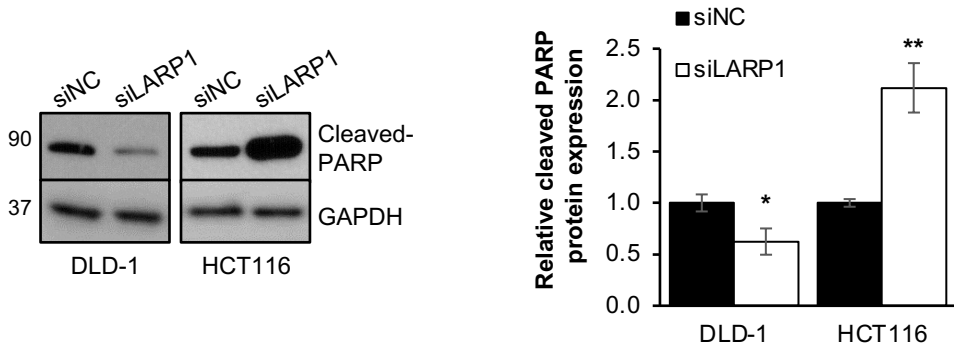
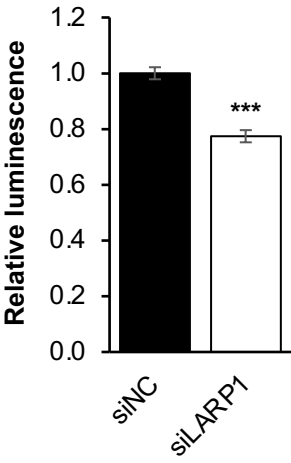


# Supplementary Fig. S1

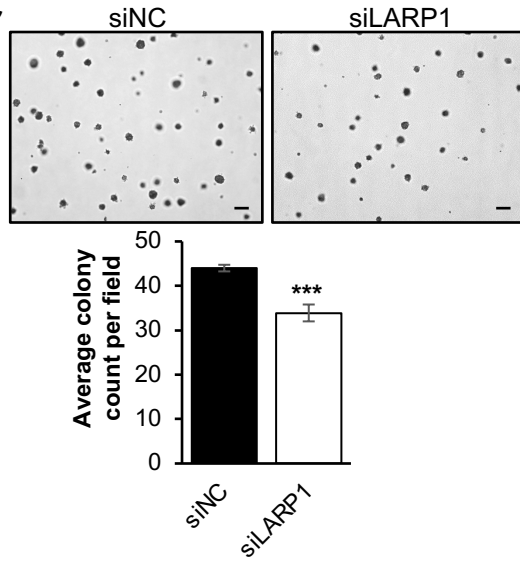
**A**



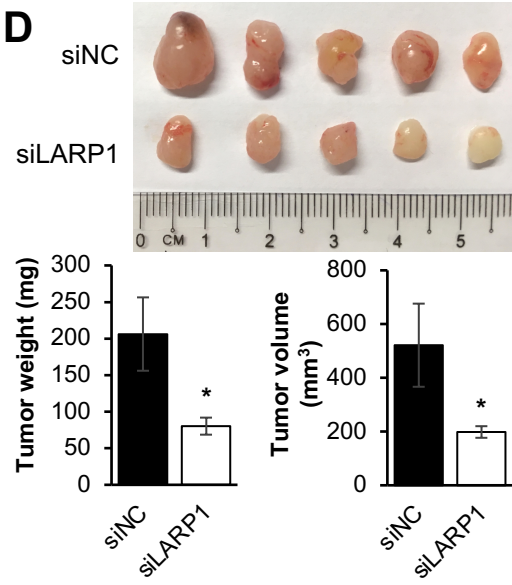
**B**



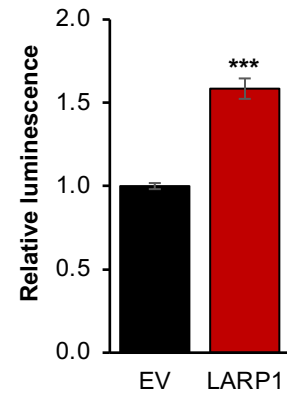
**C**



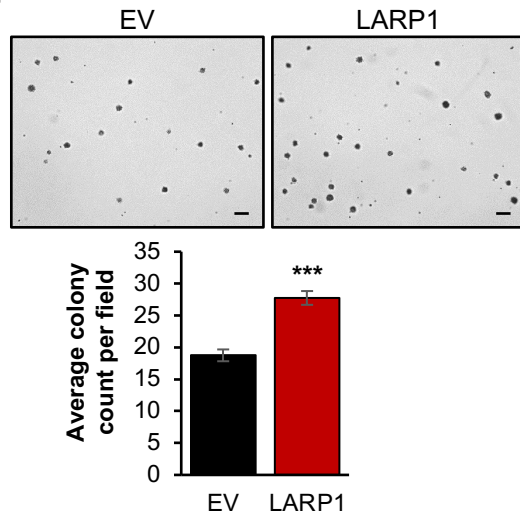
**D**



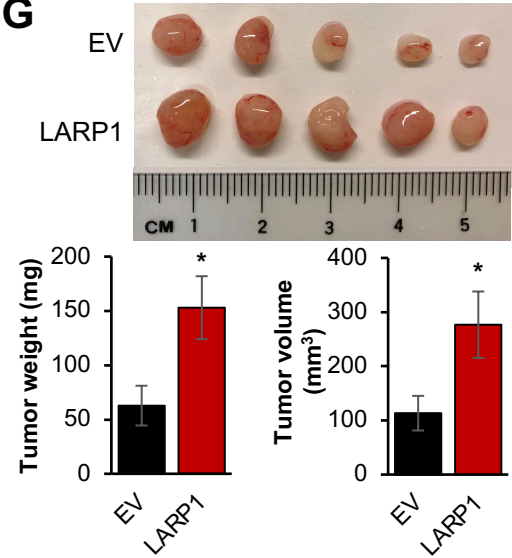
**E**



**F**

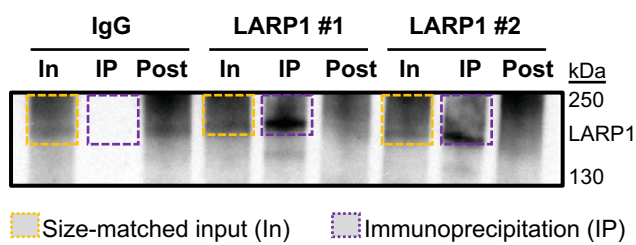


**G**

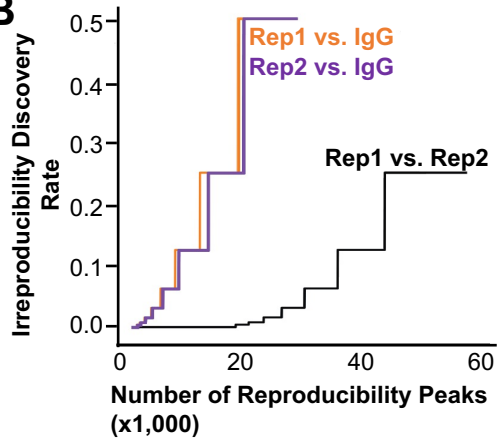


# Supplementary Fig. S2

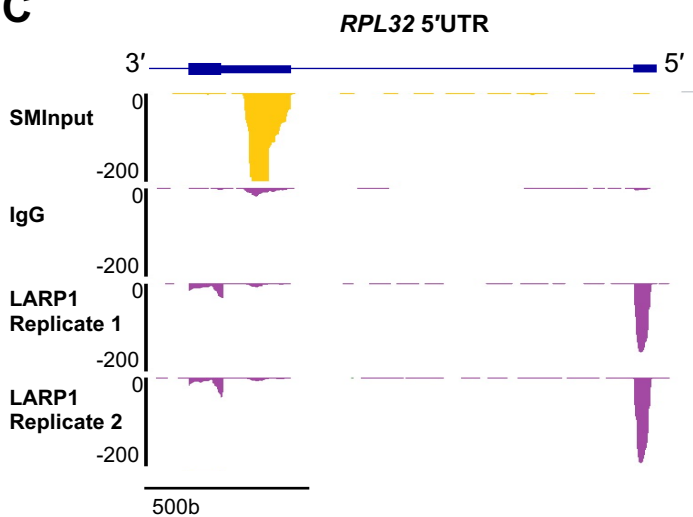
## A



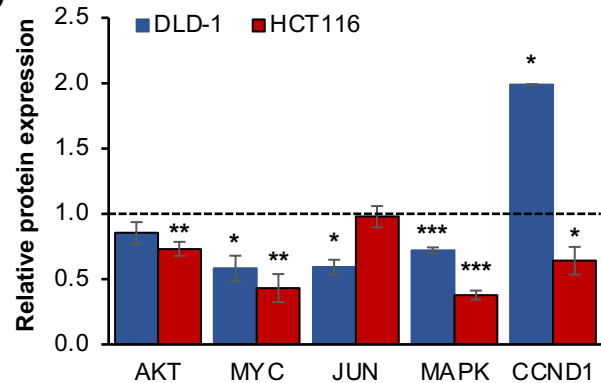
## B



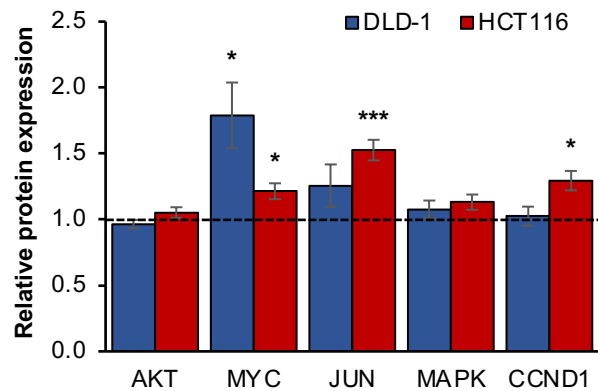
## C



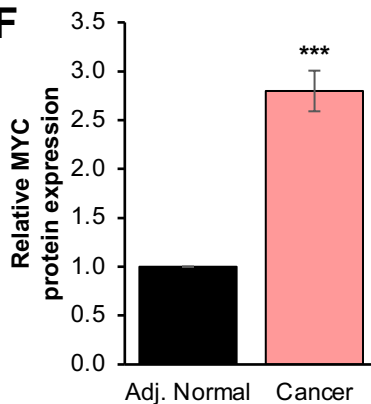
## D



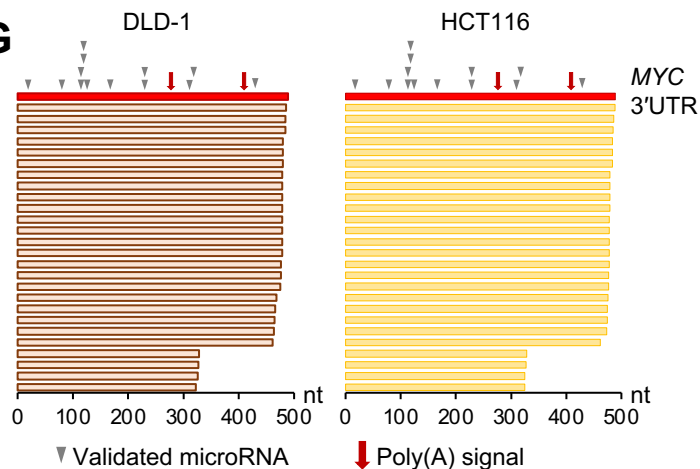
## E



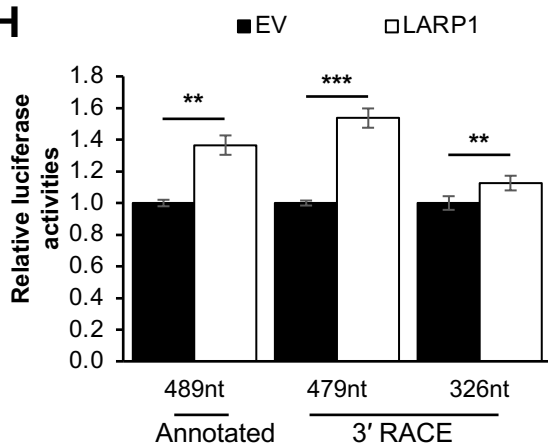
## F



## G



## H



# Supplementary Fig. S3

**A**

Gene Name	Protein Name	Peptides (95%)	Unused score
PABPC3	Polyadenylate-binding protein 3	5	10.00
ILF3	Interleukin enhancer-binding factor 3	5	10.00
IGF2BP2	Insulin-like growth factor 2 mRNA-binding protein 2	5	4.00
DSP	Desmoplakin	3	6.00
GNAI1	Guanine nucleotide-binding protein G(i) subunit alpha-1	3	6.00
TAOK1	Serine/threonine-protein kinase TAO1	3	6.00
U2SURP	U2 snRNP-associated SURP motif-containing protein	3	4.78
LARP1	La-related protein 1	2	4.00
RPL13A	60S ribosomal protein L13a	2	4.00
HADHB	Trifunctional enzyme subunit beta, mitochondrial	2	4.00
HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	2	3.33
PRPF40A	Pre-mRNA-processing factor 40 homolog A	2	2.15

**B**

**LARP1 amino acid sequence:**

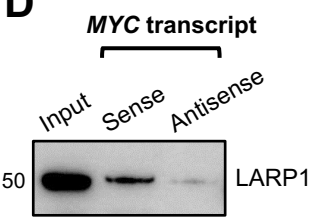
MATQVEPLLPGGATLLQAEHGGGLVRKKPPPAPEGKGEPPNDVRRGGEPDGSARRPRPPCAKPHKEGTGQQERESPRPLQLPGAEGPAIS  
 DGEEGGGEPGAGGGAAGAAGARRDFVEAPPKVNVPWTKNALPPVLTVNGQSPPEHSAPAKVVRAAVPKQRKGSKVGDFGDAINWPTP  
 GEIAHKSVPQSHKPQPTRKLPKPKDMKEQEKGEKSDSKESPKTKSDESGEEKNGDEDCQRRGGQKKKGNKHKWVPLQIDMKPEVPREKLA  
 SRPTRPPEPRHIPANRGEIKGSSEATYVPVAPPTPAWQPEIKPEAWHDQDETSSVKSDGAGGARASFRGRGRGRGRGRGRGRGRGGTRTHF  
 DYQFGYRKFDGVEGPRTPKYMNNITYYFDNVSSTELYSVDQELLKDYIKRQIEYYFSVDNLERDFFLRKMDADGFLPITLIASFHRVQALTTDI  
 SLIFAALKDSKVVIEVDEKVRREEPEKWLPLPIVDYSQTDFSQLNCPFVPRQHYQKETESAPGSRAVTPVPTKTEEVSNLKTLPKGLSAS  
 LPDLSENWIEVKKRPRPSPARPKKSEESRFSHLTSLPQQQLPSQQLMSKDQDEQEELDFLDEEMEQQMDGRKNTFTAWSDEESDYEIDDRD  
 VNKILIVTQTPHYMRRRHPGGDRTGNHTSRAKMSAELAKVINDGLFYEQDLWAEKFEPEYSQIKQEVENFKKVNMSIREQFDLTLPPEPVDPN  
 QEVPPGPPR**FQQVPTDALANKLFGAPEPSTIAR**SLPTTVPESPNYRNRTRPTRTPQLKDDSSQTSRFYFPVVEKGRTLDAKMPRKRKTRHSS  
 NPPLSHVGVWVMDSREHRRRTASISSPSEGTPVGSYGCTPQSLPKFKQHPHSHELLKENGFTQHVYHKYRRRLNCRKLGIGQSQEMNTL  
 FRFWSF<sup>1</sup>LRDFHFNKMYE<sup>2</sup>EFKQ<sup>3</sup>LALEDAKEGYRY<sup>4</sup>GLECLFRYYSYGLEKKFRLDIFKDFQEETVKDYEAGQLYGLEKFWAFLKYSKAKNLDID  
 PKLQ<sup>5</sup>EYLGKFRRLDFRVDPPMGE<sup>6</sup>EGNHKRHSVVA<sup>7</sup>GGGGGEGRKRCPSSSSRPAAMISQPPTPPTGQPVREDAKWTSQHSNTQTLGK  
**FQQVPTDALANK** **LFGAPEPSTIAR**

**C**

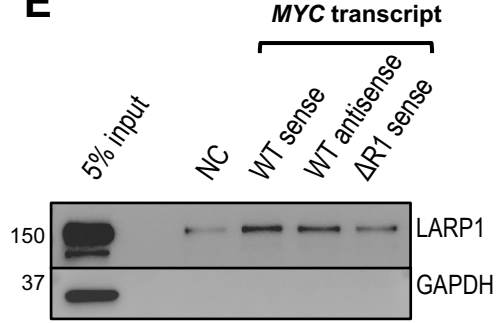
**Amino acid alignment:**

FDTLTPEPPVDPNQEVPPGPPR**FQQ** - - - - - **VP** - - - - **TDALANKLFGAPEPSTIA** - - RSLPTTVPESP **LARP1**  
 F+ LTPE P + PNQEV P + +Q +P TD LA KLF E ++ A SLPT VPESP **Matched residues**  
 FENLTPELPFE PNQEVVAPSQRSRGGVQGVLHPIPKKDLTDELAQKLFVSEITSAMVHSLPTAVPESP **LARP2**

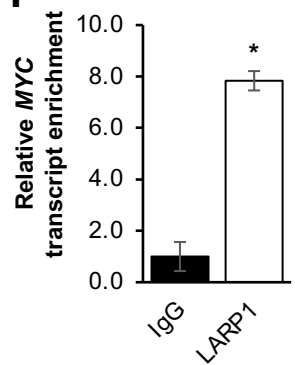
**D**



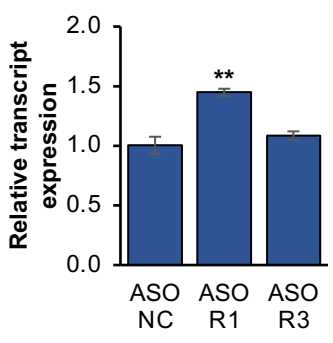
**E**



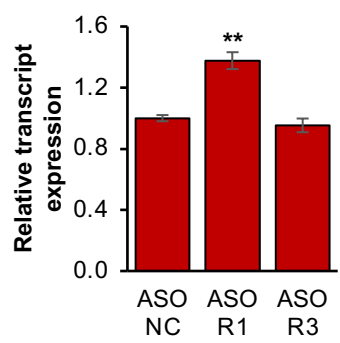
**F**



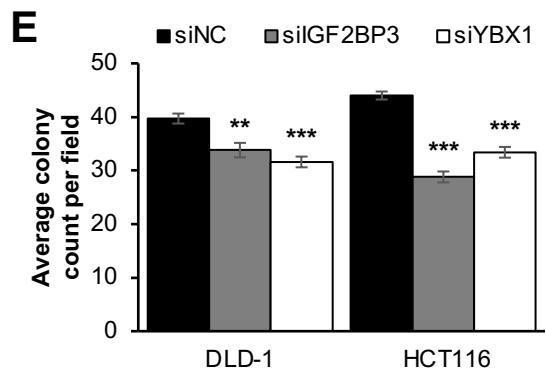
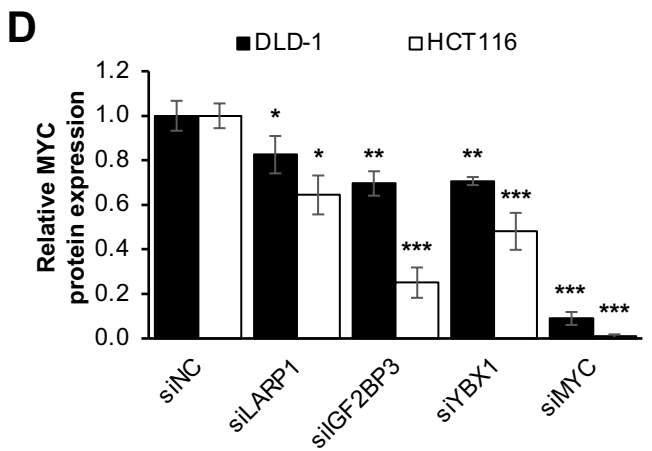
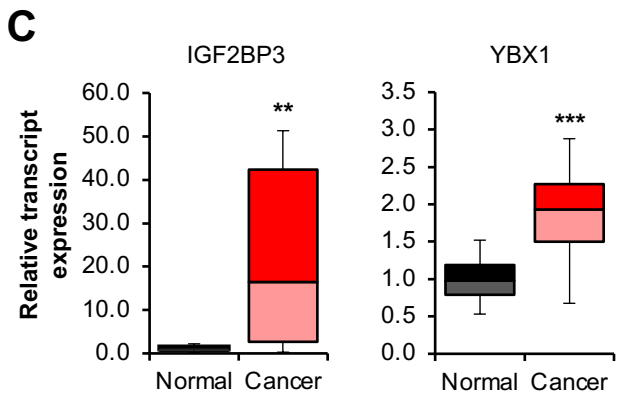
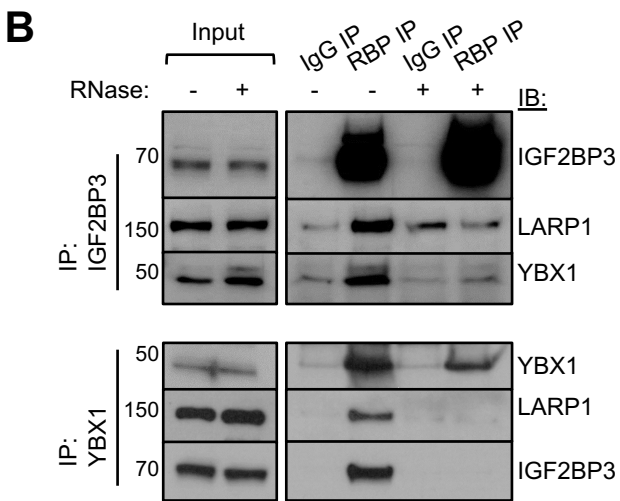
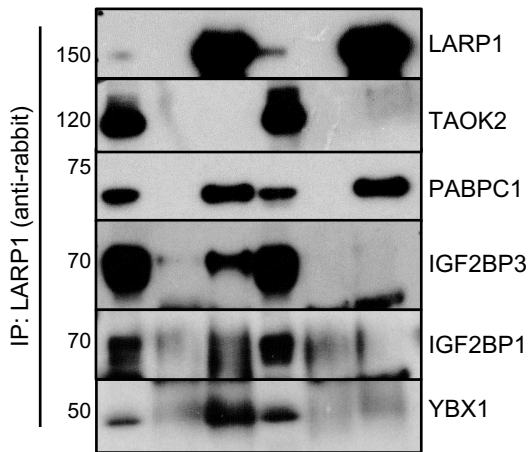
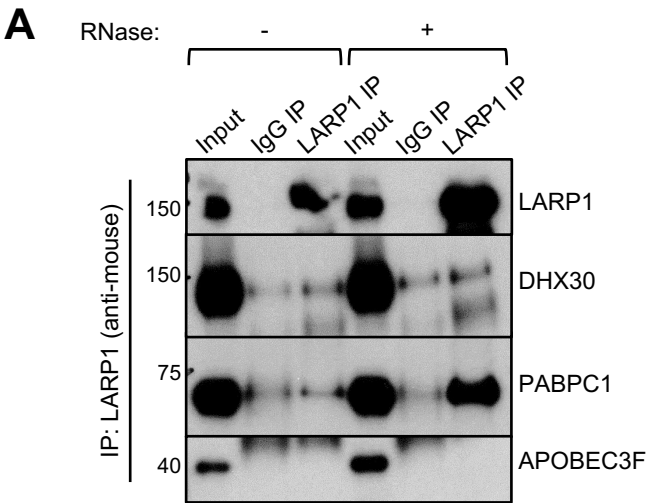
**G**



**H**



# Supplementary Fig. S4





# Supplementary Fig. S5

