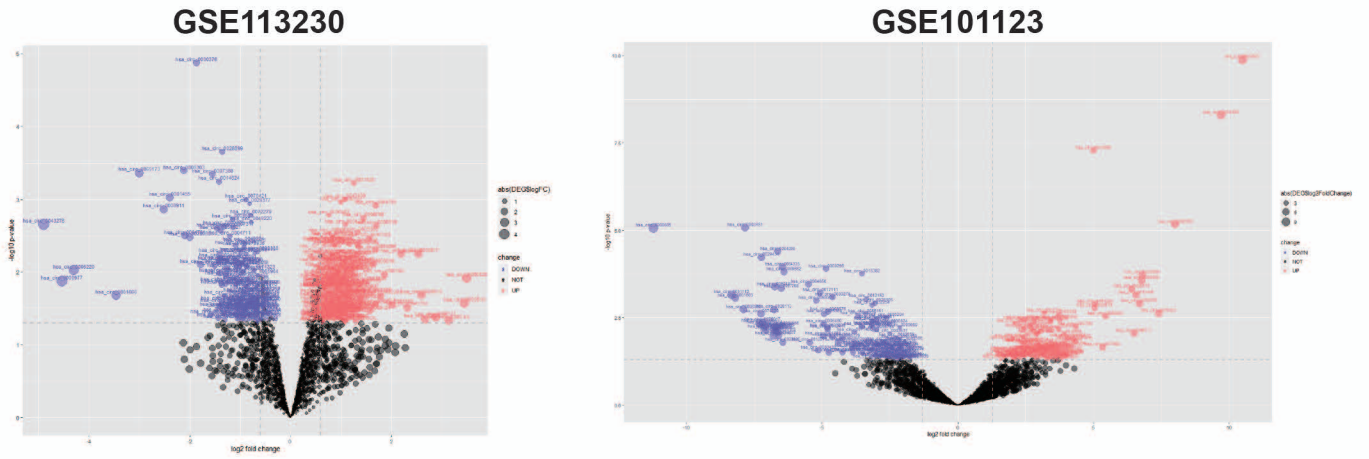
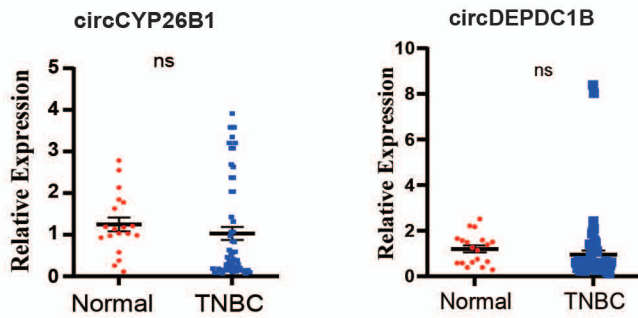


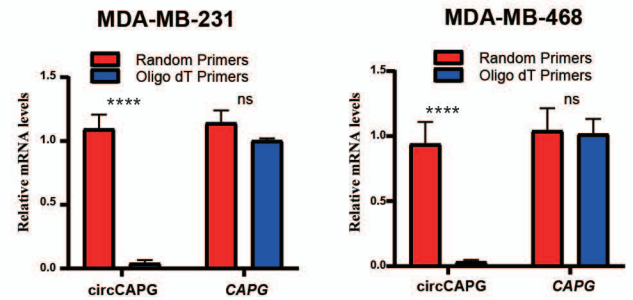
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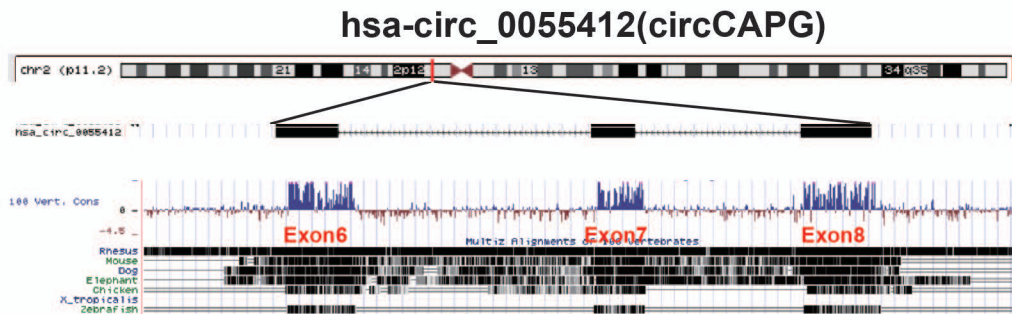
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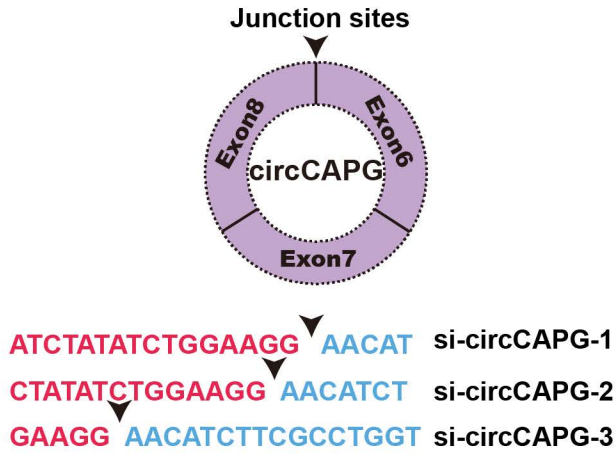
D



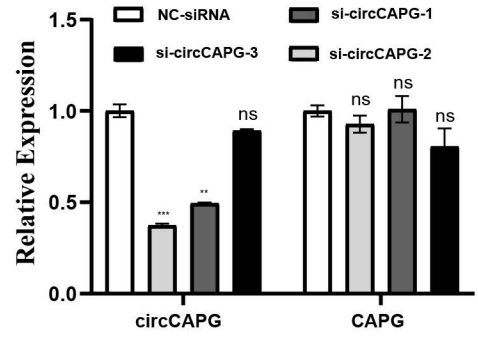
C



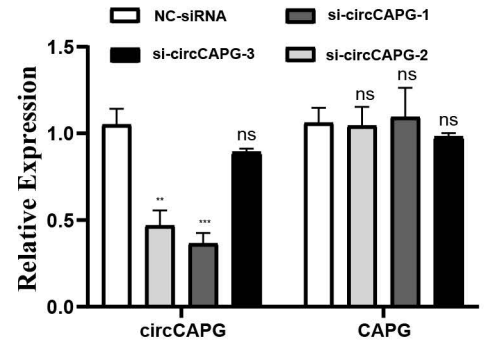
A



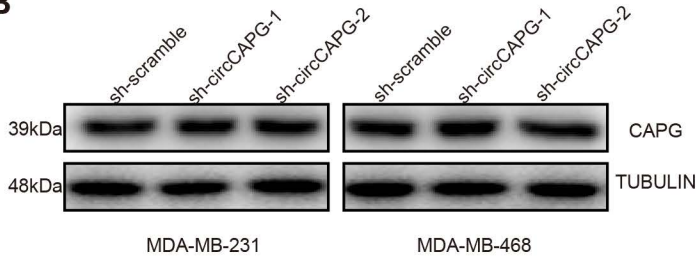
MDA-MB-231



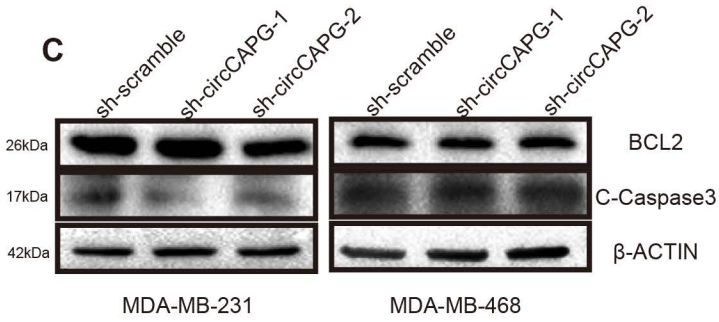
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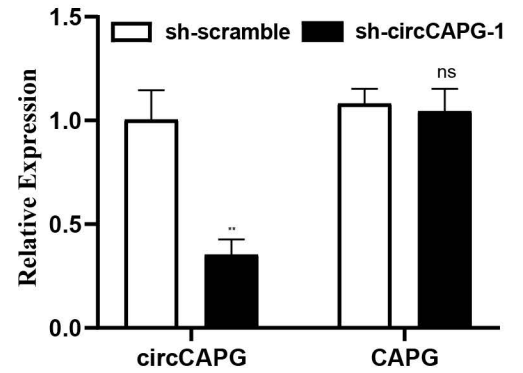
B



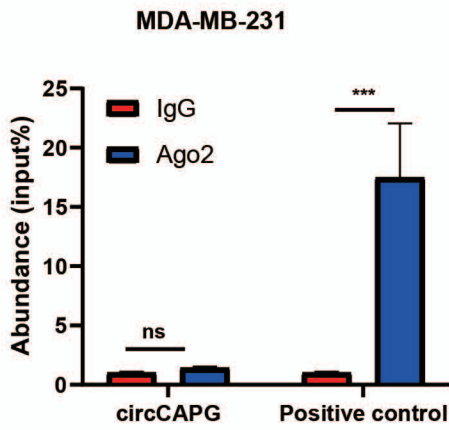
C



D



A



B

Transcript id	NM_001256139		
Exon	Exon Number	Exon id (total)	Exon Sizes
	3	3,4,5 (18)	133, 93, 150
Spliced seq length	376 nt		
Sequence	AACATCTTCG CCTG6T6T6G T66AAGTCC AACATCTCG AACSCAACA G6GAG6GAC CT6CCCTG6 CCATCC6GGA CA6T6G6C6A CA6G6C6A6G6 C6CA6G6T6G6A GAT6T6T6CACT GAT6G6G6A6G6 A6C6T6C6T6G6A GAT6AT6C6C6A6 G6T6C6T6G6C6C CC6A6G6C6T6G6 T6C6T6A6A6G6A6G6 G6C6A6C6C6C6T6 A6G6A6A6G6A6C6T6 C6A6C6T6G6A6C A6A6G6C6A6A6T6 C6C6A6G6C6C6C A6C6T6T6T6A6 A6G6T6C6T6G6 A6T6C6A6C6T6G6 A6C6A6T6G6A6C C6T6A6C6A6G6 T6G6C6T6G6A6C C6A6C6A6T6T6 G6C6C6T6G6A6C T6C6T6G6A6T6C T6A6T6G6A6C T6T6T6G6C6T6G6 A6C6A6C6G6G6C C6T6T6G6C6A6G A6T6A6T6A6T6C G6A6A6G		
Protein coding potential			
IRES Elements	Parameter Index		
	Position (start-end)	R Score	With Pseudoknot (YN)
	26-39	1.467281	Y
	29-86	1.466247	Y
Open Reading Frame (ORF)	Start Position	End Position	Protein Length
	323	2+86	171 aa
<p>MTALCWTGTS VARSISGRNI FAWCGGKSNI LERNKARDLA LAIRDSEKQ KAQVEIVTDG EEPAEIQVL GPKPALKEGNPEEDLTADKANAQAALYKVS DATGQMNLTKVADSSPFALLELLISDDCFVLDNGLCGKIYIWKGRKAN EKERQAALQVAEGFISRMQYAPNTQVEILPQGRESPIFKQFFKDWK</p> <p>Note: (1), nr represents n rounds(n<3); (2), * represents a stop codon.</p>			

C

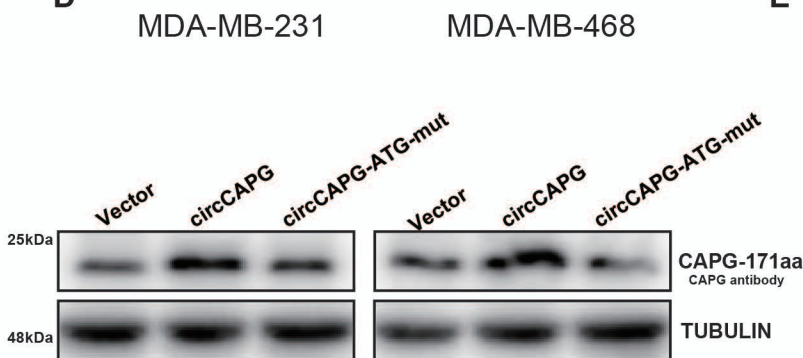
CAPG full length
 MYTAIPQSGSPFPGSVQDPGLHVWRVEKLPVPVAQENQGVFFSGDSYLVLHNGPEEVSH
 LHLWIGQQSSRDEQGACAVLAVHLNLTLLGERPVQHREVQGNESDLFMSYFPRGLKYQEGG
 VESAFHKTSTGAPAAIKKLYQVKGKKNIRATERALNWDSFNTGDCFILDLGQ **NIFAWCGGKSNILERNKARDLALAIRDSERQGKAQVEIVTDGEEPAEMIQVLGPKPALKEGNPEEDLTADKANAQAALYKVS
 DATGQMNLTKVADSSPFALLELLISDDCFVLDNGLCGKIYIWKGRKAN**
 ANEKERQAALQVAEGFISRMQYAPNTQVEILPQGHESPIFKQFFKDWK

CAPG-171aa
 MTALCWTGTS VARSISGRNI **FAWCGGKSNI LERNKARDLA LAIRDSEKQ KAQVEIVTDG
 EEPAEIQVL GPKPALKEGN PEEDLTADKANAQAALYKVS
 DATGQMNLTKVADSSPFALLELLISDDCFVLDNGLCGKIYIWK**EHLRLVW WKVQHPGTQQ GEGPGPGHPG Q

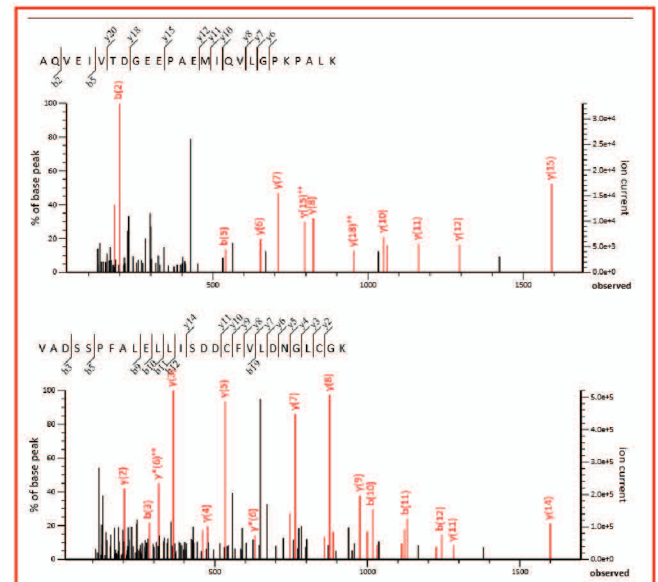
CAPG Polyclonal antibody(Proteintech #10194-1-AP)
 HLWIGQQSSRDEQGACAVLAVHLNLTLLGERPVQHREVQGNESDLFMSYFPRGLKYQEGGV
 ESAFHKTSTGAPAAIKKLYQVKGKKNIRATERALNWDSFNTGDCFILDLGQ **NIFAWCGGKSNILERNKARDLALAIRDSERQGKAQVEIVTDGEEPAEMIQVLGPKPALKEGNPEEDLTADKANA
 QAALYKVS
 DATGQMNLTKVADSSPFALLELLISDDCFVLDNGLCGKIYIWK**GRKAN
 EKERQAALQVAEGFISRMQYAPNTQVEILPQGRESPIFKQFFKDWK
 (62-348 aa encoded by BC000728)

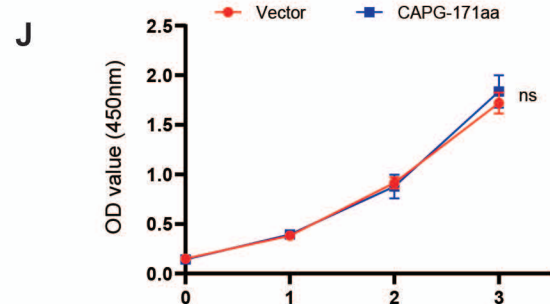
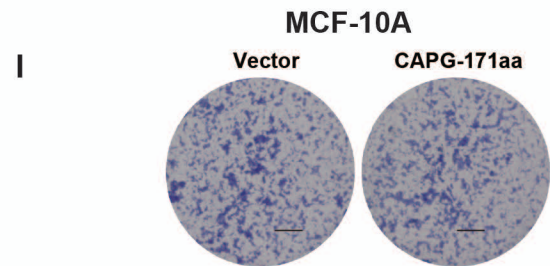
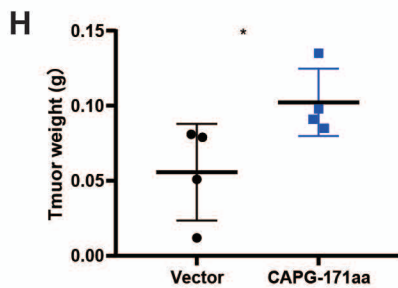
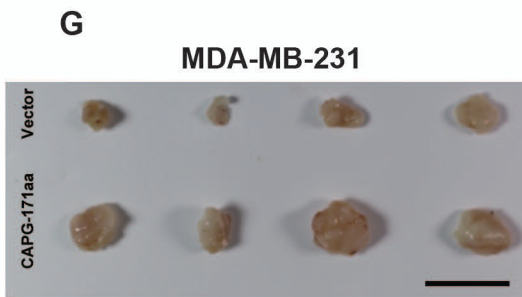
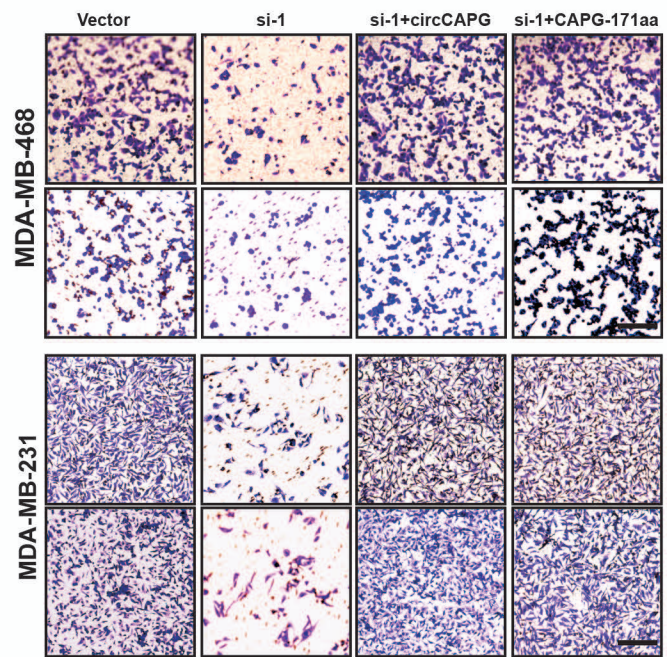
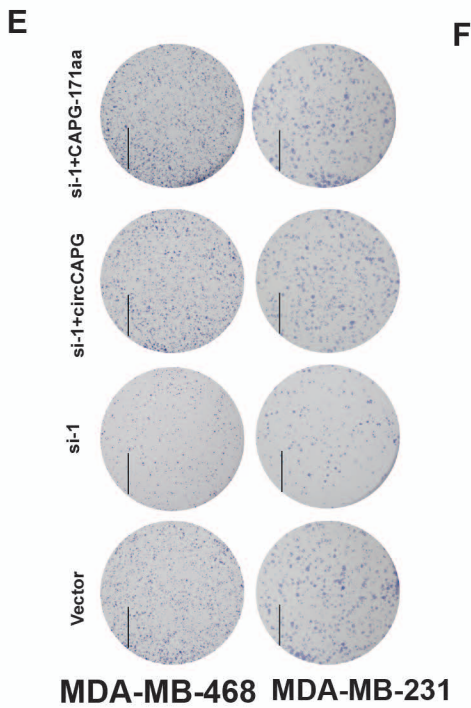
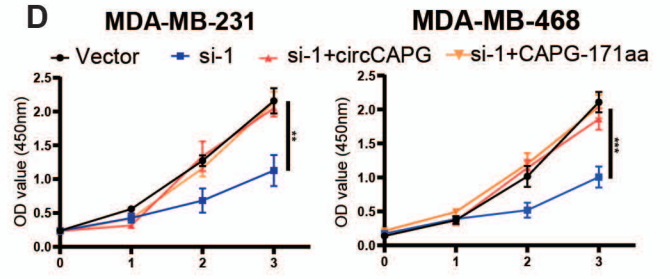
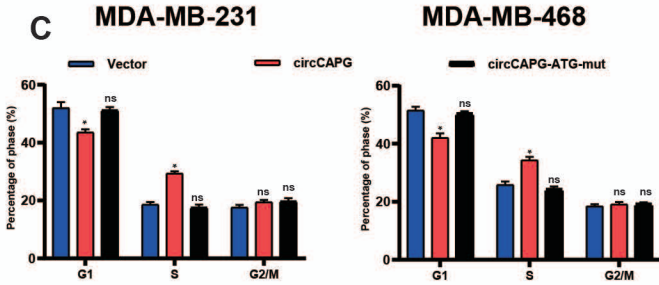
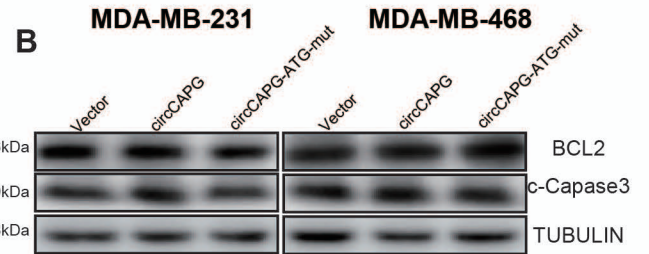
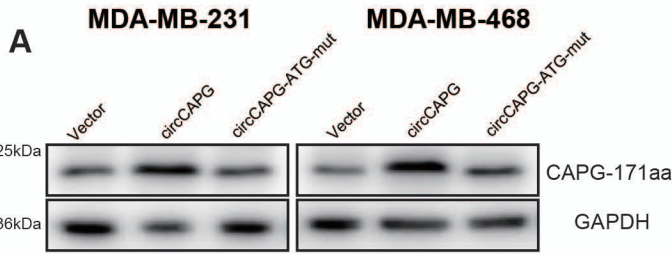
Blue marked CAPG antibody targeting sequence

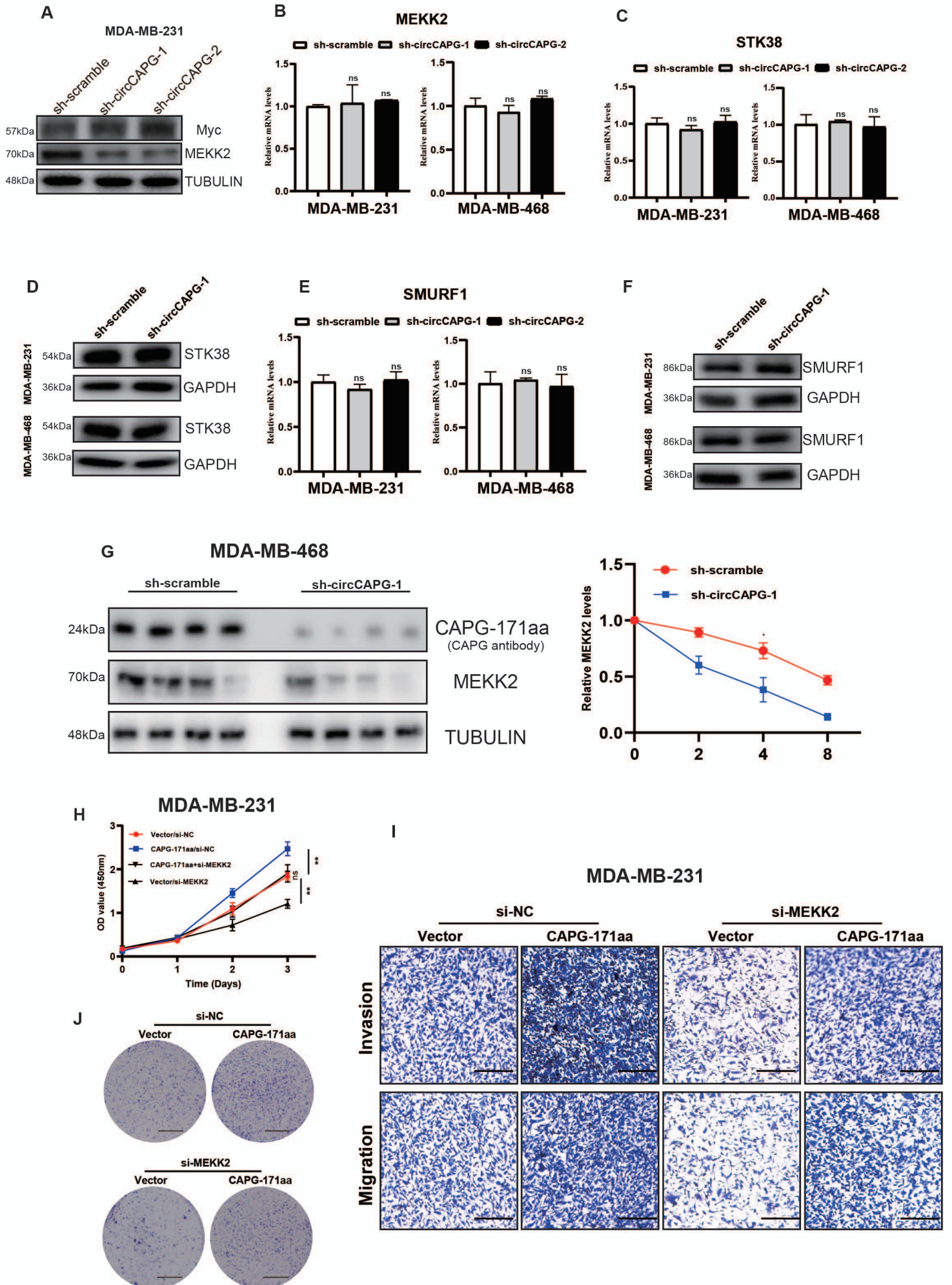
D



E





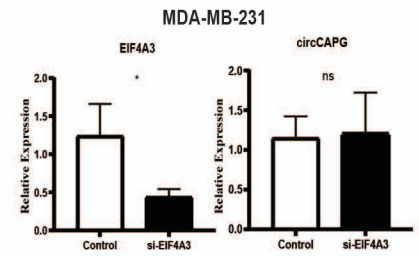


A

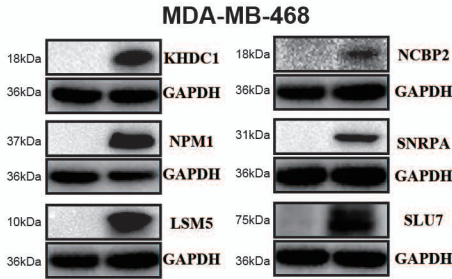
CircInteractome

circRNA	Tag Name	% Identity	Alignment Length	Mismatches	Gap Openings	Tag Start	Tag End	circRNA Start	circRNA End	Upstream/Downstream
hsa_circ_0055412	HHLE1_206509_elf4AIII_rep1_206509_32_152	100.00	152	0	0	1	152	0	+392	Downstream
hsa_circ_0055412	HHLE1_206515_elf4AIII_rep1_206515_3_43	100.00	43	0	0	1	43	-205	-163	Upstream
hsa_circ_0055412	HHLE2_673405_elf4AIII_rep2_673405_41_137	100.00	137	0	0	1	137	0	-377	Downstream

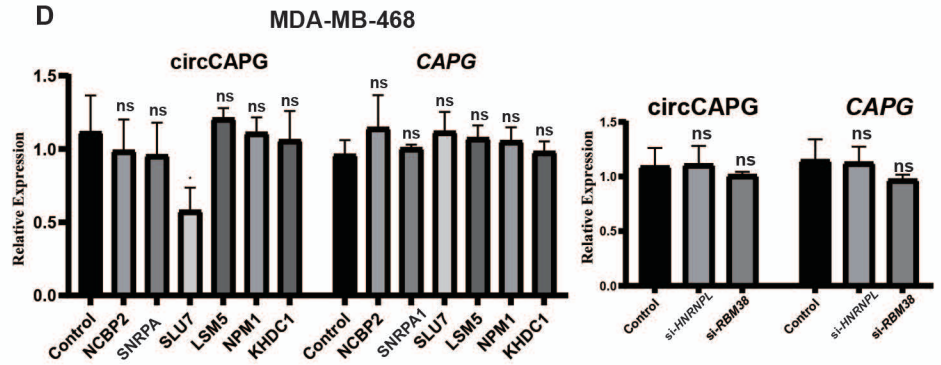
B



C

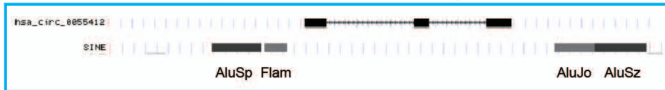


D



E

The potential SLU7 binding sites



G

The high homology between AluSp and AluSz

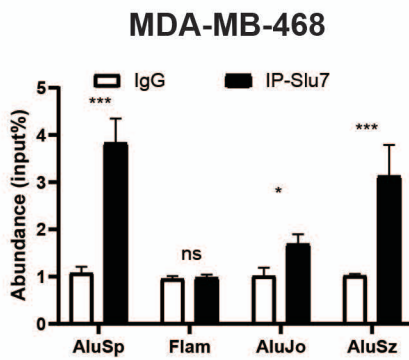
Sequence ID: Query_5125 Length: 297 Number of Matches: 1

Range 1: 7 to 293 Graphics

Next Match Previous Match

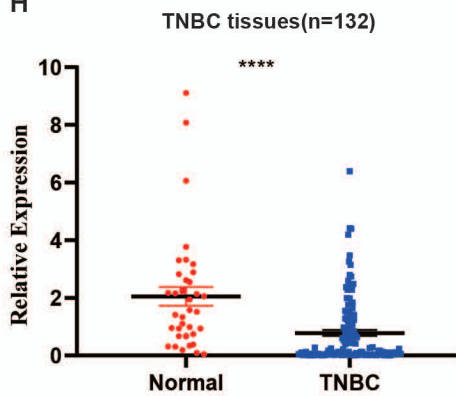
Score	Expect	Identities	Gaps	Strand
244 bits(132)	2e-69	244/296(82%)	15/296(5%)	Plus/Plus
Query 14	GCTCAGGCTGTAATTOCCAGCACTTTGGGAGGCGGAGGTGGCGAGATCACCTGAGGTC	71		
Sbjct 7	GCTCACATCTGTAATTOCCAGCACTTTGGGAGGCGGAGGCGGTCATCACTTGAAGTC	64		
Query 72	GGAGTTCGAGACCAAGGCTGACCAACATCGAGAAACCCCATCTCTACTAAAAATATAAA	130		
Sbjct 65	ACAAGTTCGAGACCAAGGCTGCTAGTCAAAACCCCATCTCTACTAAAAATACAAAA	118		
Query 131	ATTAGCCGGGCTGTTGGGCACATGCTGTAATTOCCAGCTACTCGGAGGCTGATGCAAGGA	190		
Sbjct 119	ATTAGCCAGGCTGTTGGGCACGCACTGCTACTOCCAGCTACTCGGAGGCTAAGCCAGGA	178		
Query 191	GGATCTCTTGAAGCCAGGAGGTTGGGCTGAGCTGAGATTGTACCATTGCACTTCC	250		
Sbjct 179	GAATTGCTTGAAGCCAGGAGGTTGGGCTGAGCTGAGCTGAGATTGTACCATTGCACTTCC	238		
Query 251	AGCTGGGCAACAAGAGGAACTGCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	303		
Sbjct 239	AGCTGGGTAACA-GAGCAAGATTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	293		

F

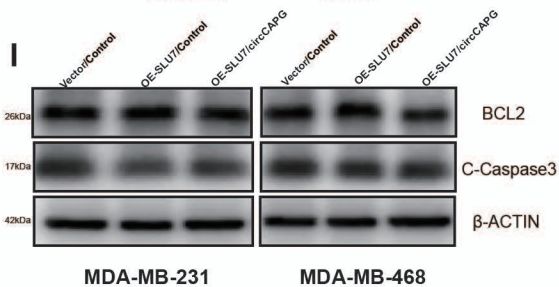


SLU7

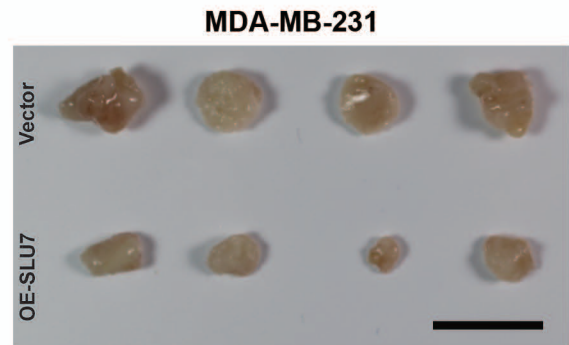
H



I



J



K

