

**Supplementary Table . The functional enrichment analysis of 100 VIPR1-related genes**

<b>ONTOLOGY</b>	<b>ID</b>	<b>Description</b>	<b>GeneRatio</b>	<b>BgRatio</b>	<b>pvalue</b>	<b>p.adjust</b>	<b>qvalue</b>
<b>BP</b>	GO:0001867	complement activation, lectin pathway	4/73	13/18670	1.50e-07	2.33e-04	1.83e-04
<b>BP</b>	GO:1904018	positive regulation of vasculature development	9/73	230/18670	2.74e-07	2.33e-04	1.83e-04
<b>BP</b>	GO:0045766	positive regulation of angiogenesis	8/73	204/18670	1.30e-06	7.36e-04	5.79e-04
<b>BP</b>	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	8/73	221/18670	2.36e-06	0.001	7.90e-04
<b>BP</b>	GO:1901342	regulation of vasculature development	10/73	422/18670	5.46e-06	0.002	0.001
<b>CC</b>	GO:0005581	collagen trimer	6/79	87/19717	1.33e-06	2.13e-04	1.95e-04
<b>CC</b>	GO:0062023	collagen-containing extracellular matrix	10/79	406/19717	4.99e-06	3.99e-04	3.65e-04
<b>CC</b>	GO:0030014	CCR4-NOT complex	2/79	17/19717	0.002	0.100	0.091
<b>CC</b>	GO:0099056	integral component of presynaptic membrane	3/79	73/19717	0.003	0.100	0.091
<b>CC</b>	GO:0046930	pore complex	2/79	23/19717	0.004	0.100	0.091
<b>MF</b>	GO:0030246	carbohydrate binding	9/70	271/17697	1.17e-06	1.99e-04	1.55e-04
<b>MF</b>	GO:0005126	cytokine receptor binding	9/70	286/17697	1.82e-06	1.99e-04	1.55e-04
<b>MF</b>	GO:0005201	extracellular matrix structural constituent	7/70	163/17697	3.64e-06	2.66e-04	2.07e-04
<b>MF</b>	GO:0048029	monosaccharide binding	4/70	75/17697	2.21e-04	0.012	0.009
<b>MF</b>	GO:0048018	receptor ligand activity	8/70	482/17697	6.14e-04	0.027	0.021

## Supplementary Figure legend

### Supplementary Figure 1 Immune infiltration analysis of VIP and ADCYAP1

**A. C.** Explored the correlation between immune infiltration and VIP and ADCYAP1 through the ssGSEA algorithm in the “GSVA” R package. **B. D.** Evaluated the correlation between Treg/Tem/NK/iDC cells and VIP, Tem/NK/iDC/Mast cells and ADCYAP by the Pearson correlation analysis.  $*P<0.05$ ,  $**P<0.01$ ,  $***P<0.001$ .

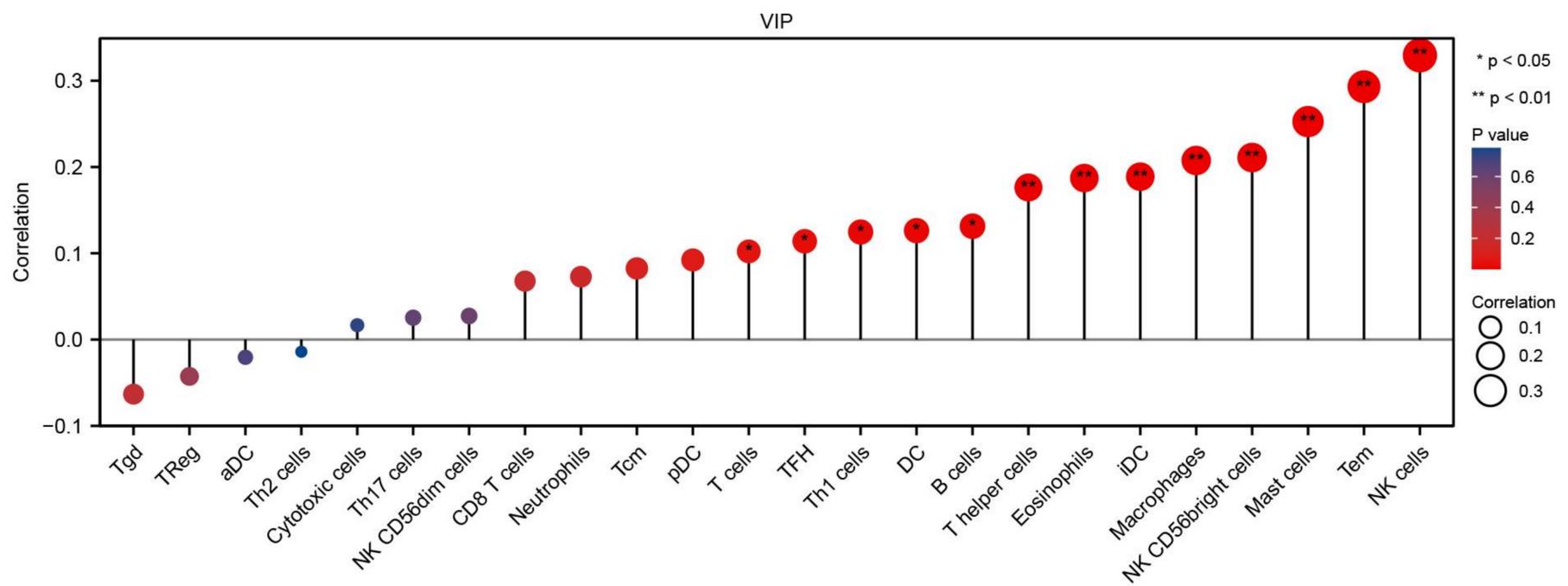
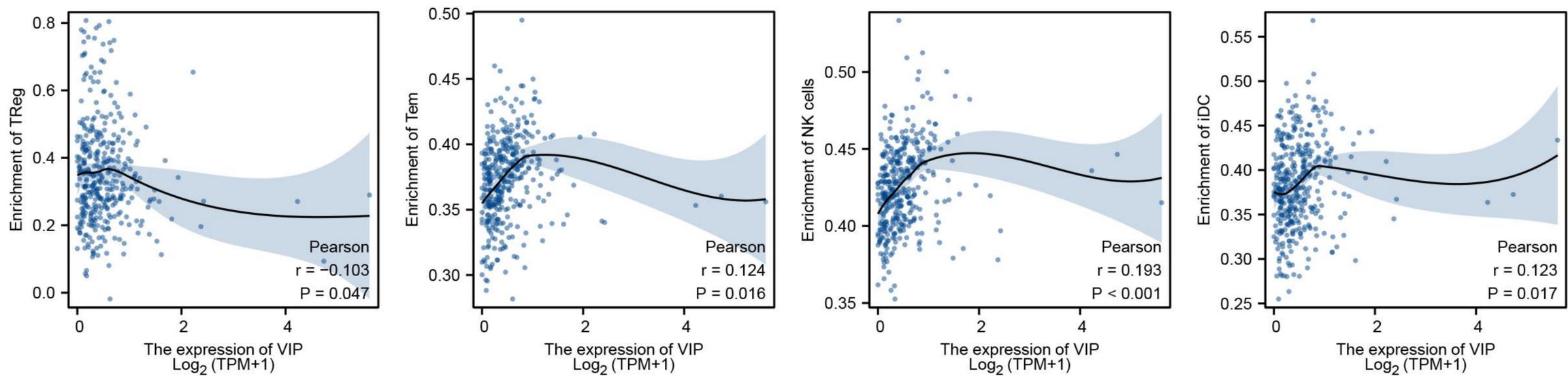
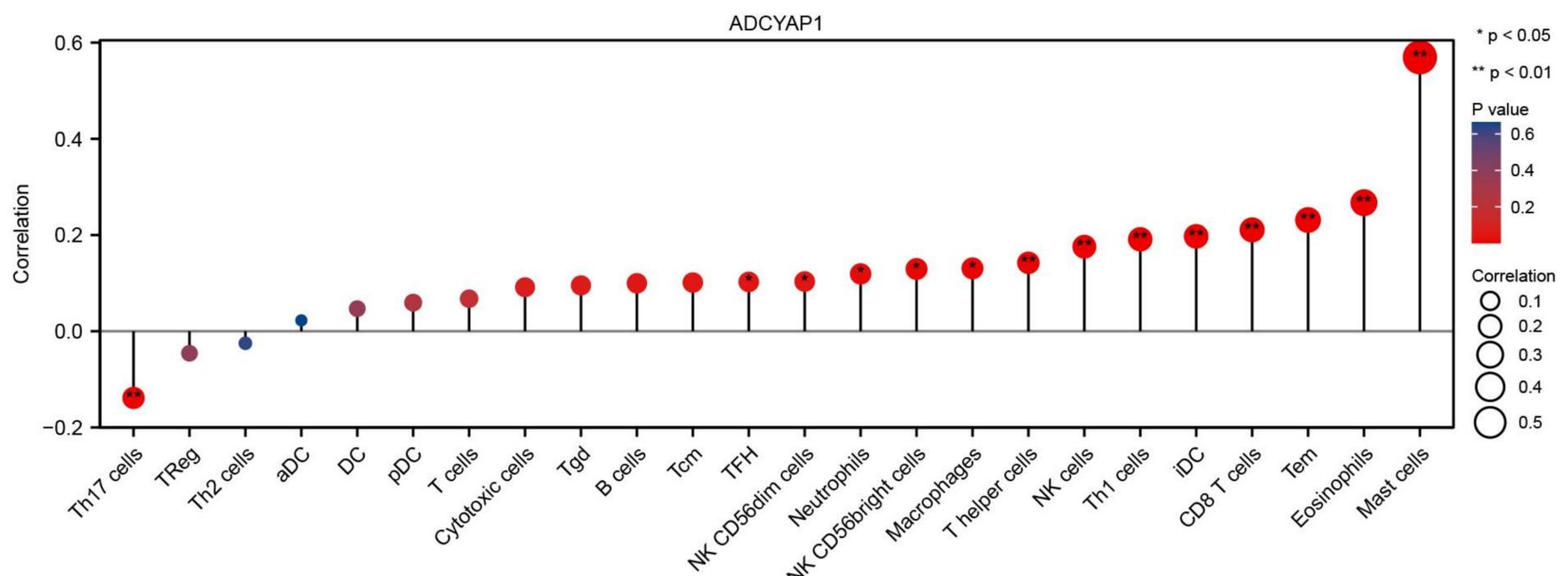
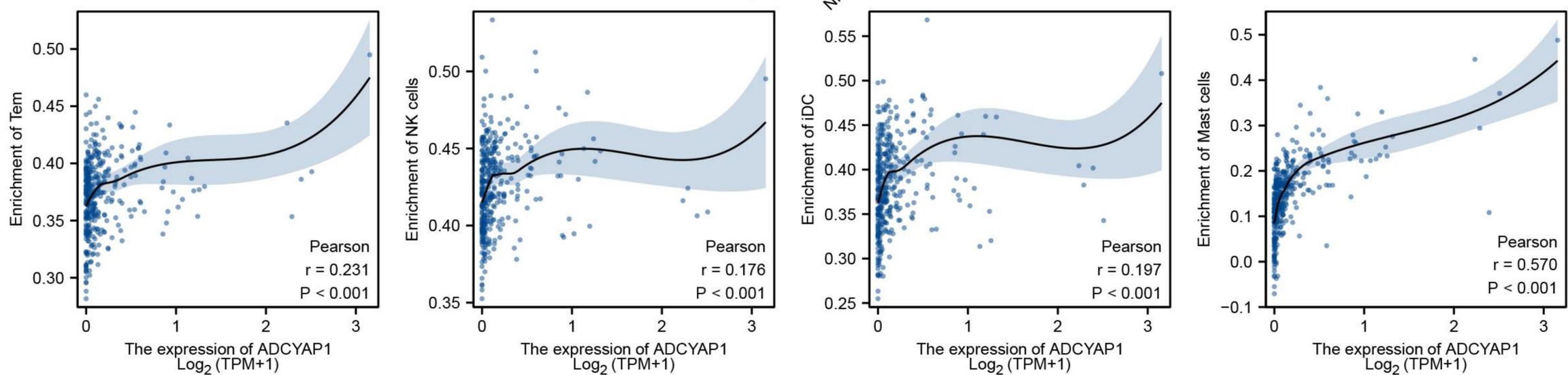
### Supplementary Figure 2 The methylation analysis of VIPR1 in HCC

**A.** The correlation between VIPR1 expression and methyltransferases in HCC. **B.** The methylation level of VIPR1 in disease tissues and normal tissues by DiseaseMeth 2.0 database. **C.** The CpG expression level of VIPR1 in HCC. **D.** The methylation site of VIPR1 DNA sequence association with gene expression was visualized using MEXPRESS. The expression of VIPR1 is illustrated by the blue line in the center of the plot. Pearson’s correlation coefficients and p values for methylation sites and query gene expression are shown on the right side.

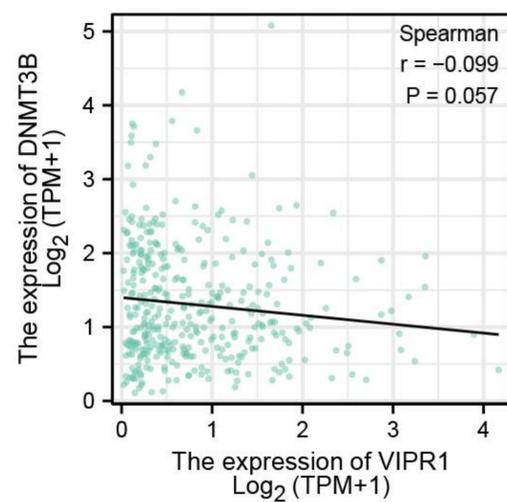
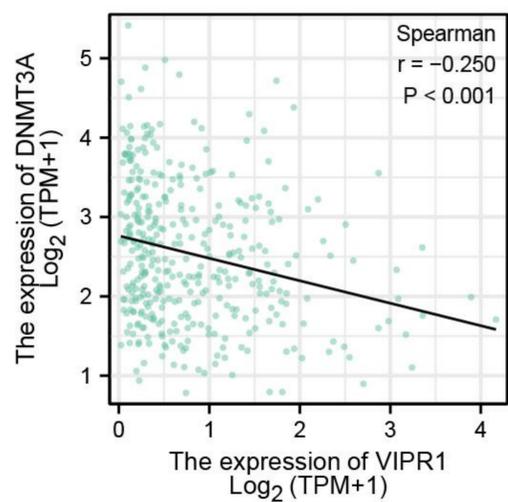
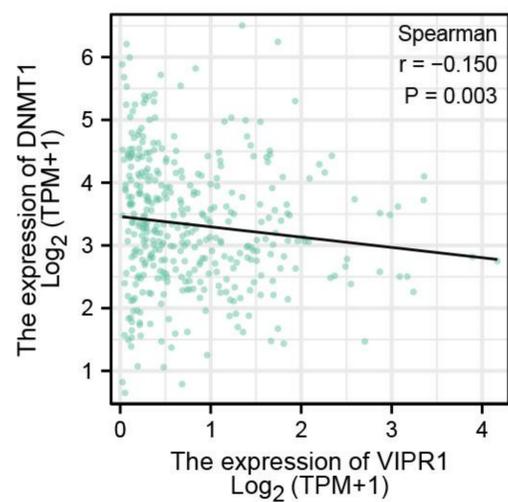
**Supplementary Figure 3** Confirmation of the stable downregulation of lncRNA-AC079061.1 transfected with lncRNA-AC079061.1 siRNA into MHCC97H and HCCLM3 HCC cells by qRT-PCR.  $*P<0.05$ ,  $**P<0.01$ ,  $***P<0.001$ .

### Supplementary Figure 4

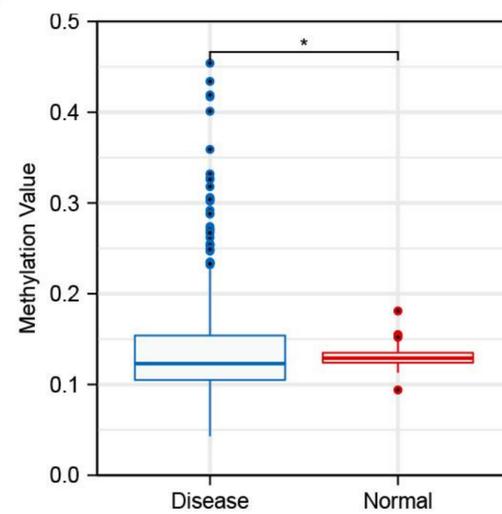
The correlation between drugs and the VIPR1 mRNA expression of HCC in CTRP and GDSC database.

**A****B****C****D**

A



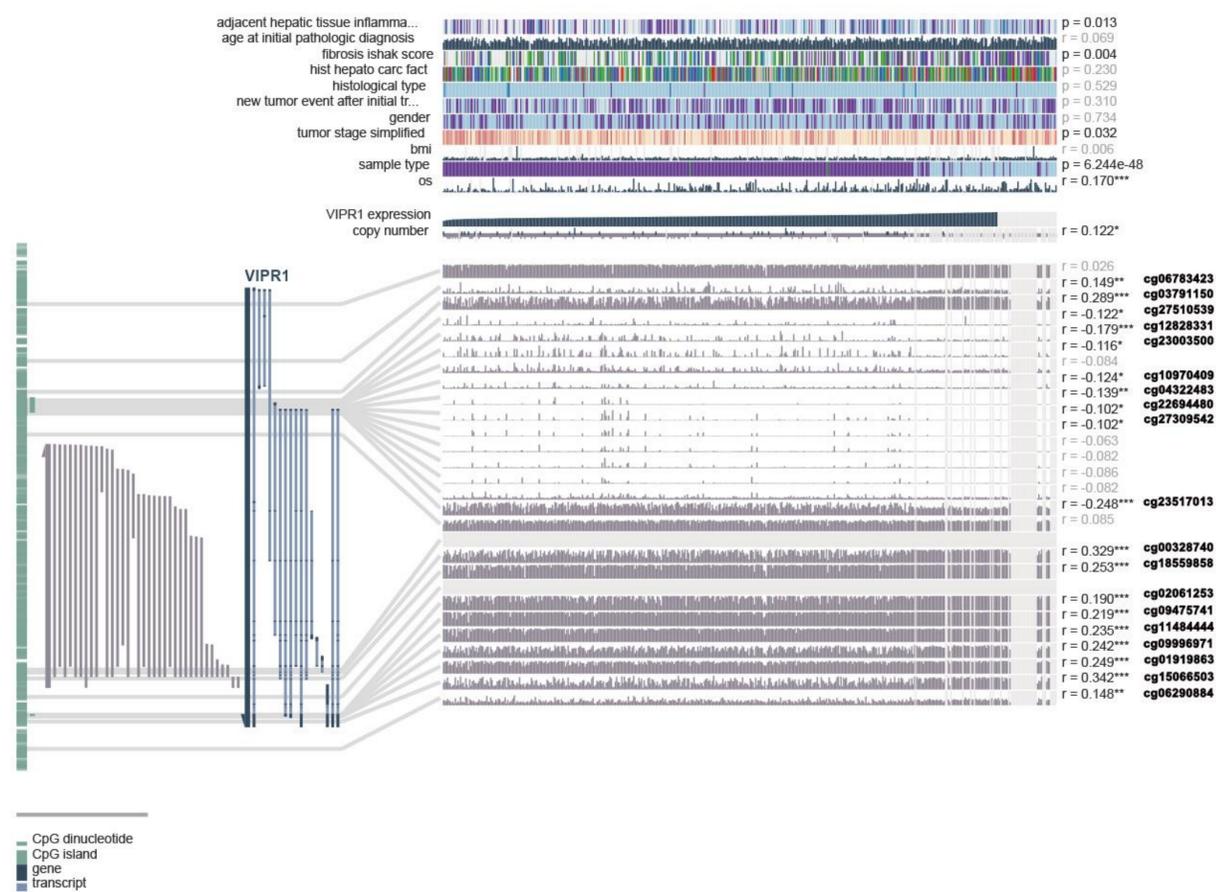
B



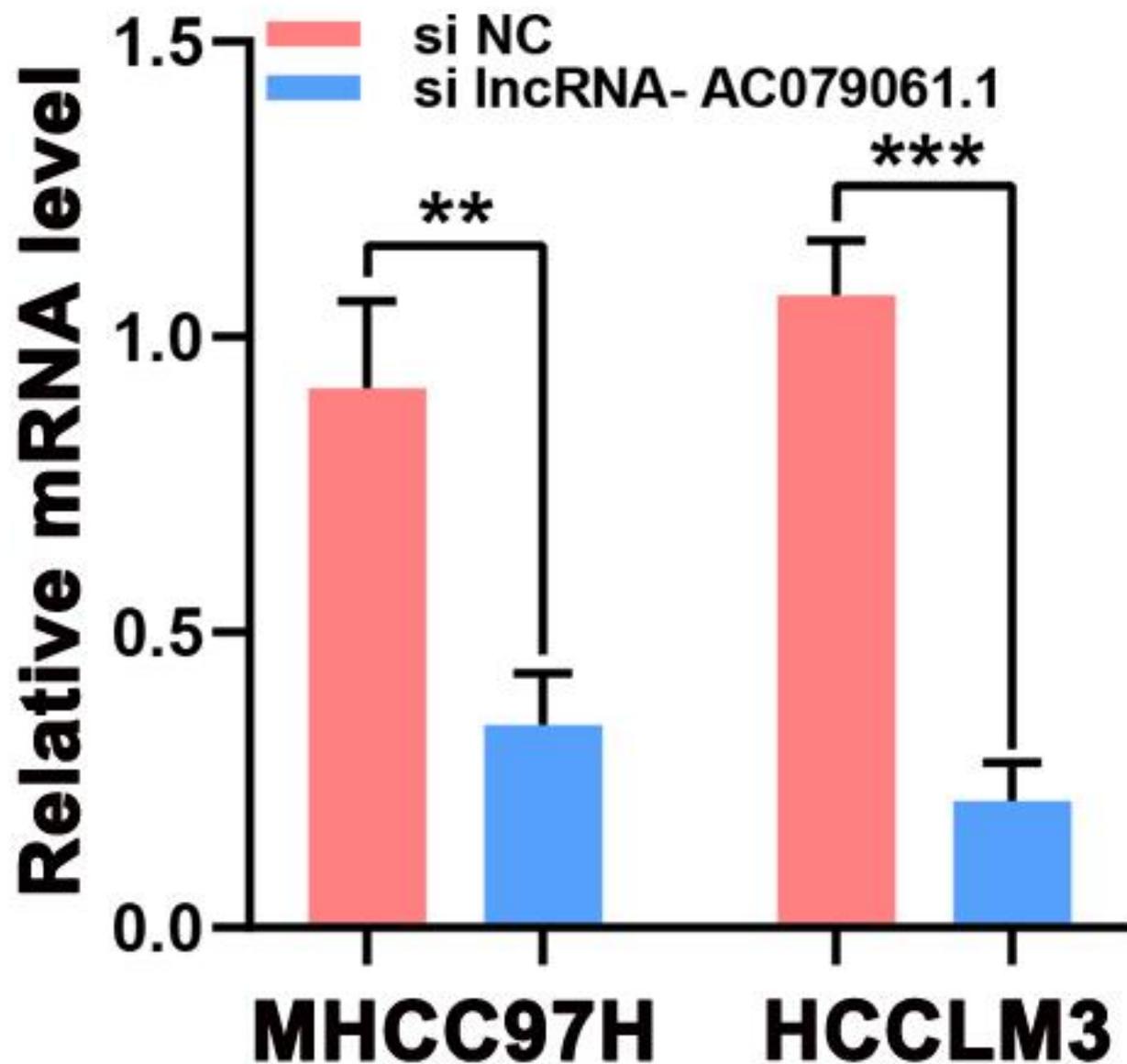
C



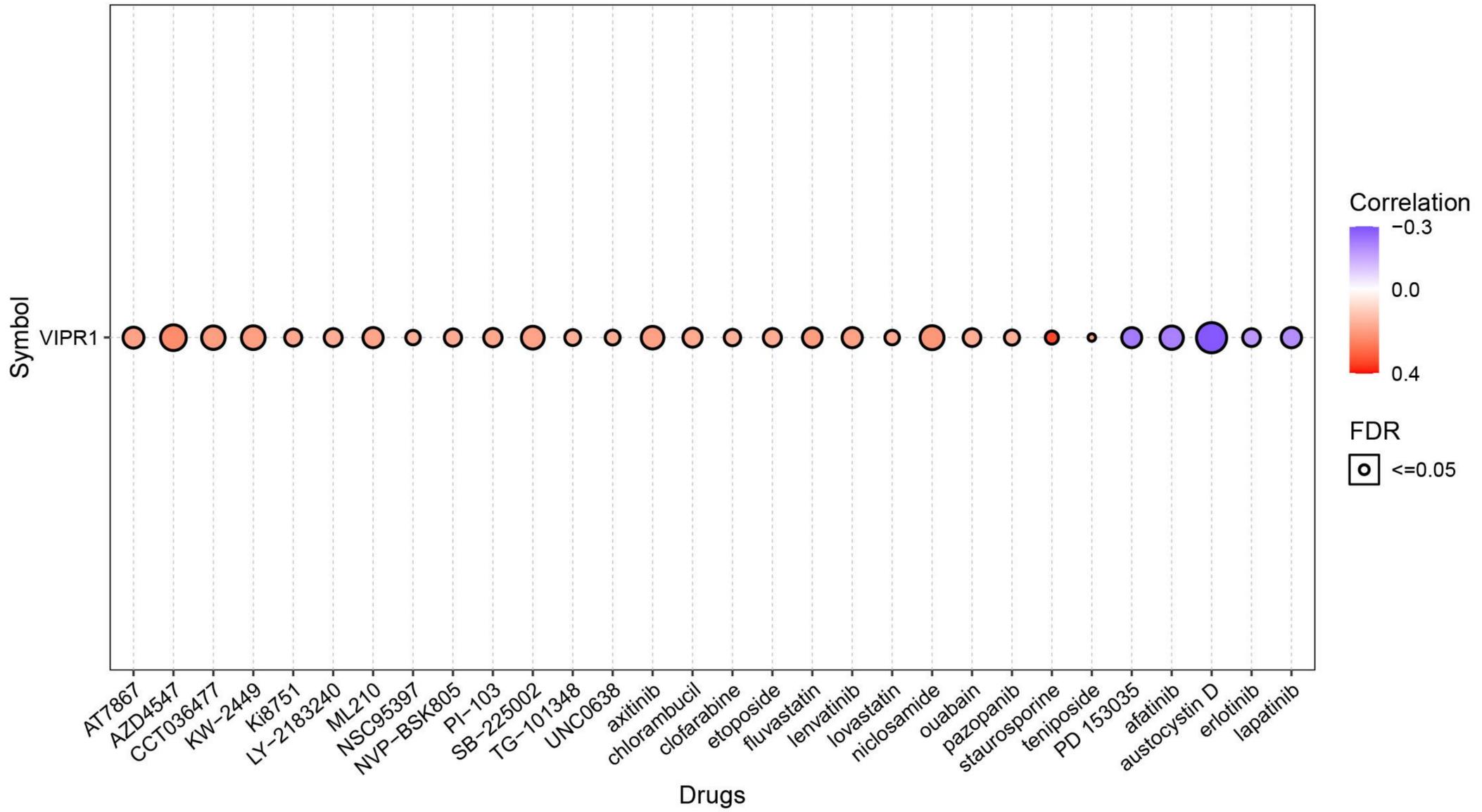
D



## lncRNA- AC079061.1



Correlation between CTRP drug sensitivity and mRNA expression



Correlation between GDSC drug sensitivity and mRNA expression

