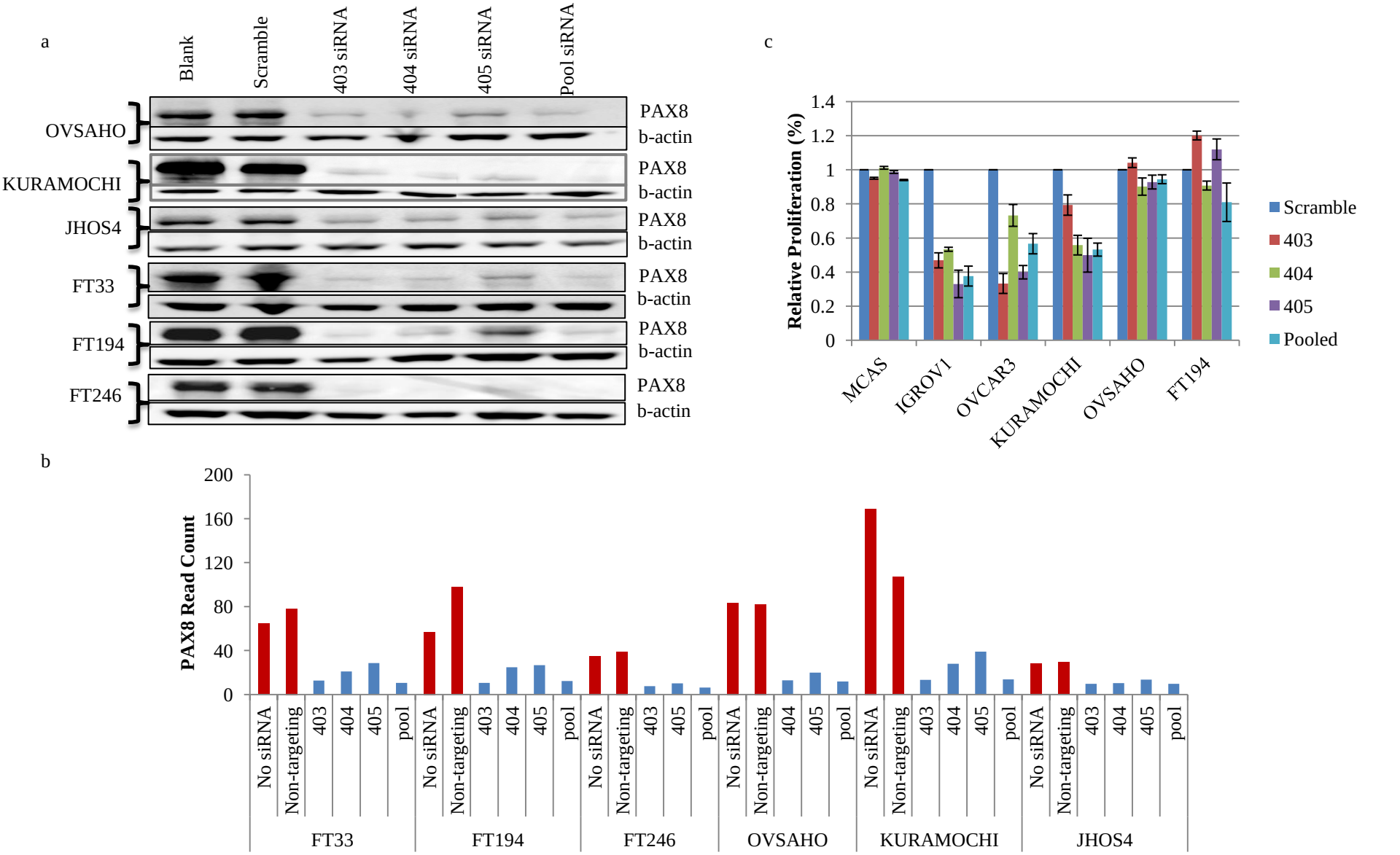
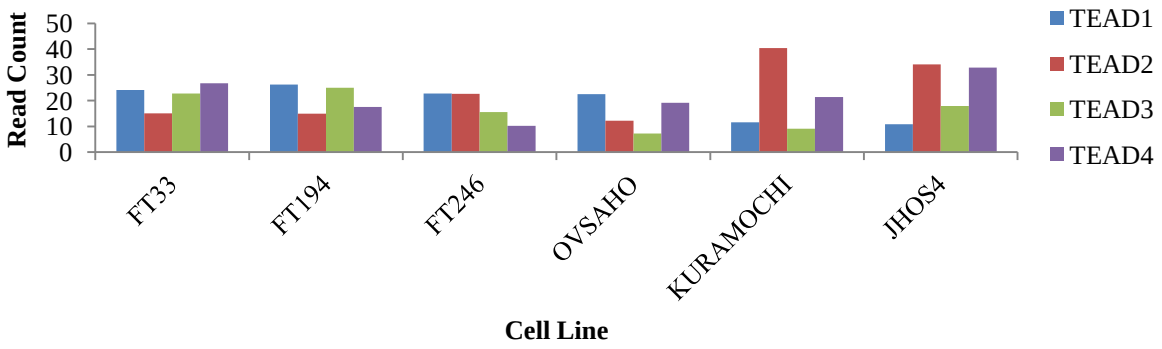


Figure S1. Characteristics of PAX8 knockdown assays. Related to Figure 1a, Supplemental Datasets 1 and 2, and Table 1.

Cells were cultured without siRNA, a scramble siRNA control, or siRNA oligonucleotides targeted against PAX8. PAX8 knockdown by siRNA was confirmed after 72 hours by (a) western blot and (b) RNA-seq. Separately, cells were cultured for 144 hours after siRNA transfection with either scramble siRNA or siRNA oligonucleotides targeted against PAX8 and assessed. Cell proliferation was assessed using CellTiter-Glo and compared relative to the scramble siRNA control (c). Data show the summary of three independent experiments with the average relative proliferation ± SEM.

a



b

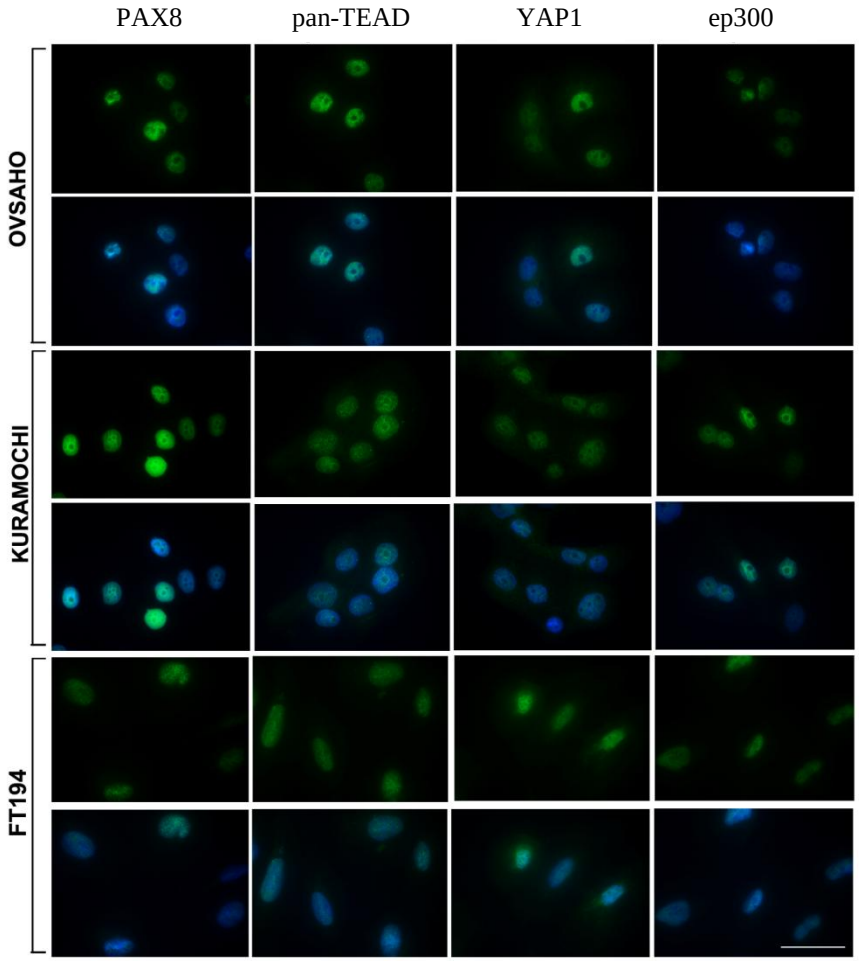


Figure S2. Expression of TEAD homologs in cell lines. Related to Figure 5a.

(a) Expression of TEAD homologs in Müllerian cell lines by RNA-seq. (b) Protein expression of PAX8, pan-TEAD, YAP1, and ep300 in select cell lines by immunofluorescence. White scale bar = 20 μm.

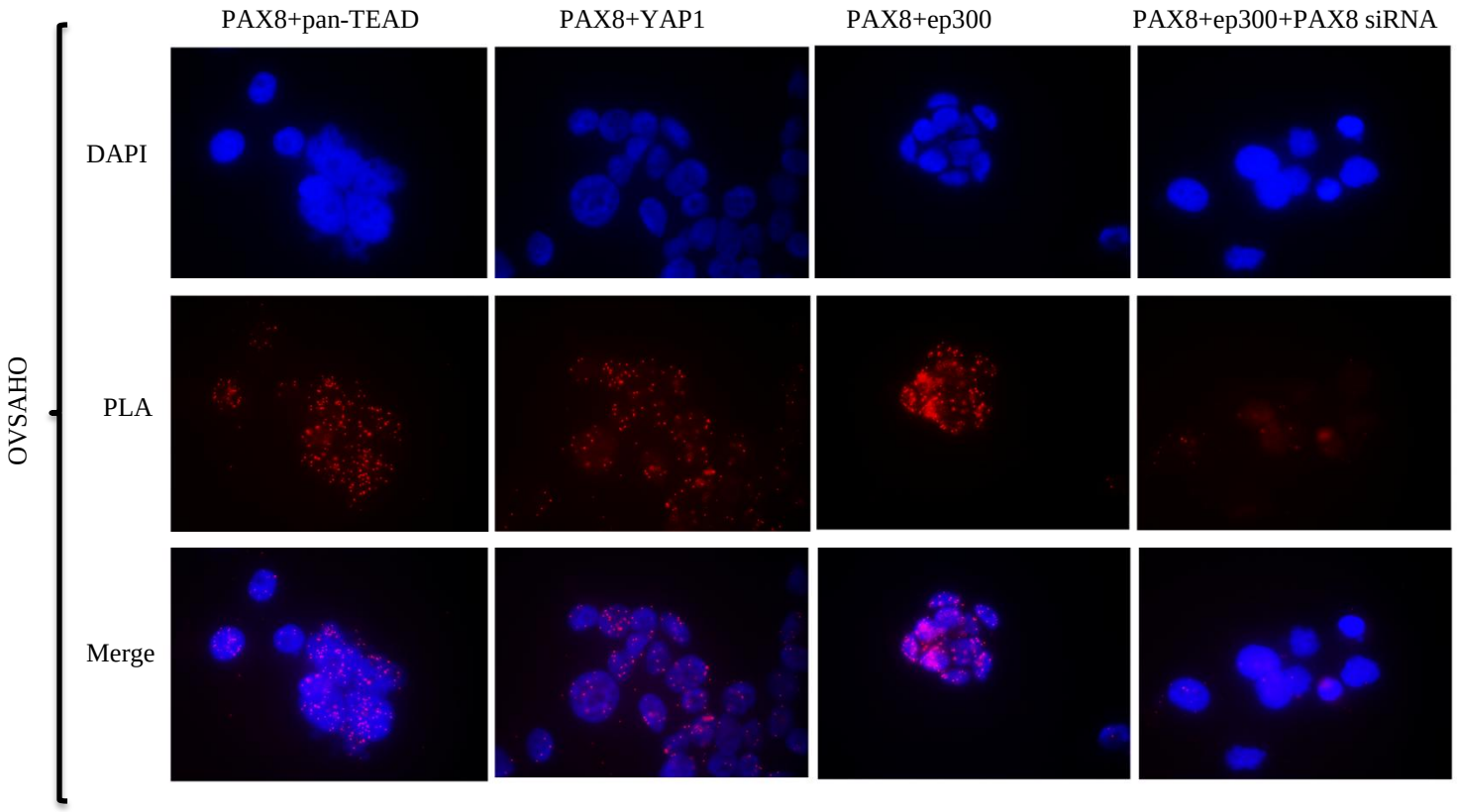


Figure S3. In situ interactions between PAX8, YAP1, and TEAD. Related to Figure 5b.

An in situ proximity ligation assay (PLA) performed in OVSAHO cells showing the interaction between endogenous PAX8 and YAP1 protein and PAX8 and pan-TEAD protein. Each red dot represents a single interaction. Nuclei were counterstained with DAPI (blue). The previously reported interaction between PAX8 and p300 serves as a positive control and incubation with PAX8 siRNA serves as a negative control.

Table S1. Characteristics of ChIP-Seq experiment. Related to Figure 2.

Sample Name	Conc. (ng/ul)	Total Reads (M)	Uniq Mapped (M)	Total Peaks	10xPeaks	FriP (%)	Top Motif
FT33 CHIP	91.4	18.0	13.9	3139	822	0.64	PAX2
FT33 INPUT	82.2						
FT194 CHIP	84.8	30.2	22.9	1604	335	0.4	PAX2
FT194 INPUT	69.8						
FT246 CHIP	30.2	24.1	17.6	2632	877	0.54	PAX2
FT246 INPUT	81.8						
KURAMOCHI CHIP	90.2	21.3	16.5	5984	862	0.97	PAX2
KURAMOCHI Input	80.2						
OVSAHO CHIP	86.4	21.9	16.3	5696	1306	1.06	PAX2
OVSAHO Input	48.8						
JHOS4 CHIP	89.2	24.5	18.5	1122	302	0.46	PAX2
JHOS4 Input	83.6						

FRiP (Fraction of Reads in Peaks), is a quality measure for ChIP-Seq and Dnase-Seq experiments. FRiP is simply the percentage of all tags that fall in 'hotspots', regions of local enrichment of short-read sequence tags mapped to the genome, i.e. MACS peaks. FRiP scores are positively correlated with true positive rates and replicate reproducibility.

Table S2. Top secondary transcription factor binding motifs in ChIP-seq analysis. Related to Figure 5a.

Sample Name	**Top Secondary Motifs**	
FT33 CHIP	fos/jun	tead
FT33 INPUT		
FT194 CHIP	tead	runx
FT194 INPUT		
FT246 CHIP	tead	CP2/HLH
FT246 INPUT		
KURAMOCHI CHIP	EGR	tead
KURAMOCHI Input		
OVSAHO CHIP	tead	CP2/HLH
OVSAHO Input		
JHOS4 CHIP	tead	ets
JHOS4 Input		