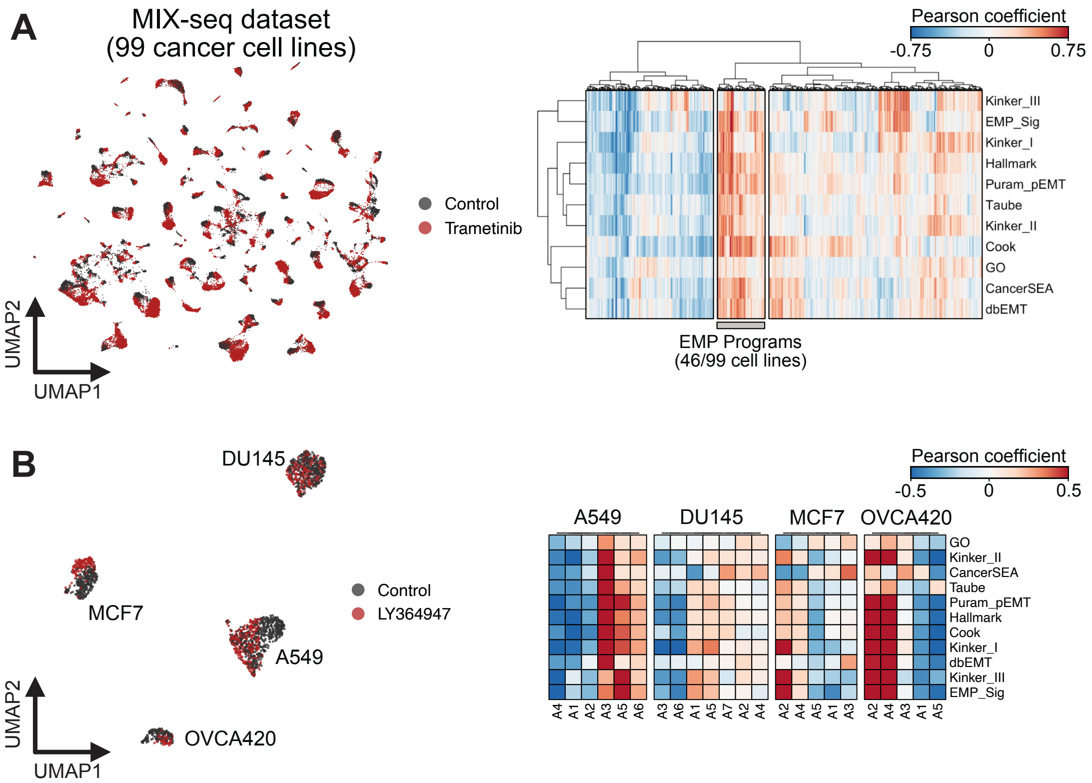


Figure S7. Identifying EMP signatures in cancer cell lines. (A) UMAP embedding of 99 cancer cell lines from the MIX-seq data set (60) (left) and pearson correlation coefficients of archetype activity scores and EMT gene set scores for all cells. (B) Same as (A), but for scRNA-seq data of A549, DU145, MCF7, and OVCA420 cells from Cook & Vanderhyden (8).

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