

Genomic and transcriptomic analysis of a library of small cell lung cancer patient-derived xenografts

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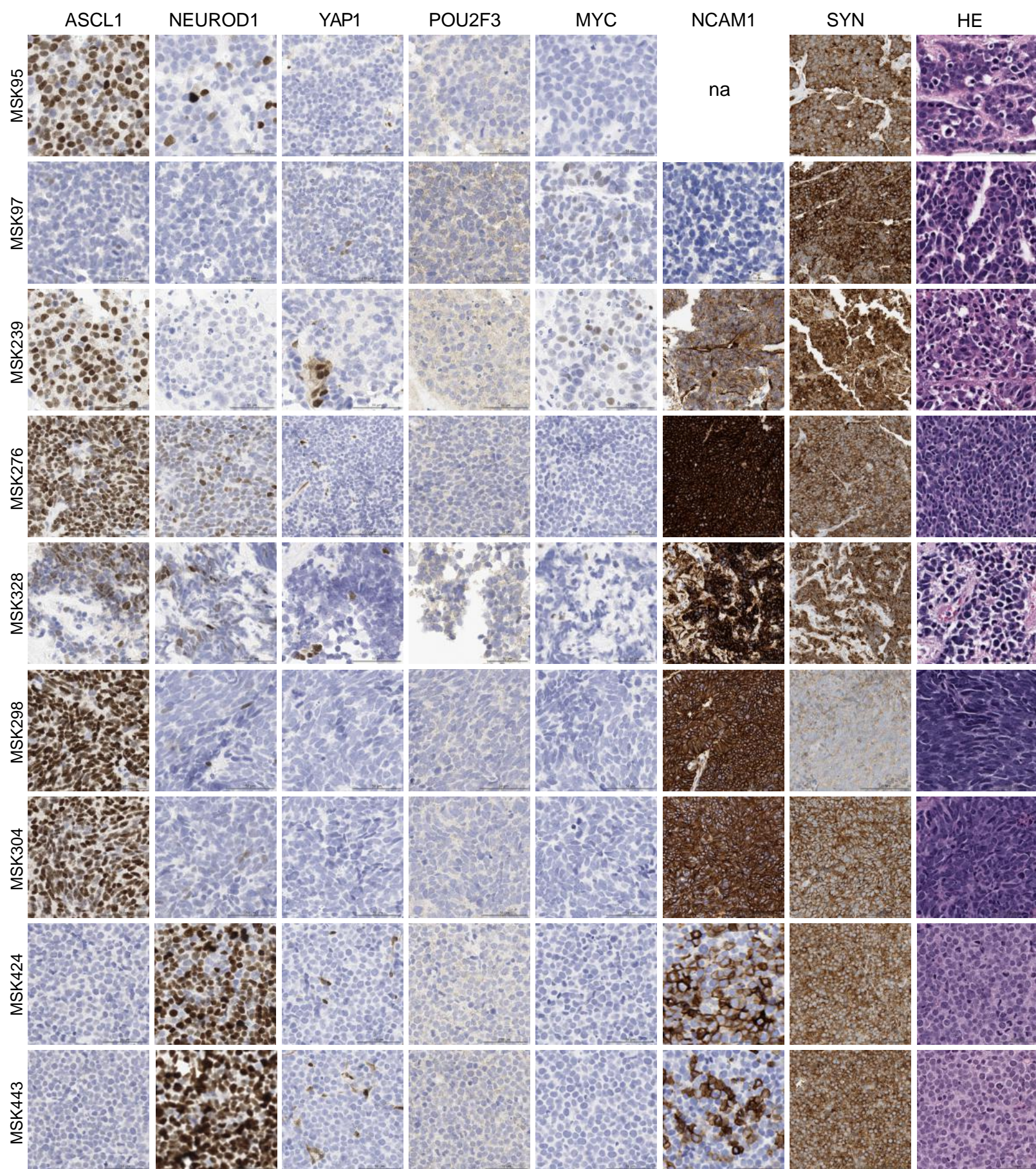
Supplementary Table 1 Program versions used in RNA-seq analysis

Program	Version
HTSEQ	htseq/HTSeq-0.5.3
PICARD	picard/picard-tools-1.124
R	R/R-3.2.0
STAR	star/STAR-STAR_2.5.0a
SAMTOOLS	samtools/samtools-0.1.19

Supplementary Table 2 Antibodies used for the immunohistochemical evaluation of PDX and clinical samples

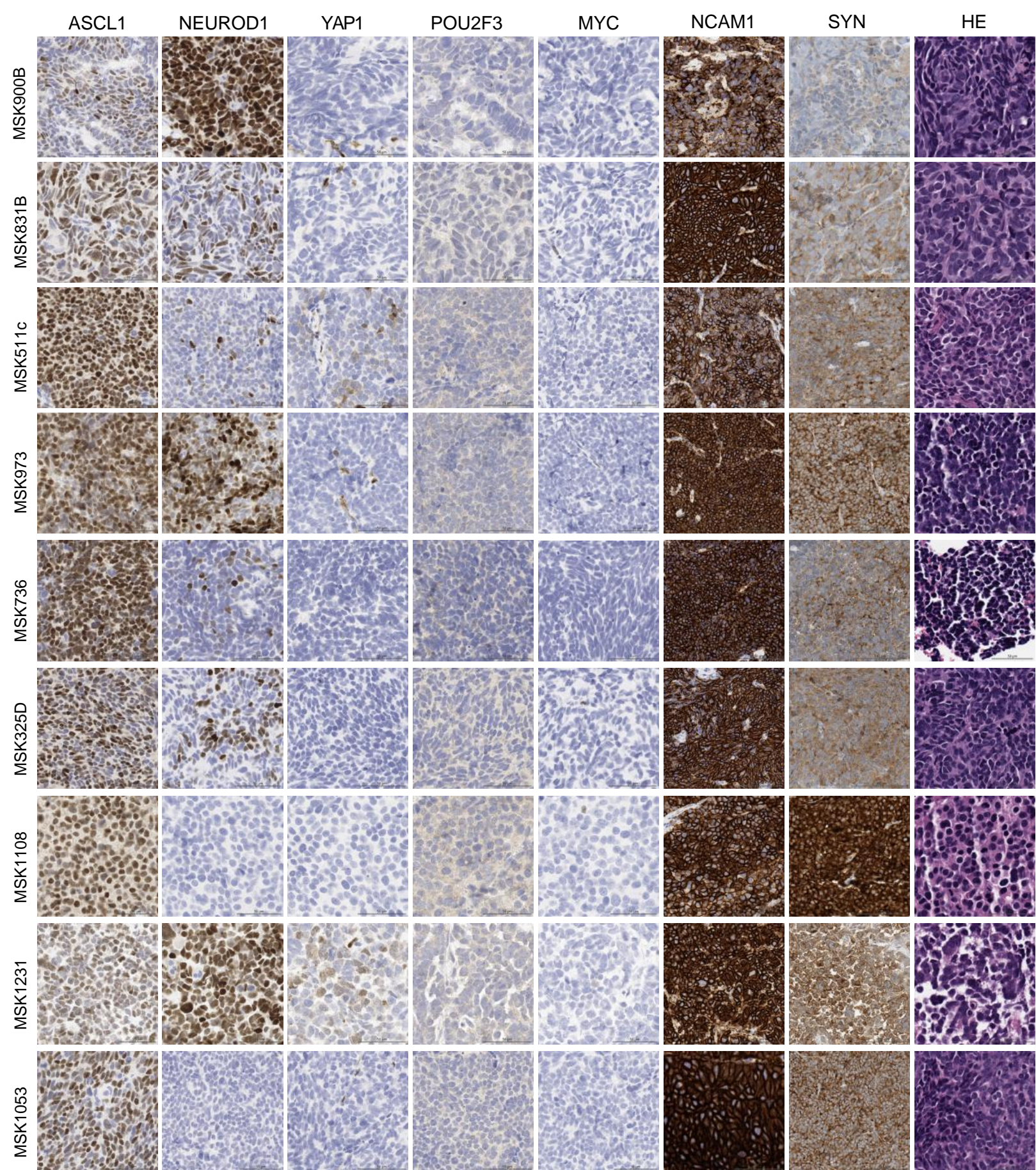
Antibody	Clone	Species	Dilution	Manufacturer	Platform
ASCL1	24B72D11.11	Mouse (m)	1:100	BD	Leica Bond-RX
CD56	MRQ42	Rabbit (m)	1:100	Cell Marque	Leica Bond-RX
MYC	Y69	Rabbit (m)	1:250	Abcam	Leica Bond-RX
NEUROD1	EPR 17084	Rabbit (m)	1:50	Abcam	Leica Bond-RX
POU2F3	6D1	Mouse (m)	1:600	Santa Cruz	Leica Bond-RX
Synaptophysin	SNP88	Mouse (m)	1:1000	BioGenex	Ventana Discovery Ultra
YAP1	63.7	Mouse (m)	1:2000	Santa Cruz	Leica Bond-RX

(m): monoclonal



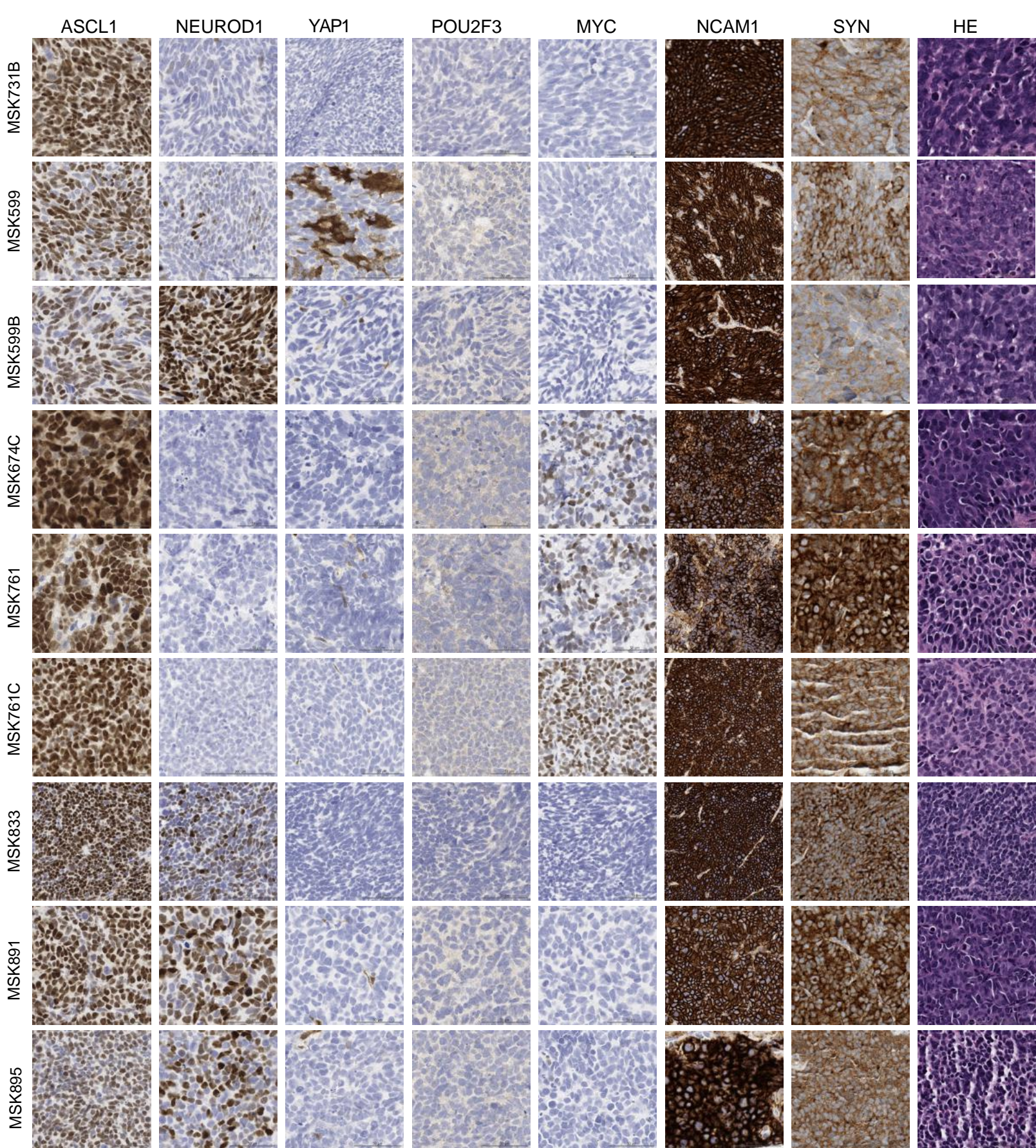
Supplementary Figure 1 Histologic analysis of PDX/CDX samples

H&E and immunohistochemistry images for the indicated proteins are shown for the 37 patient-derived/circulating tumor cell-derived xenograft (PDX/CDX) samples (9 samples shown here). Three independent cores per sample were stained for H&E and the indicated protein with a representative example shown here. Scale bar as indicated, 50µM.



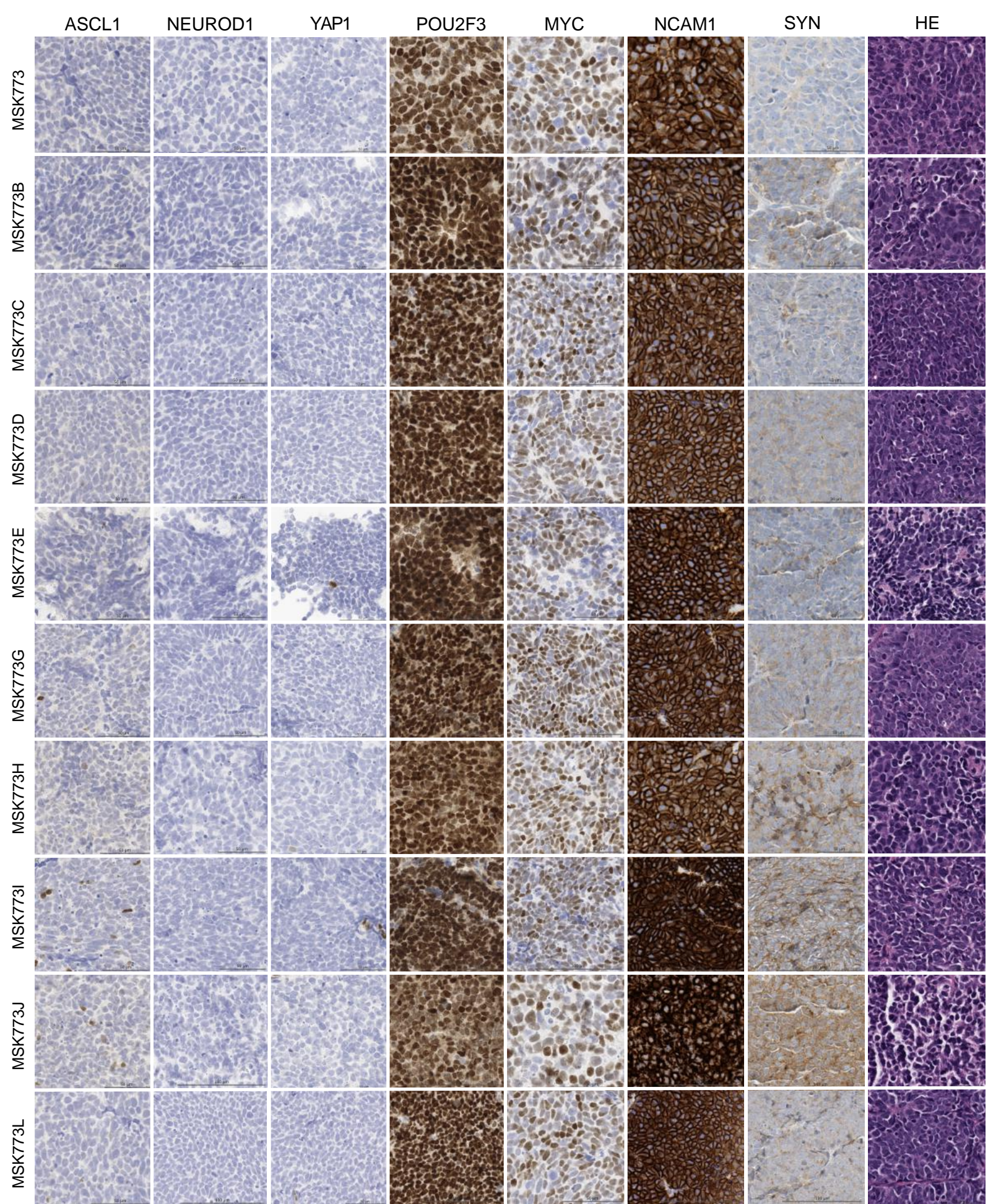
Supplementary Figure 2 Histologic analysis of PDX/CDX samples

H&E and immunohistochemistry images for the indicated proteins are shown for the 37 patient-derived/circulating tumor cell-derived xenograft (PDX/CDX) samples (9 samples shown here). Three independent cores per sample were stained for H&E and the indicated protein with a representative example shown here. Scale bar as indicated, 50µM.

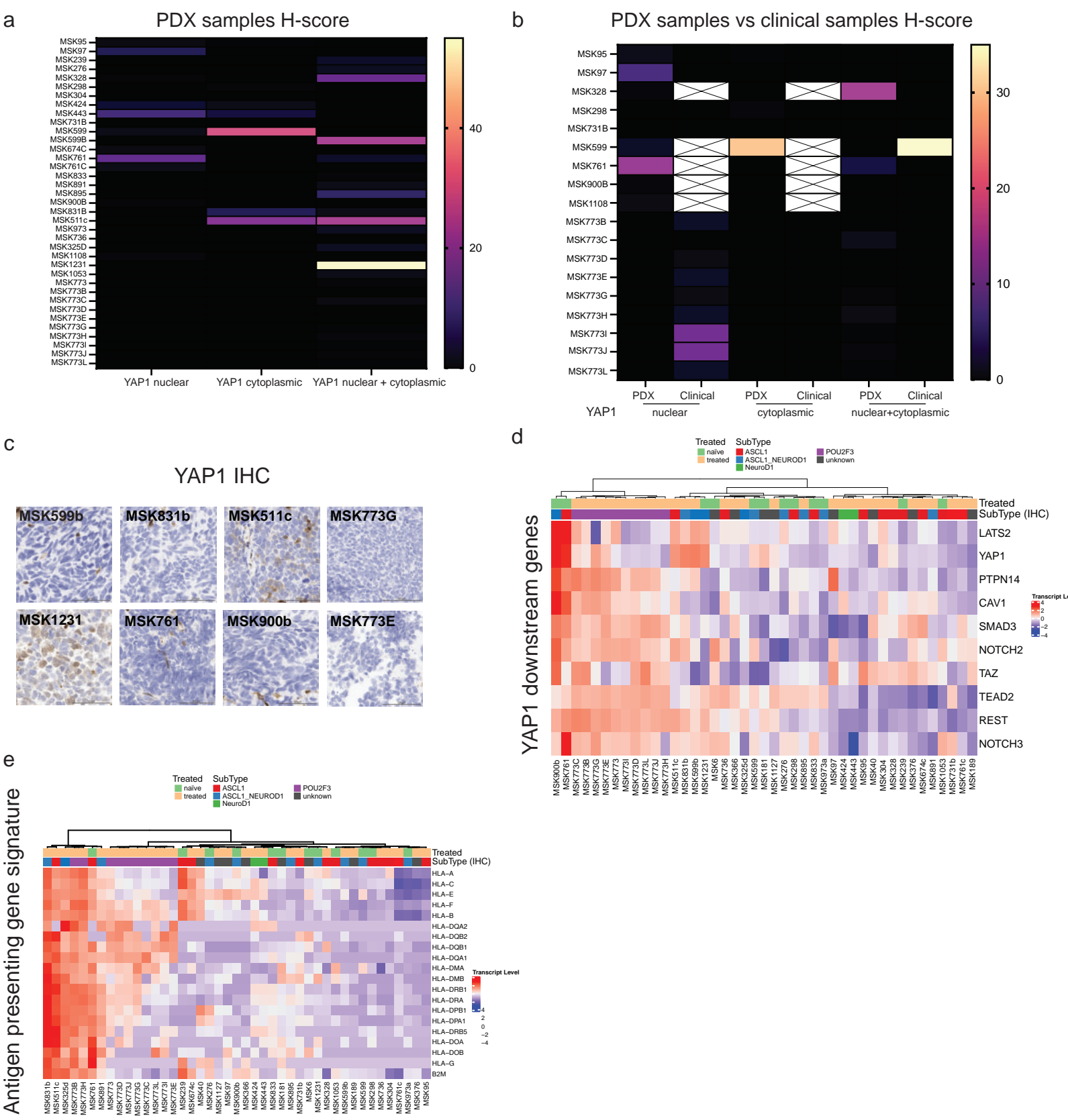


Supplementary Figure 3 Histologic analysis of PDX/CDX samples

H&E and immunohistochemistry images for the indicated proteins are shown for the 37 patient-derived/circulating tumor cell-derived xenograft (PDX/CDX) samples (9 samples shown here). Three independent cores per sample were stained for H&E and the indicated protein with a representative example shown here. Scale bar as indicated, 50µM.

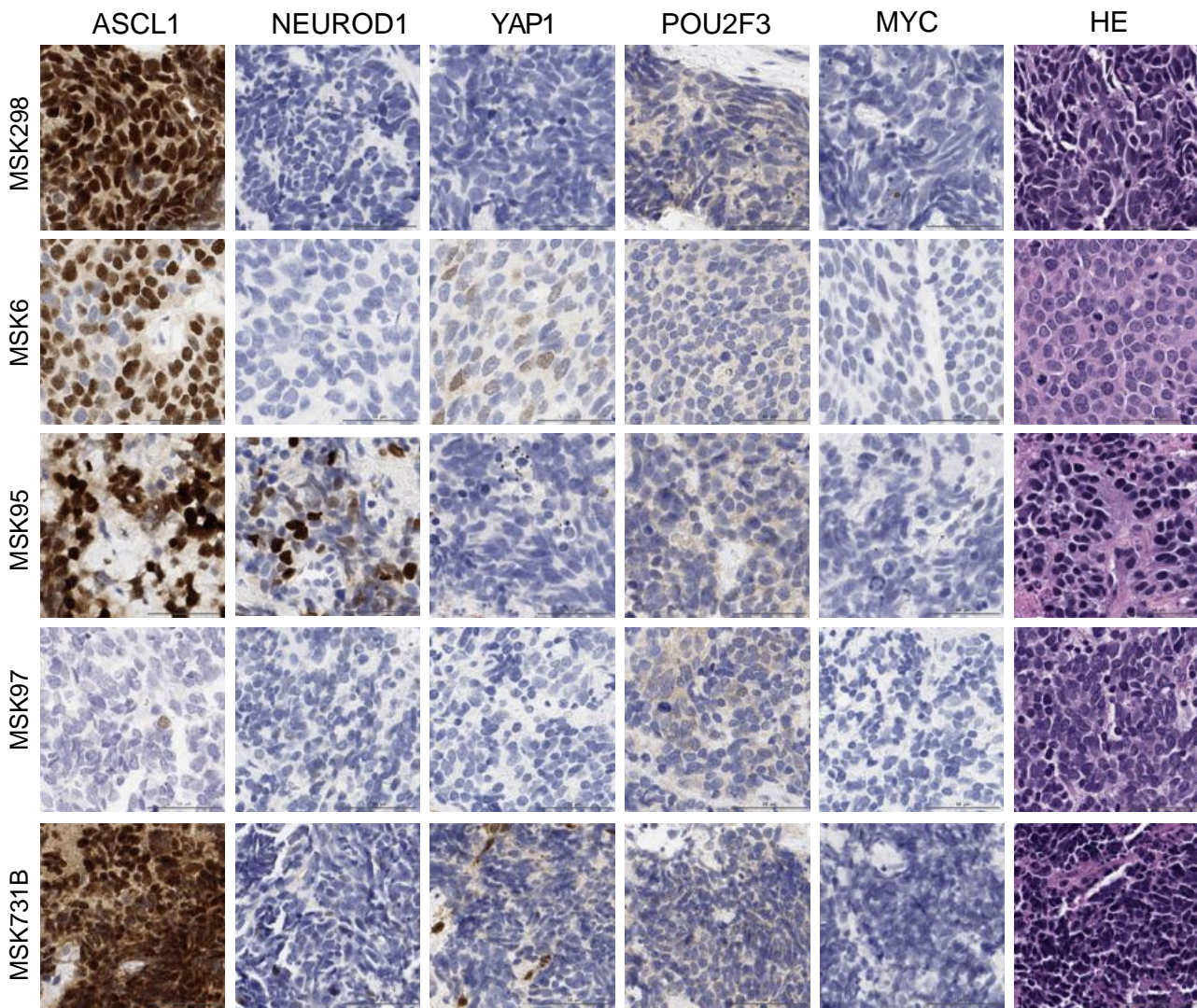


Supplementary Figure 4 Histologic analysis of PDX/CDX samples
H&E and immunohistochemistry images for the indicated proteins are shown for the 37 patient-derived/circulating tumor cell-derived xenograft (PDX/CDX) samples (10 samples shown here). Three independent cores per sample were stained for H&E and the indicated protein with a representative example shown here. Scale bar as indicated, 50µM.



Supplementary Figure 5 YAP1 expression in PDX/CDX and clinical samples

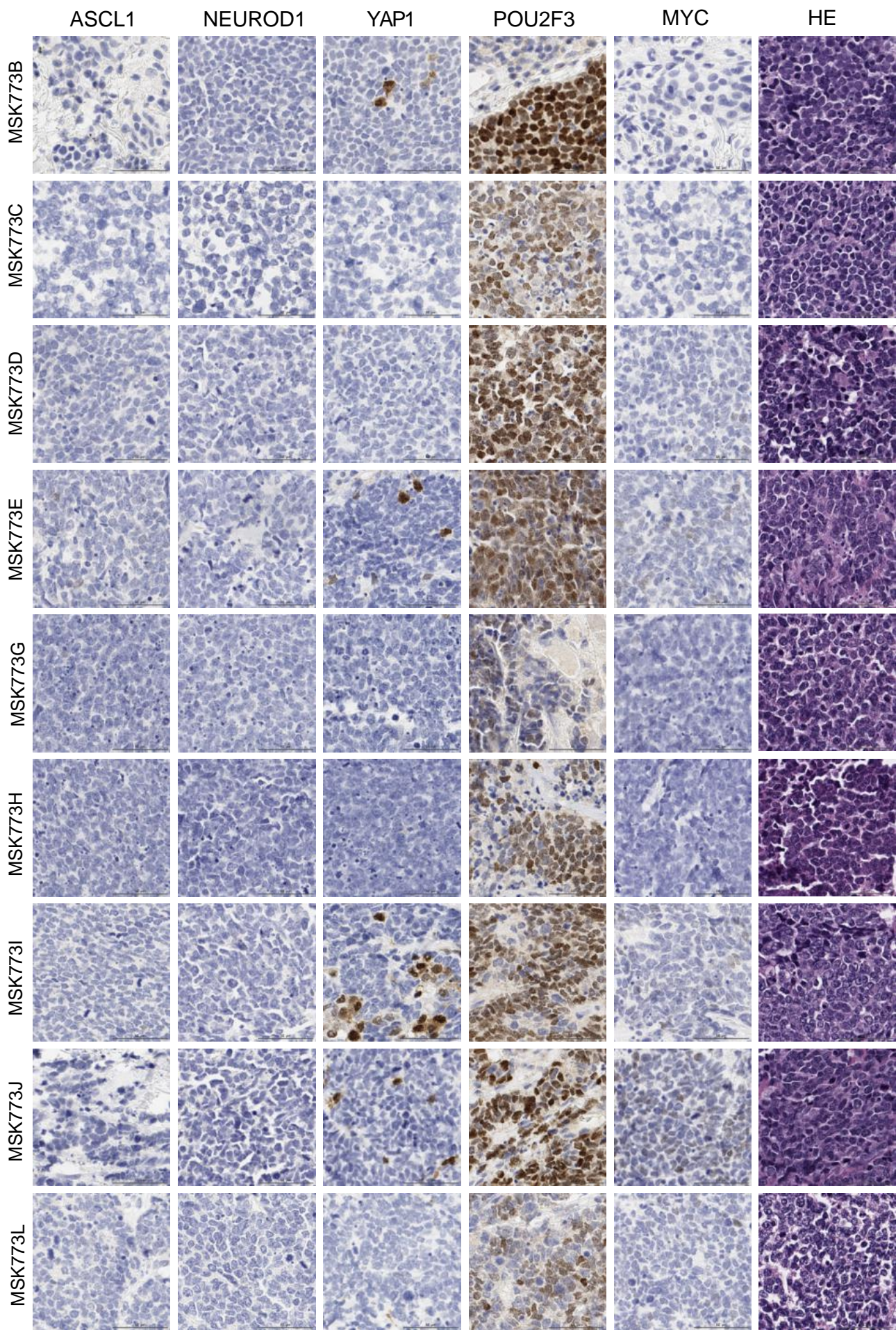
a Heatmap depicts H-scores derived from 37 scored patient-derived xenograft (PDX) tumors for the fraction of positive cells and staining intensity, for YAP1 nuclear, cytoplasmic, and combined. Source data are provided as a Source Data file. **b** Heatmap depicts H-scores derived from 18 paired PDX tumors and clinical samples for the fraction of positive cells and staining intensity, for YAP1 nuclear, cytoplasmic and combined. White boxes with cross indicate scoring was not performed based on nuclear or cytoplasmic, only combined. Source data are provided as a Source Data file. **c** Immunohistochemistry images for YAP1 are shown for six selected PDX samples as indicated. Three independent cores per sample were stained for YAP1 with a representative example shown here. Scale bar as indicated, 50µm. **d** Heatmap of gene expression of 43 PDX samples for YAP1 downstream genes³⁰. Color-coded panel on top depicts treatment status (naïve or treated) and subtype annotation based on IHC. Source data are provided as a Source Data file. **e** Heatmap of gene expression of 43 PDX samples for antigen presenting genes¹². Color-coded panel on top depicts treatment status (naïve or treated) and subtype annotation based on IHC. Source data are provided as a Source Data file..



Clinical Samples

Supplementary Figure 6 Histologic analysis of clinical samples

H&E and immunohistochemistry images for the indicated proteins are shown for 14 clinical specimens (5 shown here). One core per sample was stained for H&E and the indicated protein with a representative example shown here. Scale bar as indicated, 50µM.

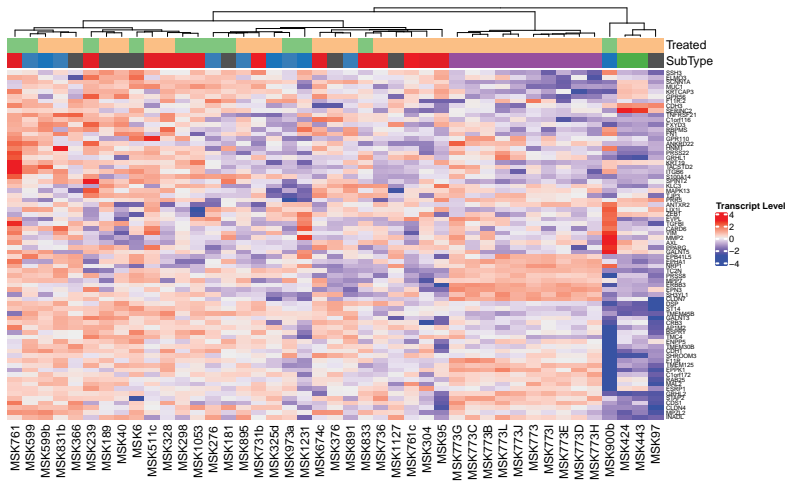


Supplementary Figure 7 Histologic analysis of clinical samples

H&E and immunohistochemistry images for the indicated proteins are shown for 14 clinical specimens (9 shown here). One core per sample was stained for H&E and the indicated protein with a representative example shown here. Scale bar as indicated, 50µM.

Treated SubType
 naive ASCL1 POU2F3
 treated ASCL1_NEUROD1 unk
 NeuroD1

EMT gene signature



Supplementary Figure 8 EMT gene signature of PDX samples

Heatmap of gene expression of 43 patient-derived xenograft (PDX) samples for epithelial to mesenchymal transition (EMT) gene signature taken from 34. Color-coded panel on top depicts treatment status (naïve or treated) and subtype annotation based on IHC. Source data are provided as a Source Data file.