Supplemental Table S1. PCR TOPO cloning Primer Pairs Sequences and Amplicon Sizes.

Supplemental Table 1

PCR TOPO Cloning Primer Pair Sequences and Amplicon Sizes

Gene	Sequence	Exon	Amplicon Size
KRAS	Forward-GTGAGTTTGTATTAAAAGGTACTGG	2	265 bp
	Reverse-GGTCCTGCACCAGTAATATGC		
KRAS	Forward-CCAGACTGTGTTTCTCCCTTC	3	286 bp
	Reverse-TGCATGGCATTAGCAAAGAC		
PIK3CA	Forward-CTGTGAATCCAGAGGGGAAA	9	269 bp
	Reverse-ACATGCTGAGATCAGCCAAA		
PIK3CA	Forward-CATTTGCTCCAAACTGACCA	20	389 bp
	Reverse-GGTCTTTGCCTGCTGAGAGT		
TP53	Forward-CACTTGTGCCCTGACTTTCA	5	267 bp
	Reverse-AACCAGCCCTGTCGTCTCT		
TP53	Forward-CTGCTCAGATAGCGATGGTG	6	251 bp
	Reverse-CTTAACCCCTCCTCCCAGAG		
TP53	Forward-CTTGGGCCTGTGTTATCTCC	7	199 bp
	Reverse-GGGTCAGAGGCAAGCAGA		
TP53	Forward-GGGAGTAGATGGAGCCTGGT	8	274 bp
	Reverse-TAACTGCACCCTTGGTCTCC		

Supplemental Table S2. Quantitative Real-Time PCR Primer Pairs. Amplicon sizes are within the range from 80 to 250 bp.

Supplemental Table 2
Quantitative Real-Time PCR Primer Pairs

Gene	Sequence
ALDH1A1	CTCAAGGCCCTCAGATTGAC
	GTTTGGCCCCTTCTTTCTTC
OCT4	AGTGAGAGGCAACCTGGAGA
	ACACTCGGACCACATCCTTC
CD44	GGCGCAGATCGATTTGAATA
	GAAAGCCTTGCAGAGGTCAG
CD133	AATTCACCAGCAACGAGTCC
	TCCAACAATCCATTCCCTGT
CD117	AAGTGGATGGCACCTGAAAG
	AGGGGCTGCTTCCTAAAGAG
CXCR4	TTGTGCCCTTAGCCCACTAC
	CACTTCCAATTCAGCAAGCA
NANOG	CAGAAGGCCTCAGCACCTAC
	ACTGGATGTTCTGGGTCTGG
RPL18	GGATGATCCGGAAGATGAAG
	CCGCACATCATCAGTTATGG

Supplemental Table S3. Summary of Identified Mutations.

Supplemental Table 3

Summary of Identified Mutations

p53		Exon 5						Exon 6		Exon 7				Exon 8	
Control	CDS									703 c.703A>C AAC>CAC N235H Substitution					
	Codon														
100 mM	CDS	384 c.384T>C CCT>CCC	387 c.387C>T GCC>GCT	386 c.386C>T GCC>GTC	470 c.470T>G GTC>GGC			590 c.590T>C GTG>GCG							
	Codon	P128P **Transition**	A129A **Transition**	A129V **Transition**	V157G **Transversion**			V197A **Transition**							
300 mM	CDS	384 c.384T>C CCT>CCC	388 c.388C>A CTC>ATC	427 c.427G>C GTG>CTG	436 c.436T>C TGG>CGG	488 c.488A>G TAC>TGC	537 c.537T>C CAT>CAC	658 c.658T>G TAT>GAT		703 c.703A>C AAC>CAC N235H					
	Codon	P128P **Transition**	L130I **Transversion**	V143L **Transversion**	W146R **Transition**	Y163C **Transition**	H179H **Transition**	Y220D **Transversion**		Substitution					
500 mM	CDS	384 c.384T>C CCT>CCC	386 c.386C>T GCC>GTC					658 c.658T>G TAT>GAT	688 c.688A>T ACC>AGC	703 c.703A>C AAC>CAC	710 c.710T>A ATG>AAG	746 c.746G>C AGG>ACG	751 c.751A>C ATC>ATA	911 c.911C>A ACC>AAC	914 c.914A>G AAA>AGA
	Codon	P128P **Transition**	A129V **Transition**					Y220D **Transversion**	T230S Substitution	N235H Substitution	M237K Substitution	R249T Substitution	I251I Substitution	T304N Substitution	K305R Substitution

Transition	10
Transversion	5
Substitution	9

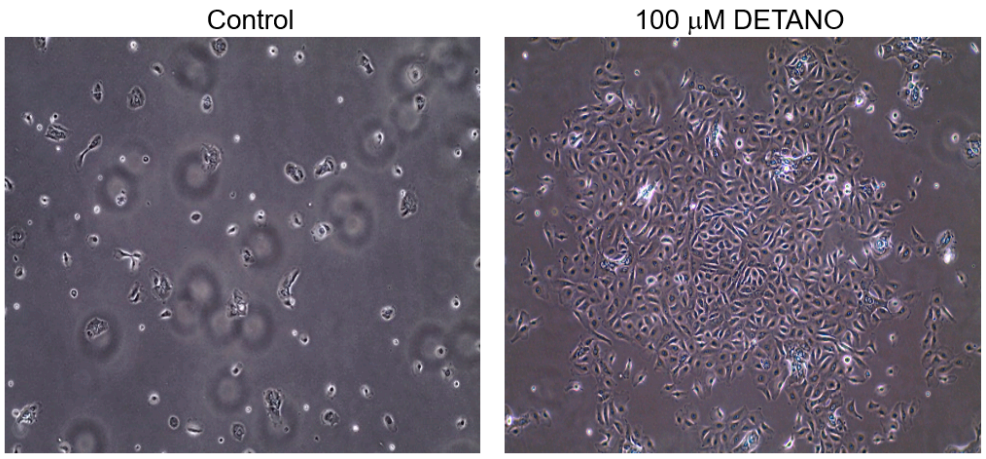
PIK3CA		Exon 9			Exon 20		
Control	CDS	1634 c.1634A>C GAG>GCG	1658 c.1658delG AGT>ACC	1659 c.1659T>C		3088 c.3088A>G ACT>GCT	
	Codon	E545A **Transversion**	S553T Substitution	**Transition**		T1030A **Transition**	
100 mM	CDS	1634 c.1634A>C GAG>GCG	1658 c.1658delG AGT>ACC	1659 c.1659T>C			
	Codon	E545A **Transversion**	S553T Substitution	**Transition**			
300 mM	CDS	1570 c.1570A>T AGG>TGG	1658 c.1658delG AGT>ACC	1659 c.1659T>C		3088 c.3088A>G ACT>GCT	3226 c.3226A>G
	Codon	R524W **Transversion**	S553T Substitution	**Transition**		T1030A **Transition**	**Transition**
500 mM	CDS	1623 c.1623T>C TCT>TCC	1634 c.1634A>C GAG>GCG	1658 c.1658delG AGT>ACC	1659 c.1659T>C	3224 c.3224A>G	
	Codon	S541S **Transition**	E545A **Transversion**	S553T Substitution	**Transition**	**Transition**	

Transition	9
Transversion	4
Substitution	4

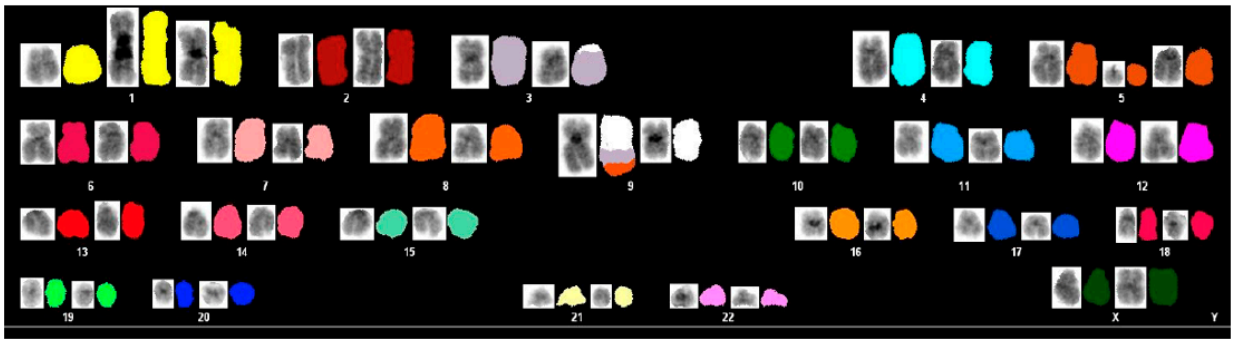
KRAS		Exon 1	Exon 2			
Control	CDS	89 c.89A>G GAC>GGC	144 c.144A>T GGA>GGT	209 c.209A>G CAG>CGG	234 c.234T>C TTT>TTC	284 c.284A>G CAT>CGT
	Codon	D30G **Transition**	G48G **Transversion**	E70R **Transition**	F78F **Transition**	H95R **Transition**
100 mM	CDS		183 c.183A>G CAA>CAG			
	Codon		Q61Q **Transition**			
300 mM	CDS	86 c.86T>C GTG>GCG	188 c.188A>G GAG>GGG			
	Codon	V29A **Transition**	E63G **Transition**			
500 mM	CDS		162 c.162T>C GAT>GAC	285 c.285T>C CAT>CAC		
	Codon		D54D **Transition**	H95H **Transition**		

Transition	9
Transversion	1
Substitution	0

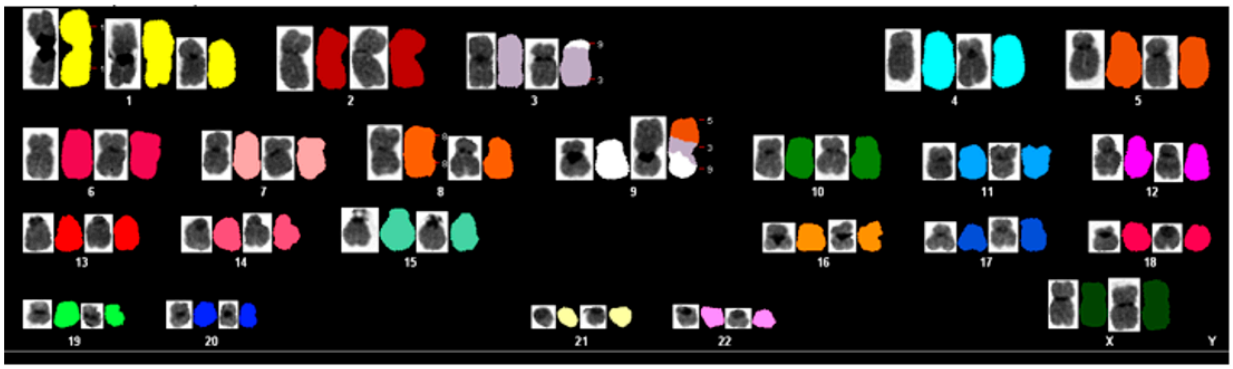
Supplementary Figure S1: Colony formation in SIT Media. Control and 100 μM DETANO treated cells were evaluated for growth in serum-free media supplemented with 5 ng/ml selenium, 5 g/ml insulin, and 5 g/ml transferrin (SIT). $1x10^5$ cells were plated in 60 mm dishes with SIT media and maintained for three weeks. When compared to control, MCF10A cells previously maintained in 100μM DETANO formed colonies in the SIT media.



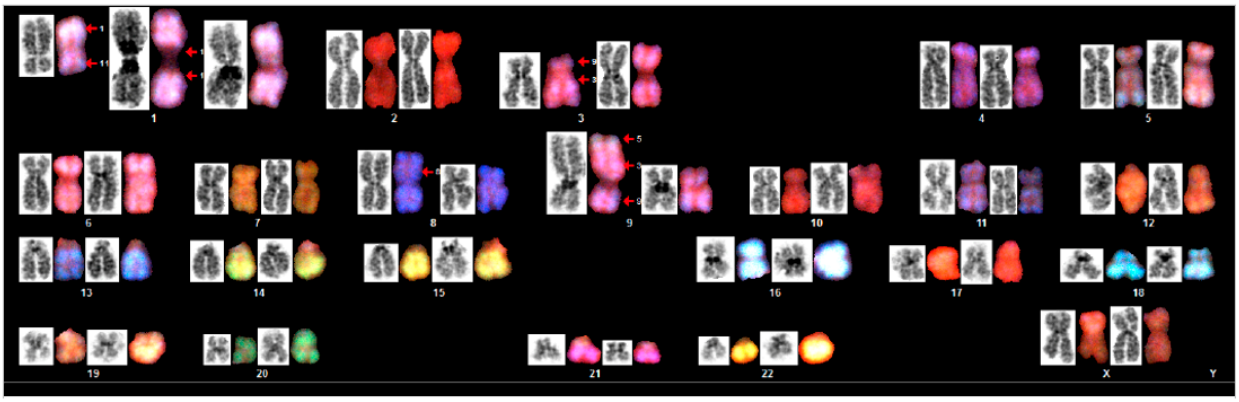
Supplementary Figure S2: Cytogenetic Analyses. Fig 4A. A dicentric Chr 1 composed by two Chr 1 long arm region 1 , band 1; a derivative Chr 1; a translocation between Chr 3 short arm region 1, band 3 and Chr 9 short arm region 2, band 2; an isochromosome 8 form by two Chr 8 long arm region 1, band 1; a translocation involved partial Chr 9 Chr 3 & Chr 5; a deletion of Chr 21; and a translocation between Chr X short arm region 2, band 2 and Chr 21 long arm region 2, band 1. Fig 4B. Chromosome 21 was showed here in green by whole chromosome painting. The Chr 21 appeared normal in this FISH assay. TIMP1 is stained in orange. An Aqua X Control probe for region Xp13.2 stain. Fig 4C. Spectrum karyotyping of Control, 100 or 1000 mM DETANO treated MCF10A cells. Control: 47, XX, del (1), +i (1q), del (3), add (8), der (9) t (5; 3; 9). 100 uM: 47, XX, dic(1;1)(q11;q11), +der(1),t(3;9)(p13;p22), der(8) i(8)(q11;q11), t(5;3;9). 1000 uM: 47, XX, dic(1;1)(q11;q11), +der(1), t(3;9)(p13;p22), i(8)(q11;q11), t(3;5;9).



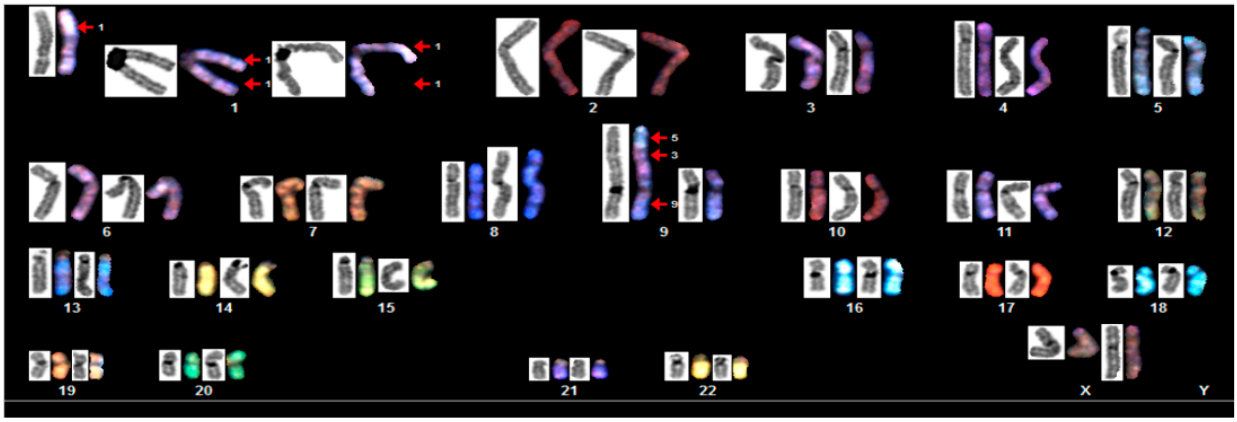
Control untreated; 47,XX, dic(1;1)(q11;q11),+der(1),-1,-3,t(3;9)(p13;22),-5,del(5),-8,i(8)(q11;q11),-9,t(9;3;5)



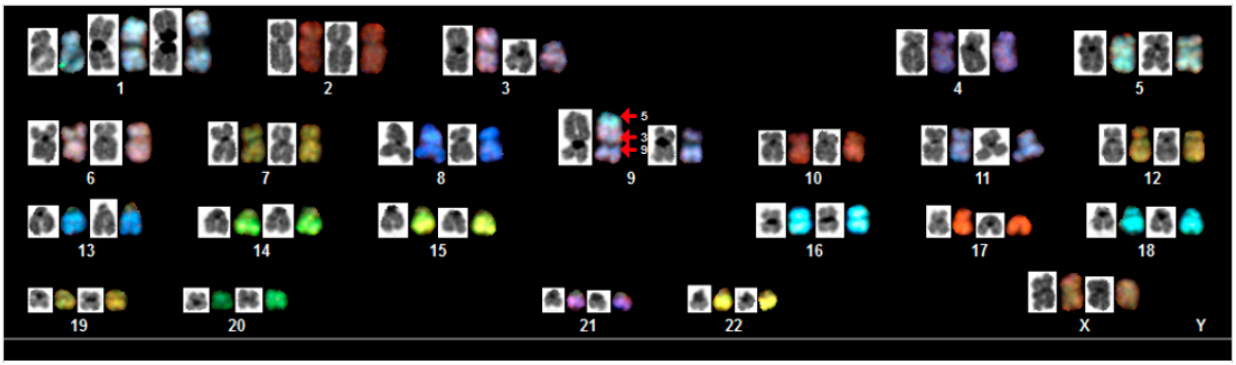
100 uM: 47, XX, dic(1;1)(q11;q11),+der(1),t(3;9)(p13;p22), der(8) i(8)(q11;q11), t(5;3;9)



2-1 100 uM: 47,XX, der(1) t(1;11),+dic(1q;1q),der(3)t(9;3),der(8),der(9)t(9;3;5)



2-2 100 uM: 47,XX, der(1),+(1q), dek(3),der(8),t(9:3:5)



2-3 100 uM: 47,XX, der(1),+dic(1q;1q),der(3)t(9;3),der(8),der(9)t(9:3:5)