

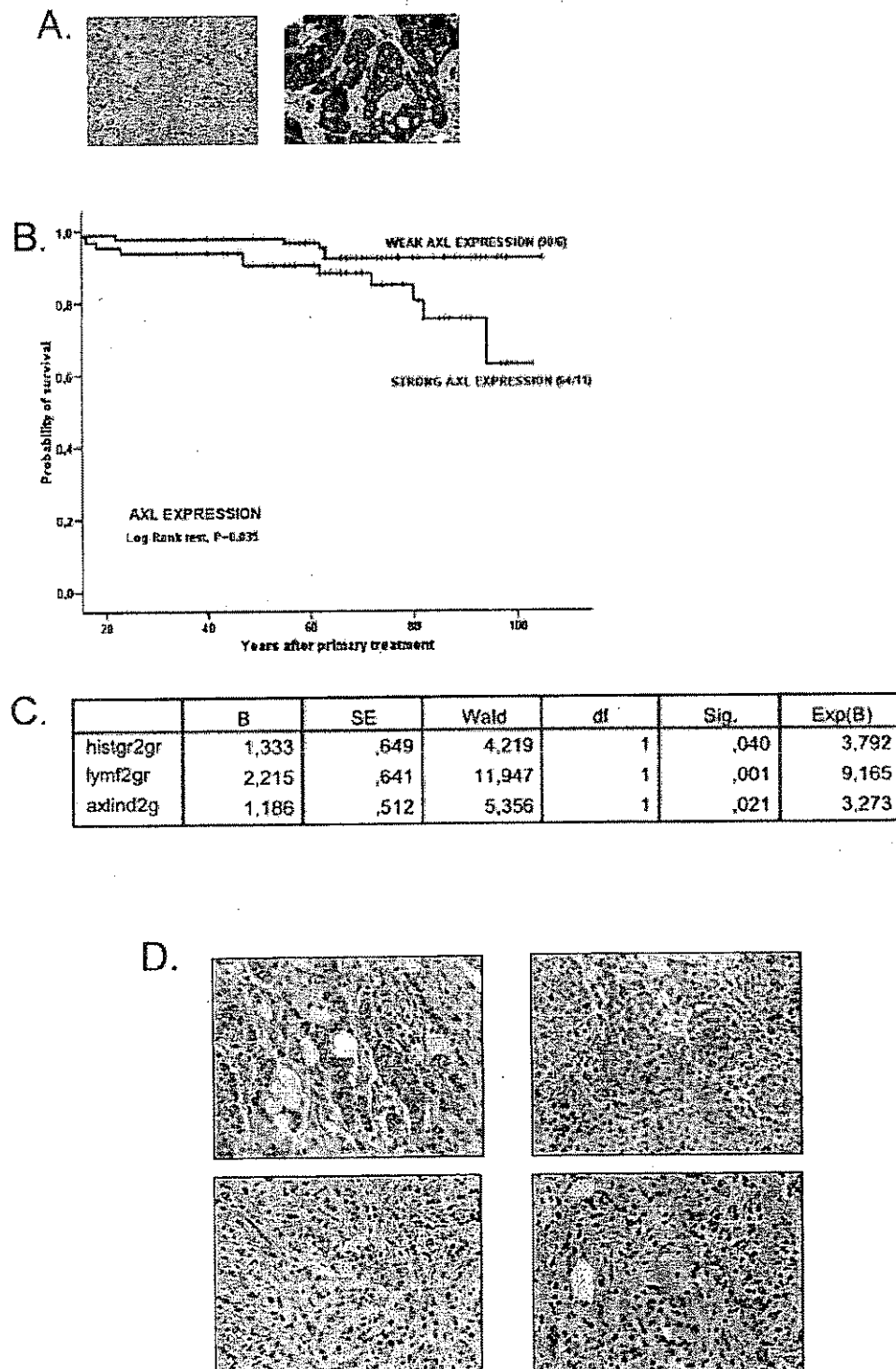


FIGURE 1

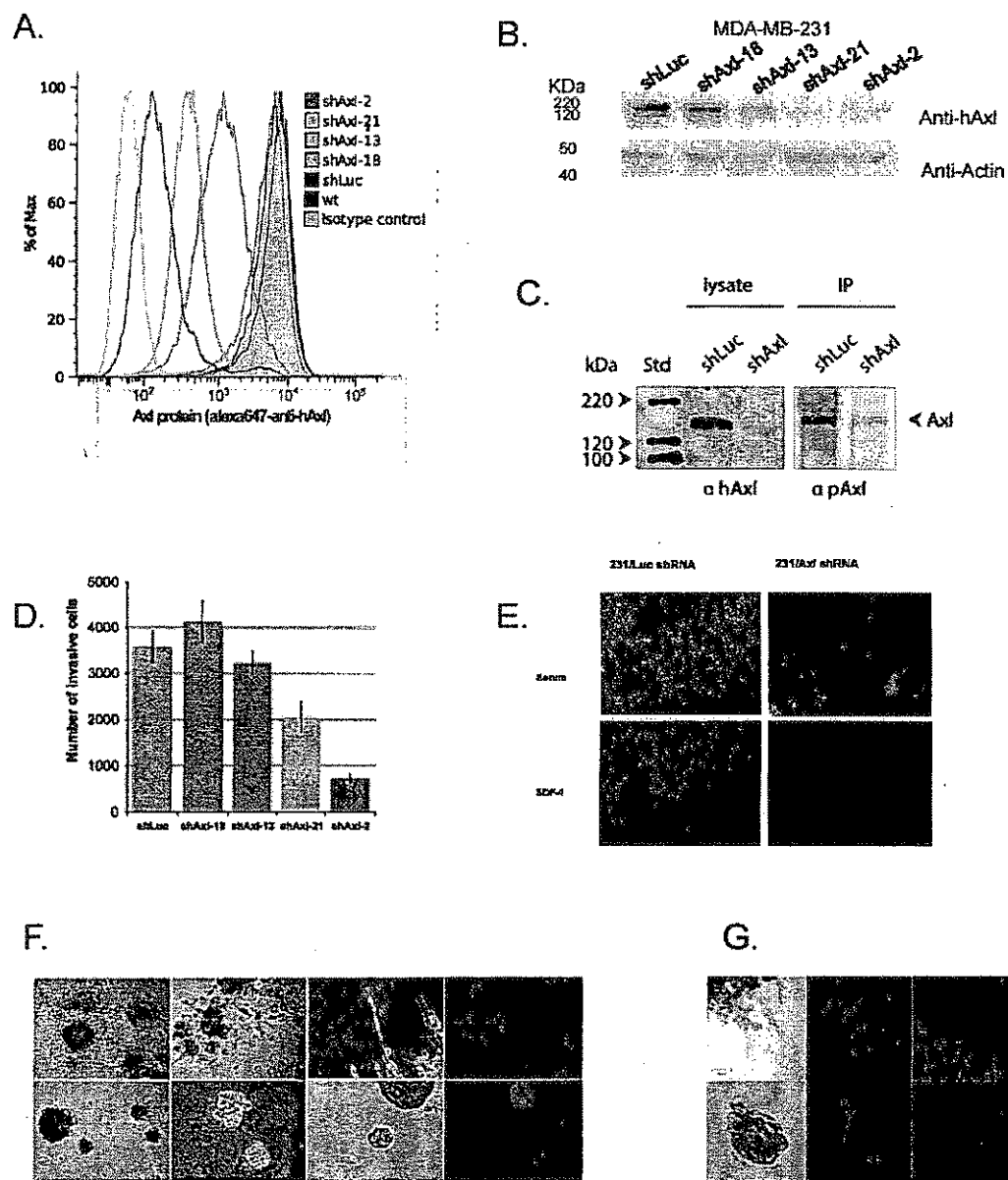


FIGURE 2

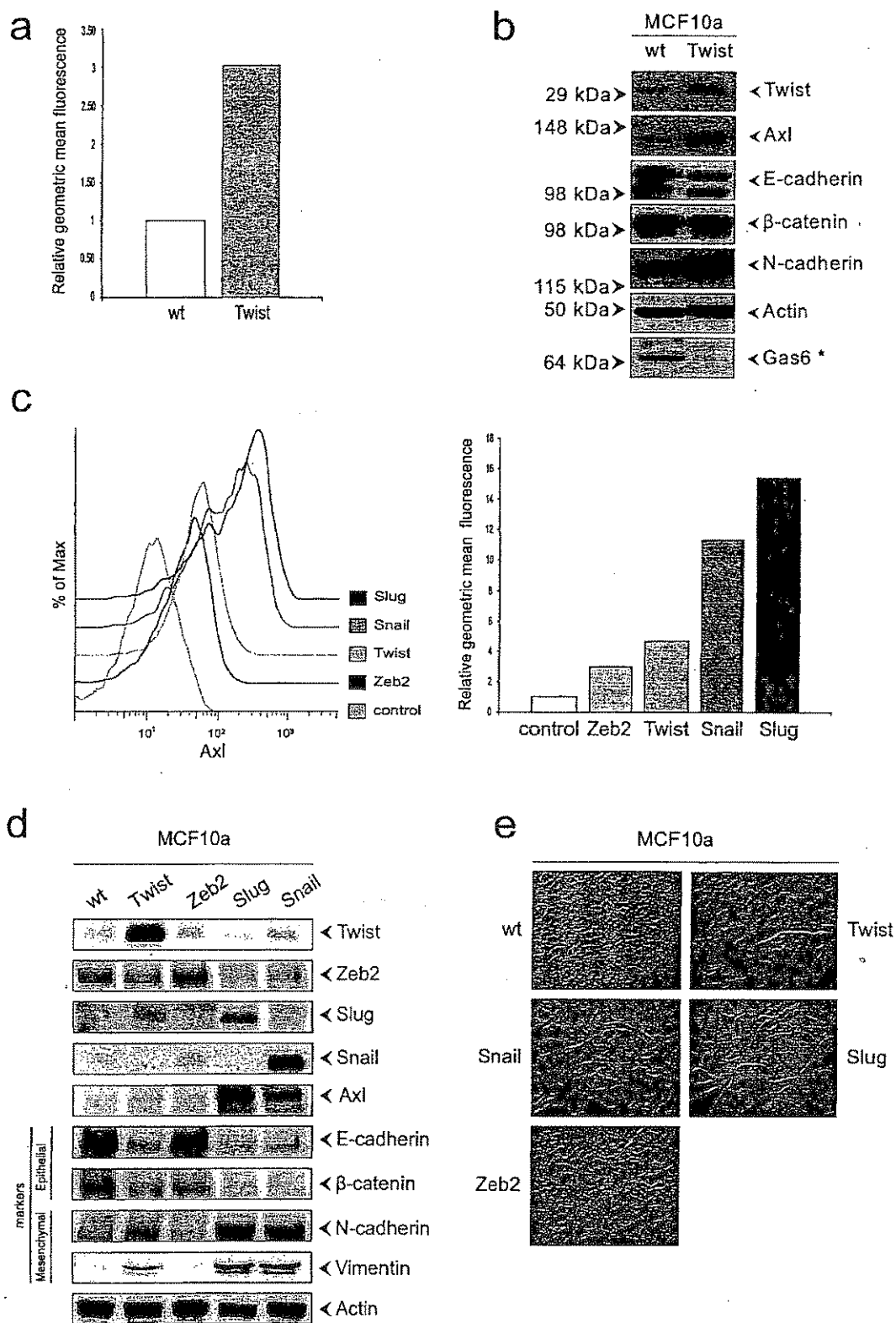


FIGURE 3

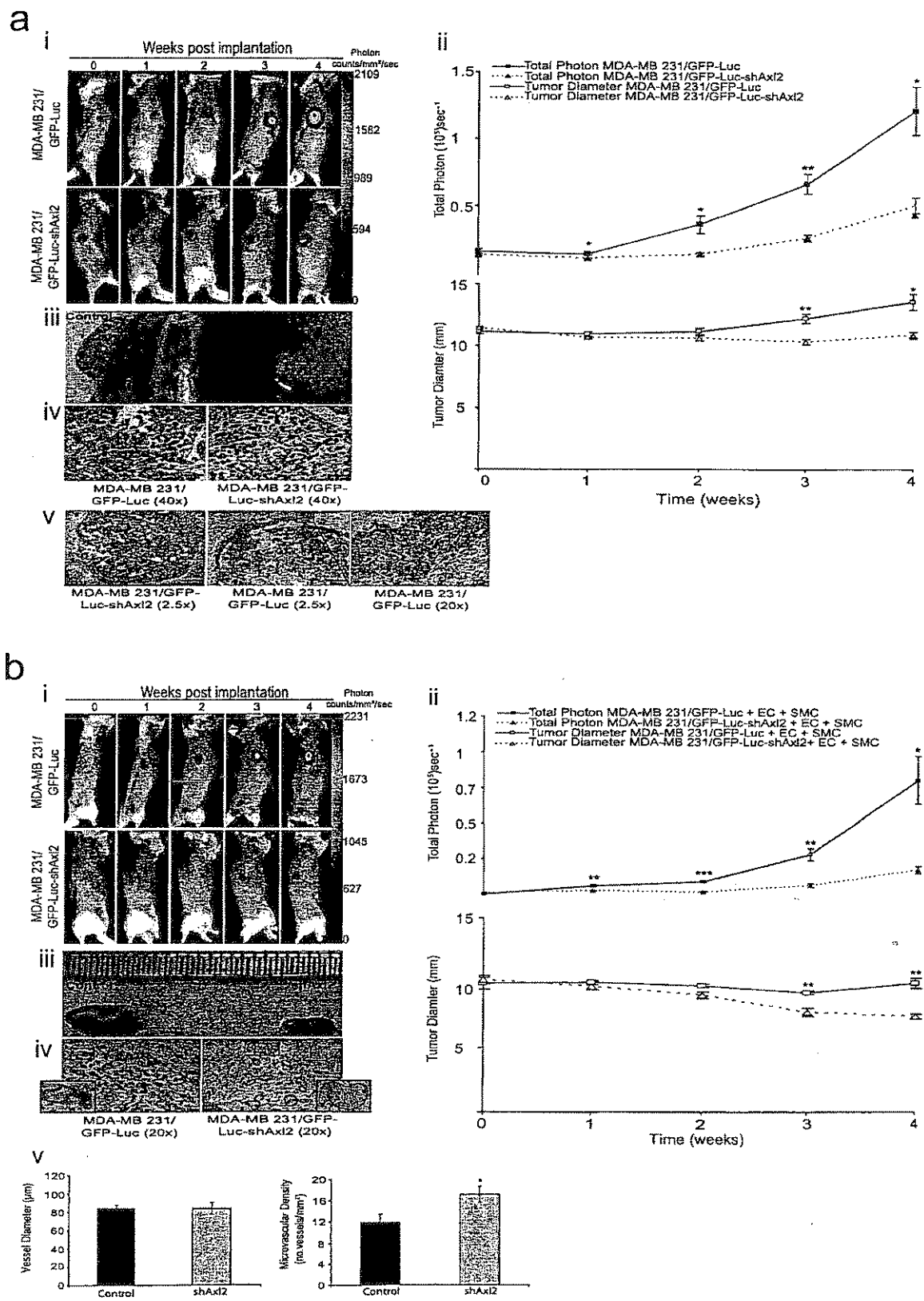
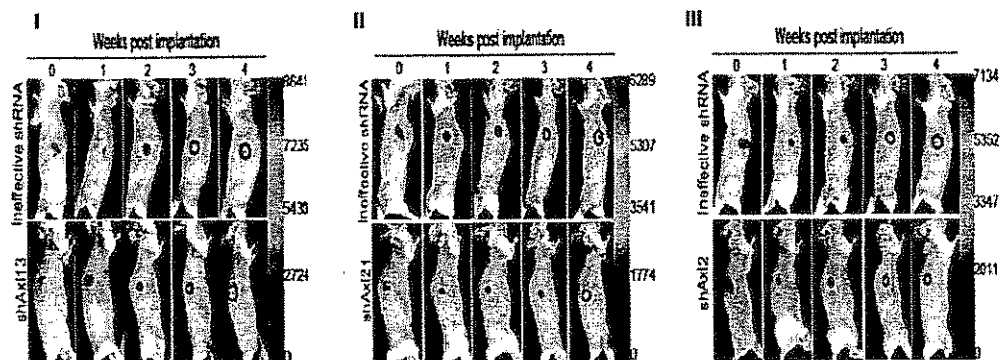


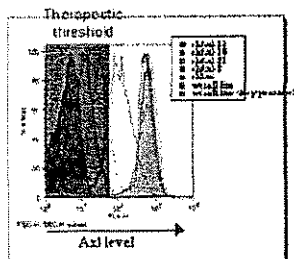
FIGURE 4

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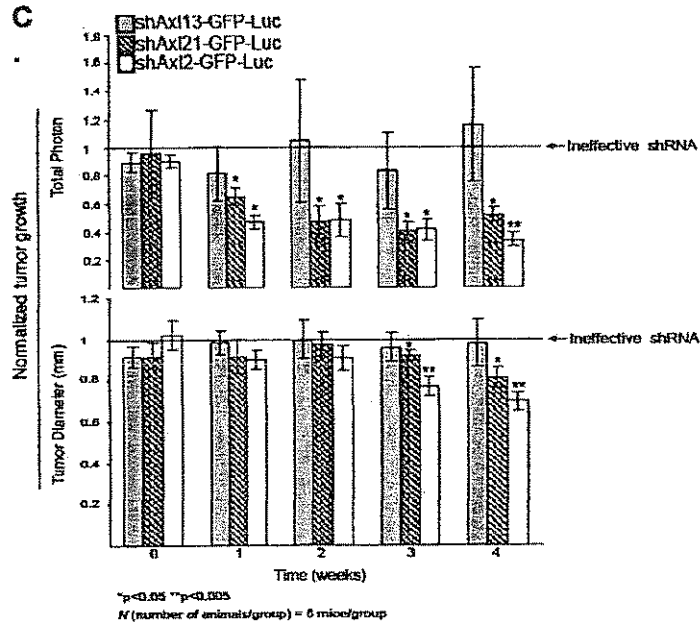
A.



B.



C.



D.

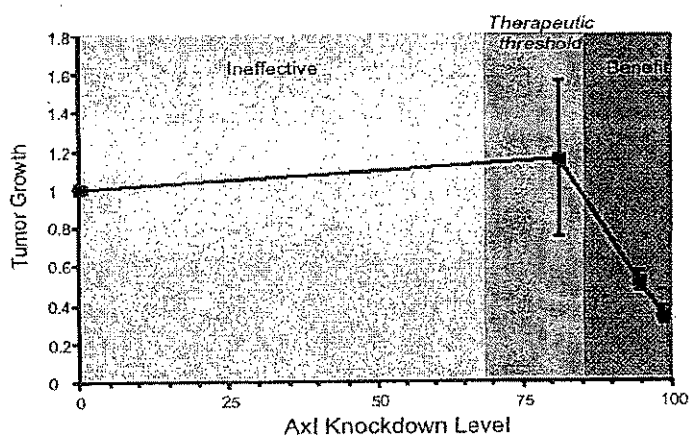
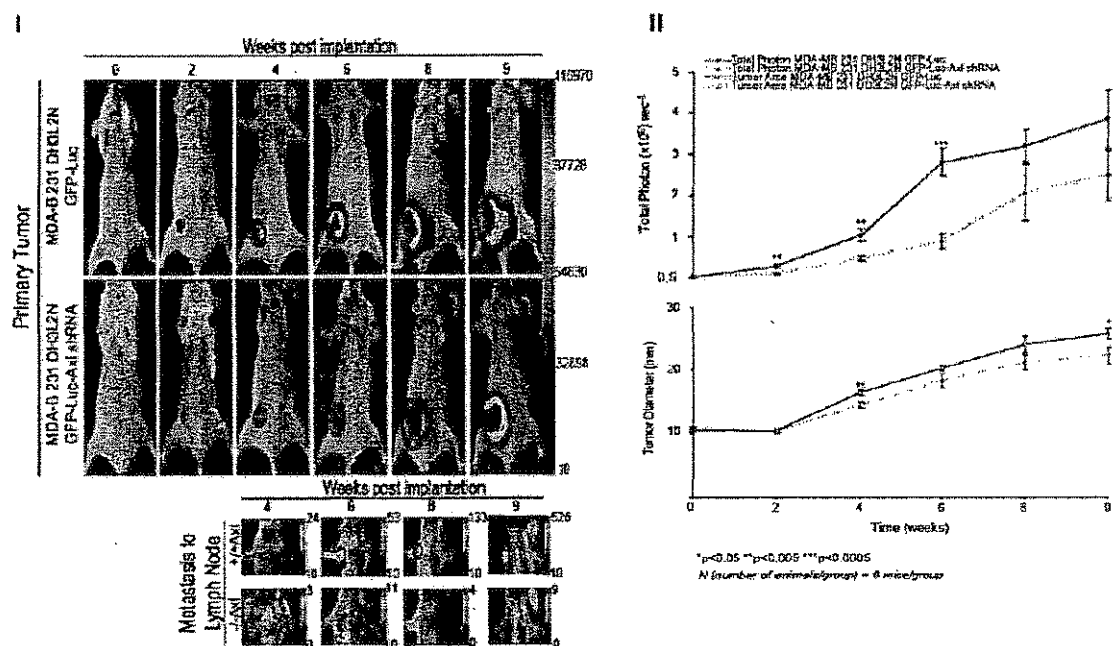


FIGURE 5

A.



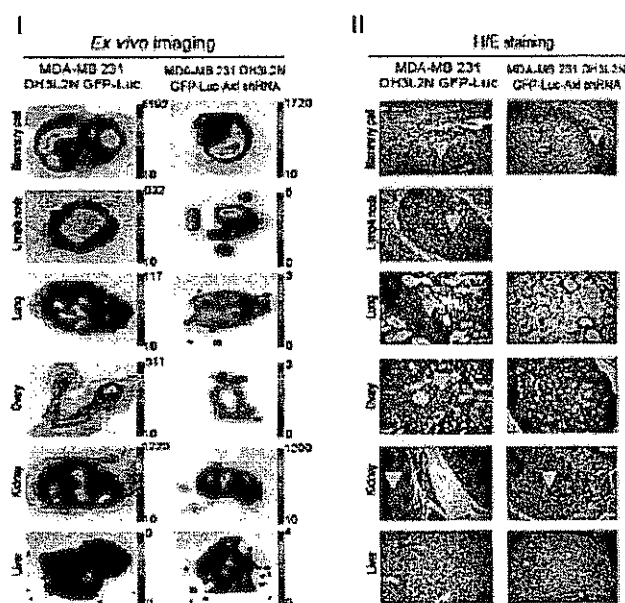
B.

Detected metastases

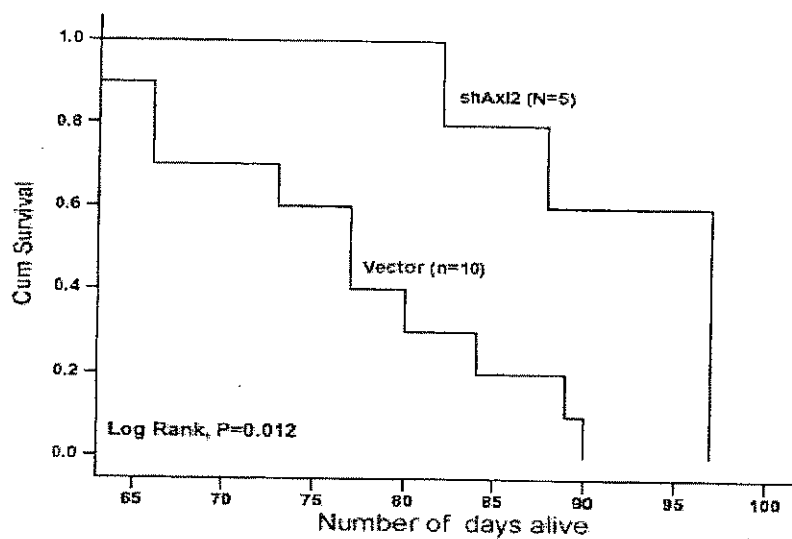
Cell line	<i>In vivo</i>	<i>Ex vivo</i>				
	Lymph node	Lungs	Kidneys	Ovaries	Liver	
MDA-MB 231 DRLN GFP-Luc	5/6	4/6	3/5	2/6	0/6	
MDA-MB 231 DRLN GFP-Luc Ad shRNA	0/6	0/6	1/6	0/6	0/6	

N(number of animals/group) = 6 mice/group

C.



FIGURES 6A-C



Number of days alive		
Cell line	Mean	Median
MDA-MB 231/DHLN-GFP-Luc	72.20	77.00
MDA-MB 231/DHLN-GFP-Luc-shAx12	92.20	97.20

Test statistics	
	Number of days alive
Mann-Whitney U	5.000
Wilcoxon W	60.000
Z	-2.463
Asymp. Sig. (2-tailed)	.014
Exact Sig. [2*(1-tailed Sig.)]	.013(a)

FIGURE 6D

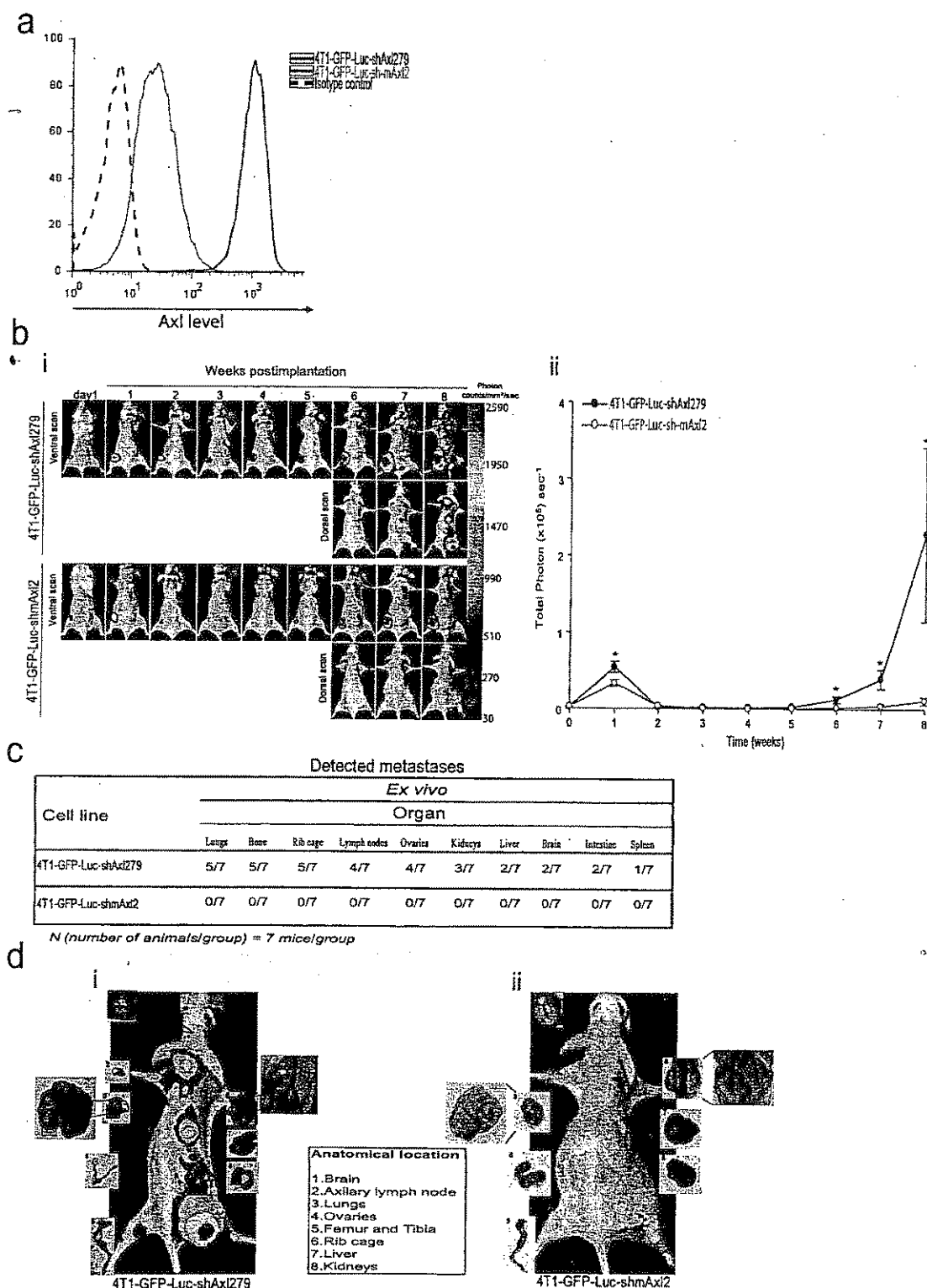


FIGURE 7

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61 CGCGTTACAT AACTTACGGT AAATGGCCCC CCTGGCTGAC CGCCCAACGA CCCCCGCCA
121 TTGACGTCAA TAATGACGTA TGTTCCCATTA GTAAACGCCAA TAGGGACTTT CCATTGACGT
181 CAATGGGTGG AGTATTTTACG GTAAACTGCC CACTTGGCAG TACATCAAGT GTATCATATG
241 CCAAGTACGC CCCCTATTGA CGTCAATGAC GGTAAATGGC CCGCCTGGCA TTATGCCCAG
301 TACATGACCT TATGGGACTT TCCTACTTGG CAGTACATCT ACGTATTAGT CATCGCTATT
361 ACCATGGTGA TGCGGTTTTG GCAGTACATC AATGGGCGTG GATAGCGGTT TGACTCACGG
421 GGATTTCCAA GTCTCCACCC CATTGACGTC AATGGGAGTT TGTTTTGGCA CCAAAATCAA
481 CGGGACTTTC CAAAATGTCG TAACAACCTC GCCCATTGA CGCAAATGGG CGGTAGGCAT
541 GTACGGTGGG AGGTCTATAT AAGCAGAGCT CAATAAAAGA GCCCACAACC CCTCACTCGG
601 CGCGCCAGTC CTCCGATTGA CTGAGTCGCC CGGGTACCCG TGTATCCAAT AAACCCTCTT
661 GCAGTTGCAT CCGACTTGTG GTCTCGCTGT TCCTTGGGAG GGTCTCCTCT GAGTGATTGA
721 GATCCCGTCA GCGGGGGTCT TTCATTTGGG GGCTCGTCCG GGATCGGGAG ACCCTGCCC
781 AGGGACCACC GACCCACCAC CGGGAGGTAA GCTGGCCAGC AACTTATCTG TGTCTGTCCG
841 ATTGTCTAGT GTCTATGACT GATTTTATGC GCCTGCGTCG GTACTAGTTA GCTAACTAGC
901 TCTGTATCTG GCGGACCCGT GGTGGAACCT ACGAGTTCGG AACACCCGGC CGCAACCCTG
961 GGAGACGTCT CAGGGACTTC GGGGGCCGTT TTTGTGGCCC GACCTGAGTC CAAAATCCC
1021 GATCGTTTTG GACTCTTTGG GACCTTTTGG TGACCCCCC ATAGAGGAGG GATATGTGGT TCTGGTAGGA
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1141 AGCCGCGCCG CGCGTCTTGT CTGCTGCAGC ATCGTCTGT GTTGTCTCTG TCTGACTGTG
1201 TTTCTGTATT TGTCTGAAAA TATGGGCCCG GGCCAGACTG TTACCACTCC CTTAAGTTTG
1261 ACCTTAGGTC ACTGGAAGA TGTCGAGCGG ATCGTCACTA ACCAGTCGGT AGATGTCAAG
1321 AAGAGACGTT GGGTTACCTT CTGCTGCGCA GAATGGCCAA CCGTTAACGT CCGATGGCCG
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1441 GGCCCGCATG GACACCCAGA CCAGGTCCCC TACATCGTGA CCTGGGAAGC CTTGGCTTTT
1501 GACCCCTCTC CCTGGGTCAA GCCCTTTGTA CACCCTAAGC CTCCGCTCC TCTTCTCCA
1561 TCCGCCCCGT CTCTCCCCCT TGAACCTCCT CGTTCGACCC CGCCTCGATC CTCTCTTAT
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1681 GGCACCCCG CCCCTTGTAA ACTTCCCTGA CCCTGACATG ACAAGAGTTA CTAACAGCCC
1741 CTCTCTCCAA GCTCACTTAC AGGCTCTCTA CTAGTCCAG CACGAAGTCT GGAGACCTCT
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1921 TTACACAGTC CTGCTGACCA CCCCACCCGC CCTCAAAGTA GACGGCATCG CAGCTTGGAT
1981 ACACGCCGCC CACGTGAAGG CTGCCGACCC CGGGGGTGGG CCATCCTCTA GACTGCCGGA
2041 TCTCGAGCCA CCATGACCGA GTACAAGCCC ACGGTGCGCC TCGCCACCCG CGACGACGTC
2101 CCCCAGGCCG TACGCACCCT CGCCGCCGCG TTCGCCGACT ACCCCGCCAC GCGCCACACC
2161 GTCGACCCCG ACCGCCACAT CGAGCGGTGC ACCGAGCTGC AAGAACTCTT CTTACGCGC
2221 GTCGGGCTCG ACATCGGCAA GGTGTGGGTC GCGGACGACG GCGCCGCGGT GCGGTCTGG
2281 ACCACGCCGG AGAGCGTCGA AGCGGGGGCG GTGTTGCGCG AGATCGGTCC GCGCATGGCC
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3121 GGCAACATCC TGGGGCACA GCTGGAGTAC AACTACAACA GCCACAACGT CTATATCATG
3181 GCCGACAAGC AGAAGAACGG CATCAAGGTG AACTTCAAGA TCCGCCACAA CATCGAGGAC
3241 GGCAGCGTGC AGCTCGCCGA CCACTACCAG CAGAACACCC CCATCGGCGA CGGCCCCGTG
3301 CTGCTGCCCG ACAACCACTA CCTGAGCACC CAGTCCGCC TGAGCAAAGA CCCCACGAG
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3481 CTAAACTTGG CGGGAGACGT CGAGTCCAAC CCTGGGCCA TGGAGACGCG CAAAACATA
3541 AAGAAAGGCC CGGCGCCATT CTATCCGCTG GAAGATGGAA CCGCTGGAGA GCAACTGCAT
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3661 GAGGTGGACA TCACTTACGC TGAGTACTTC GAAATGTCCG TTCGGTTGGC AGAAGCTATG
3721 AAACGATATG GGCTGAATAC AAATCACAGA ATCGTCGTAT GCAGTGAAAA CTCTCTTCAA

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FIGURE 8

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4081 AGGGACAAGA CAATTGCACT GATCATGAAC TCCTCTGGAT CTA CTGGTCT GCCTAAAGGT
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4201 GGCAATCAAA TCATTCCGGA TACTGCGATT TTAAGTGTG TTCCATTCCA TCACGGTTTT
4261 GGAATGTTTA CTACACTCGG ATATTTGATA TGTGGATTTT GAGTCGTCTT AATGTATAGA
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4441 AATTTACACG AAATTGCTTC TGGTGGCGCT CCCCTCTCTA AGGAAGTCGG GGAAGCGGTT
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4561 GCTATTCTGA TTACACCCGA GGGGGATGAT AAACCGGGCG CGGTGCGTAA AGTTGTTCCA
4621 TTTTTTGAAG CGAAGGTTGT GGATCTGGAT ACCGGGAAAA CGCTGGGCGT TAATCAAAGA
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4801 GAAGACGAAC ACTTCTTCAT CGTTGACCGC CTGAAGTCTC TGATTAAGTA CAAAGGCTAT
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4921 GGTGTCGCGA GTCTTCCCGA CGATGACGCC GGTGAACTTC CCGCCGCCGT TGTGTTTTG
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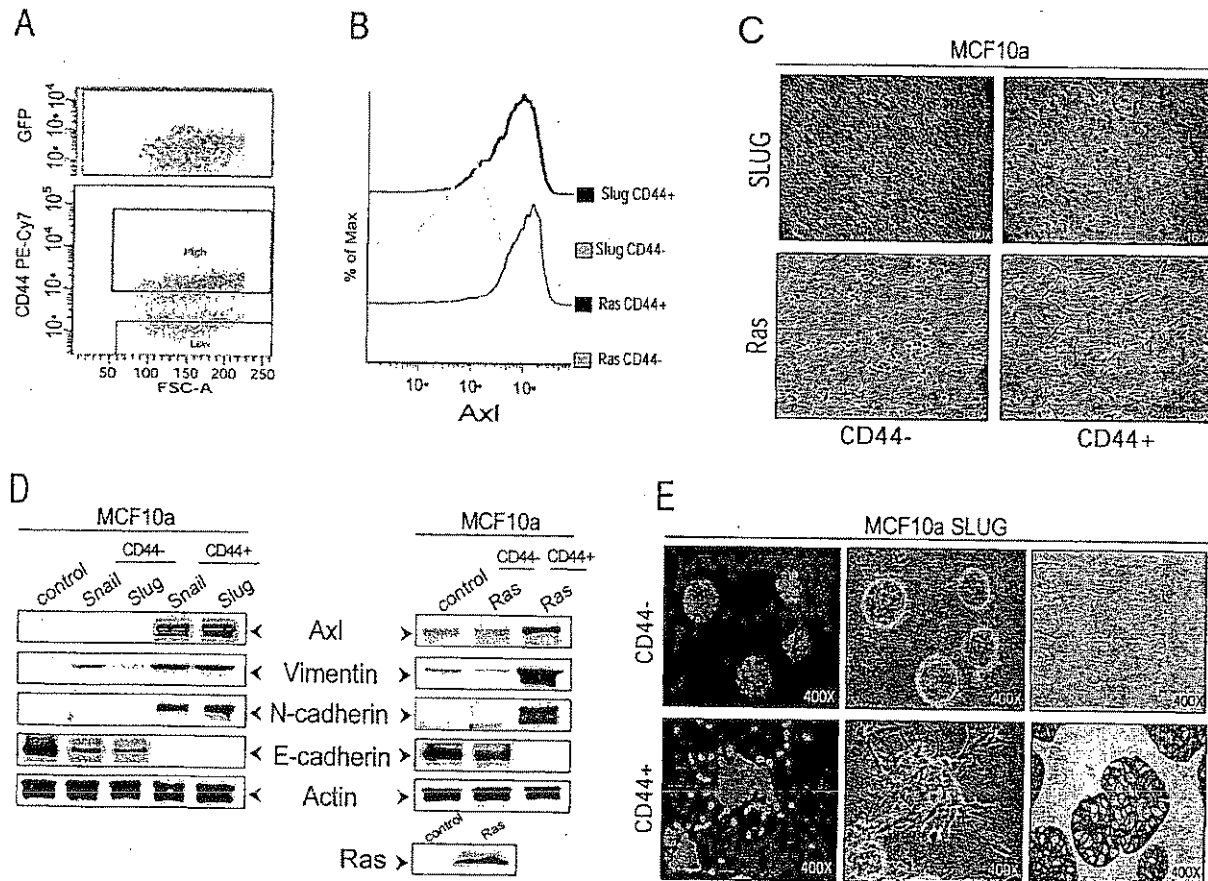
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5581 CCTGTGCGCT TATTTGAACT AACCAATCAG TTCGCTTCTC GCTTCTGTTC GCGCGCTTCT
5641 GCTCCCCGAG CTCAATAAAA GAGCCCACAA CCCCTCACTC GGGGCGCCAG TCCTCCGATT
5701 GACTGAGTCG CCCGGGTACC CGTGTATCCA ATAAACCCTC TTGCAGTTGC ATCCGACTTG
5761 TGGTCTCGCT GTTCCTTGGG AGGGTCTCCT CTGAGTGATT GACTACCCGT GACTACCCGT
5821 CTTTCATTTT CGACTTGTGG TCTCGTGCC TTGGGAGGGT CTCCTCTGAG TGATTGACTA
5881 CCCGTGAGCG GGGGTCTTCA CATGCAGCAT GTATCAAAAT TAATTTGGTT TTTTTCTTA
5941 AGTATTTACA TTAAATGGCC ATAGTTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC
6001 GGTTTGCGTA TTGGCGCTCT TCCGCTTCTT CGCTCACTGA CTCGCTGCGC TCGGTCGTTT
6061 GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAAATCAG
6121 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA
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6241 GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATAACAG GCGTTTCCCC
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6361 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT
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6481 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC
6541 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG
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7081 CCA GTGCTG AATGATACCG CGAGACCCAC GCTCACC GGC TCCAGATTTA TCAGCAATAA
7141 ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCTGCG AACTTTATCC GCCTCCATCC
7201 AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCCGA

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FIGURE 8 (cont)

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7261 ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT
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7381 CGGTTAGCTC CTTCCGGTCCT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA GTGTTATCAC
7441 TCATGGTTAT GGCAGCACTG CATAATTCTC TTA CTGTCAT GCCATCCGTA AGATGCTTTT
7501 CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT
7561 GCTCTTGCCC GGCCTCAACA CGGGATAATA CCGCGCCACA TAGCAGAACT TTA AAAGTGC
7621 TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT
7681 CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTTT ACTTTCACCA
7741 GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA
7801 CACGAAAATG TTGAATACTC ATACTCTTCC TTTTCAATA TTATTGAAGC ATTTATCAGG
7861 GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG
7921 TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CAGCTTTGCT CTTAGGAGTT TCCTAATACA
7981 TCCCAAACCTC AAATATATAA AGCATTTGAC TTGTTCTATG C
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FIGURE 8 (cont)



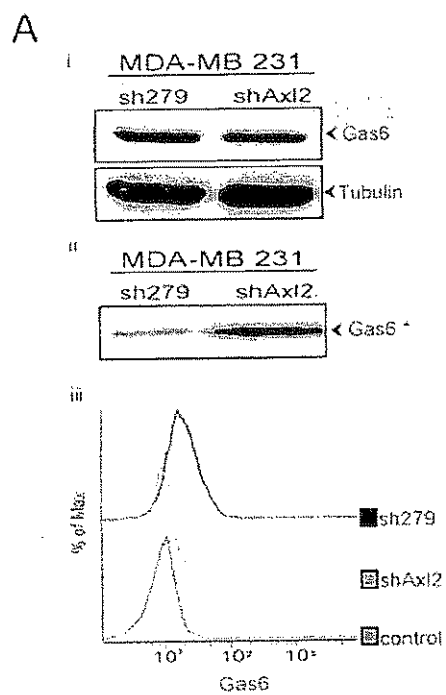


FIGURE 10

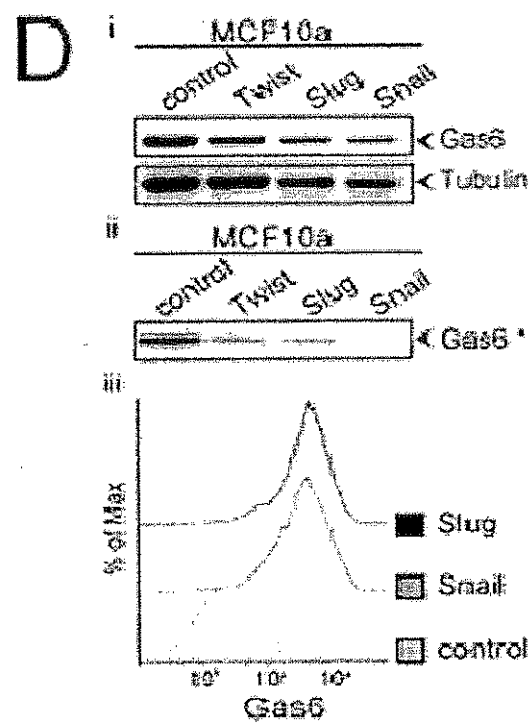


FIGURE 11