Table W1. Viral and Control Cocktail Components.

Laboratory Designation	Addgene No. or Other ID	Hyperlink
Viral cocktail		
A	shBRCA1-308*	*Homo sapiens* breast cancer 1, early onset (BRCA1) … — Nucleotide result
C	shBRCA1-4590†	*Homo sapiens* breast cancer 1, early onset (BRCA1) … — Nucleotide result
S	1774	Addgene — pBABE-neo-hTERT plasmid data
T	9058	Addgene — pBABE-hygro p53 DD plasmid data
EE	9051	Addgene — pBABE puro H-Ras V12 plasmid data
GG	11129	Addgene — pbabe-cyclin D1 + CDK4R24C plasmid data
MM	18773	Addgene — MSCV Myc T58A puro plasmid data
PP	13970	Addgene — pBABE-puro SV40 LT plasmid data
AA	10668	Addgene — pBABE GFP plasmid data
Control cocktail		
AA	10668	Addgene — pBABE GFP plasmid data
G	pMMP-mir-gl2shRNA	
Q	pBabe-puro (empty vector)	

*Sequence: 5′-TGCTGTTGACAGTGAGCG CCCACAAAGTGTGACCACATAT TAGTGAAGCCACAGATGTA ATATGTGGTCACACTTTGTGGA TGCCTACTGCCTCGGA.
†Sequence: 5′-TGCTGTTGACAGTGAGCG CGGAGCTGGACACCTACCTGAT TAGTGAAGCCACAGATGTA ATCAGGTAGGTGTCCAGCTCCT TGCCTACTGCCTCGGA.

Table W2. Antibody Information for Immunohistochemistry.

Target	Vendor	Catalog No.	Dilution
p53	Dako	M7001	1:10
Cytokeratin 7	Dako	M7018	1:800
Cytokeratin 20	Dako	M7019	1:100
WT1	Thermo Scientific	PA1-38864	1:2
PAX8	ProteinTech Group	10336-1-AP	1:200
HE4 (WFDC2)	Abcam	ab24480	1:40

Dako, Carpinteria, CA; ProteinTech, Chicago, IL; Abcam, Cambridge, MA.

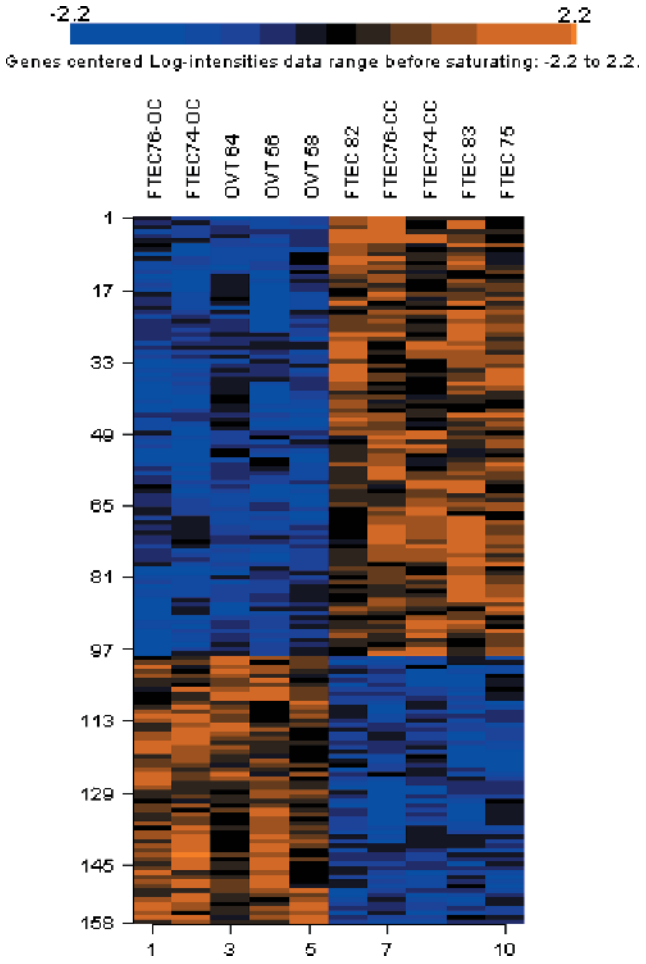

Figure W1. Hierarchical clustering of malignant signature. A total of 158 genes differentiating FTEC-OC and primary serous ovarian cancers from FTEC-CC and untreated normal primary FTEC were identified using *F* test ($P < .005$) and subjected to hierarchical clustering. Expression levels of each gene are presented in Table W3.

Gene No.	ProbeSet (	Symbol	Name	EntrezID
1	224519_at	LOC10013	hypothetica	100132167
2	201309_x_	C5orf13	chromoson	9315
3	239487_at	FAM98A	family with	25940
4	226997_at	ADAMTS1:	ADAM met	81792
5	205533_s_	CDH6	cadherin 6,	1004
6	213248_at	LOC73010	hypothetica	730101
7	1564002_a	AKD1	adenylate k	221264
8	204345_at	COL16A1	collagen, ty	1307
9	224818_at	SORT1	sortilin 1	6272
10	204966_at	BAI2	brain-speci	576
11	218963_s_	KRT23	keratin 23 (	25984
12	227236_at	TSPAN2	tetraspanin	10100
13	210943_s_	LYST	lysosomal t	1130
14	219468_s_	CUEDC1	CUE doma	404093
15	236254_at	VPS13B	vacuolar pr	157680
16	203159_at	GLS	glutaminas	2744
17	220580_at	BICC1	bicaudal C	80114
18	1557289_s	GTF2IRD2	GTF2I repe	84163
19	213349_at	TMCC1	transmemb	23023
20	209198_s_	SYT11	synaptotag	23208
21	226550_at	NA	NA	NA
22	1556051_a	BICD1	bicaudal D	636
23	215785_s_	CYFIP2	cytoplasmi	26999
24	211066_x_	NA	NA	NA
25	205717_x_	NA	NA	NA
26	209079_x_	NA	NA	NA
27	1553300_a	DGKH	diacylglyce	160851
28	1570393_a	EML5	echinodern	161436
29	216869_at	PDE1C	phosphodie	5137
30	236344_at	PDE1C	phosphodie	5137
31	221950_at	EMX2	empty spira	2018

Figure W1. (*continued*).

32	239218_at	NA	NA	NA
33	1555673_a	LOC73075	keratin ass	730755
34	202117_at	ARHGAP1	Rho GTPa	392
35	236129_at	GALNT5	UDP-N-ace	11227
36	235489_at	RHOJ	ras homolo	57381
37	243481_at	RHOJ	ras homolo	57381
38	209631_s_	GPR37	G protein-c	2861
39	235369_at	C14orf28	chromoson	122525
40	1555575_a	KDELR1	KDEL (Lys	10945
41	46142_at	LMF1	lipase matu	64788
42	202952_s_	ADAM12	ADAM met	8038
43	204797_s_	EML1	echinodern	2009
44	202439_s_	IDS	iduronate 2	3423
45	215836_s_	NA	NA	NA
46	211966_at	COL4A2	collagen, ty	1284
47	223095_at	MARVELD	MARVEL d	83742
48	228141_at	GPX8	glutathione	493869
49	223392_s_	TSHZ3	teashirt zin	57616
50	242873_at	NA	NA	NA
51	225615_at	IFFO2	intermediat	126917
52	37408_at	MRC2	mannose r	9902
53	219582_at	OGFRL1	opioid grow	79627
54	239817_at	NA	NA	NA
55	201283_s_	TRAK1	trafficking p	22906
56	229557_at	MEG3	maternally	55384
57	206806_at	DGKI	diacylglyce	9162
58	214803_at	NA	NA	NA
59	230669_at	RASA2	RAS p21 p	5922
60	228885_at	NA	NA	NA
61	202688_at	TNFSF10	tumor necr	8743
62	203662_s_	TMOD1	tropomodu	7111
63	226069_at	PRICKLE1	prickle hom	144165
64	226065_at	PRICKLE1	prickle hom	144165
65	230708_at	PRICKLE1	prickle hom	144165
66	222020_s_	NTM	neurotrimin	50863
67	227566_at	NTM	neurotrimin	50863
68	213273_at	ODZ4	odz, odd O	26011

Figure W1. (*continued*).

69	231382_at	FGF18	fibroblast g	8817
70	206987_x_	FGF18	fibroblast g	8817
71	211029_x_	FGF18	fibroblast g	8817
72	222281_s_	NA	NA	NA
73	232720_at	LINGO2	leucine rich	158038
74	227750_at	KALRN	kalirin, Rho	8997
75	202687_s_	TNFSF10	tumor necr	8743
76	203895_at	PLCB4	phospholip	5332
77	203896_s_	PLCB4	phospholip	5332
78	214329_x_	TNFSF10	tumor necr	8743
79	203157_s_	GLS	glutaminas	2744
80	228101_at	APBA1	amyloid be	320
81	225807_at	JUB	jub, ajuba h	84962
82	238827_at	NA	NA	NA
83	236038_at	NA	NA	NA
84	209453_at	SLC9A1	solute carri	6548
85	230119_at	NA	NA	NA
86	244708_at	FLJ33996	hypothetica	283401
87	236364_at	NA	NA	NA
88	1555028_a	BRD3	bromodom	8019
89	228728_at	C7orf58	chromoson	79974
90	219610_at	RGNEF	190 kDa gu	64283
91	227657_at	RNF150	ring finger p	57484
92	239582_at	PML	promyelocy	5371
93	1558622_a	ZNF548	zinc finger	147694
94	238417_at	PGM2L1	phosphoglu	283209
95	1598_g_at	GAS6	growth arre	2621
96	208712_at	CCND1	cyclin D1	595
97	210642_at	CCIN	calicin	881
98	243795_s_	LOC44090	hypothetica	440900
99	206577_at	VIP	vasoactive	7432
100	234977_at	ZADH2	zinc bindin	284273
101	1555167_s	NAMPT	nicotinamic	10135
102	210854_x_	SLC6A8	solute carri	6535
103	1566518_a	NA	NA	NA
104	216857_at	NA	NA	NA
105	227757_at	CUL4A	cullin 4A	8451

Figure W1. (*continued*).

106	225942_at	NLN	neurolysin	57486
107	1564315_a	C8orf49	chromoson	606553
108	203036_s_	MTSS1	metastasis	9788
109	212849_at	AXIN1	axin 1	8312
110	239042_at	TSR1	TSR1, 20S	55720
111	212434_at	GRPEL1	GrpE-like 1	80273
112	212656_at	TSFM	Ts translati	10102
113	216411_s_	NA	NA	NA
114	1555804_a	YSK4	YSK4 Sps1	80122
115	210215_at	TFR2	transferrin	7036
116	207463_x_	PRSS3	protease, s	5646
117	213421_x_	PRSS3	protease, s	5646
118	225078_at	EMP2	epithelial m	2013
119	213226_at	CCNA2	cyclin A2	890
120	221957_at	PDK3	pyruvate de	5165
121	211561_x_	MAPK14	mitogen-ac	1432
122	216014_s_	NA	NA	NA
123	217973_at	DCXR	dicarbonyl/	51181
124	1553031_a	GPR115	G protein-c	221393
125	213449_at	POP1	processing	10940
126	207558_s_	PITX2	paired-like	5308
127	225862_at	SLC25A26	solute carri	115286
128	236146_at	SYNCRIP	synaptotag	10492
129	206947_at	B3GALT5	UDP-Gal:b	10317
130	223292_s_	MRPS15	mitochondr	64960
131	231182_at	WIPF1	WAS/WAS	7456
132	1569588_x	PIK3C2A	phosphoinc	5286
133	217558_at	CYP2C9	cytochrome	1559
134	241606_s_	TRUB1	TruB pseuc	142940
135	203759_at	ST3GAL4	ST3 beta-g	6484
136	231099_at	FKBP15	FK506 binc	23307
137	230825_at	NA	NA	NA
138	213309_at	PLCL2	phospholip	23228
139	1555553_a	SLC22A7	solute carri	10864
140	235412_at	ARHGEF7	Rho guanir	8874
141	205449_at	SAC3D1	SAC3 dom	29901
142	218443_s_	DAZAP1	DAZ assoc	26528
143	243526_at	WDR86	WD repeat	349136
144	243033_at	TWF1	twinfilin, ac	5756
145	1556558_s	FLJ36665	hypothetica	285266
146	204798_at	MYB	v-myb mye	4602
147	214664_at	PAICS	phosphorib	10606
148	216298_at	NA	NA	NA
149	233670_at	NA	NA	NA
150	240863_at	CYP19A1	cytochrome	1588
151	229446_at	NA	NA	NA
152	214540_at	HIST1H2B	histone clu	8348
153	227925_at	FLJ39051	hypothetica	399972
154	1554314_a	C6orf141	chromoson	135398
155	1560460_a	NA	NA	NA
156	244523_at	MMD	monocyte t	23531
157	218590_at	C10orf2	chromoson	56652
158	220616_at	ZNF384	zinc finger	171017

Figure W1. (*continued*).

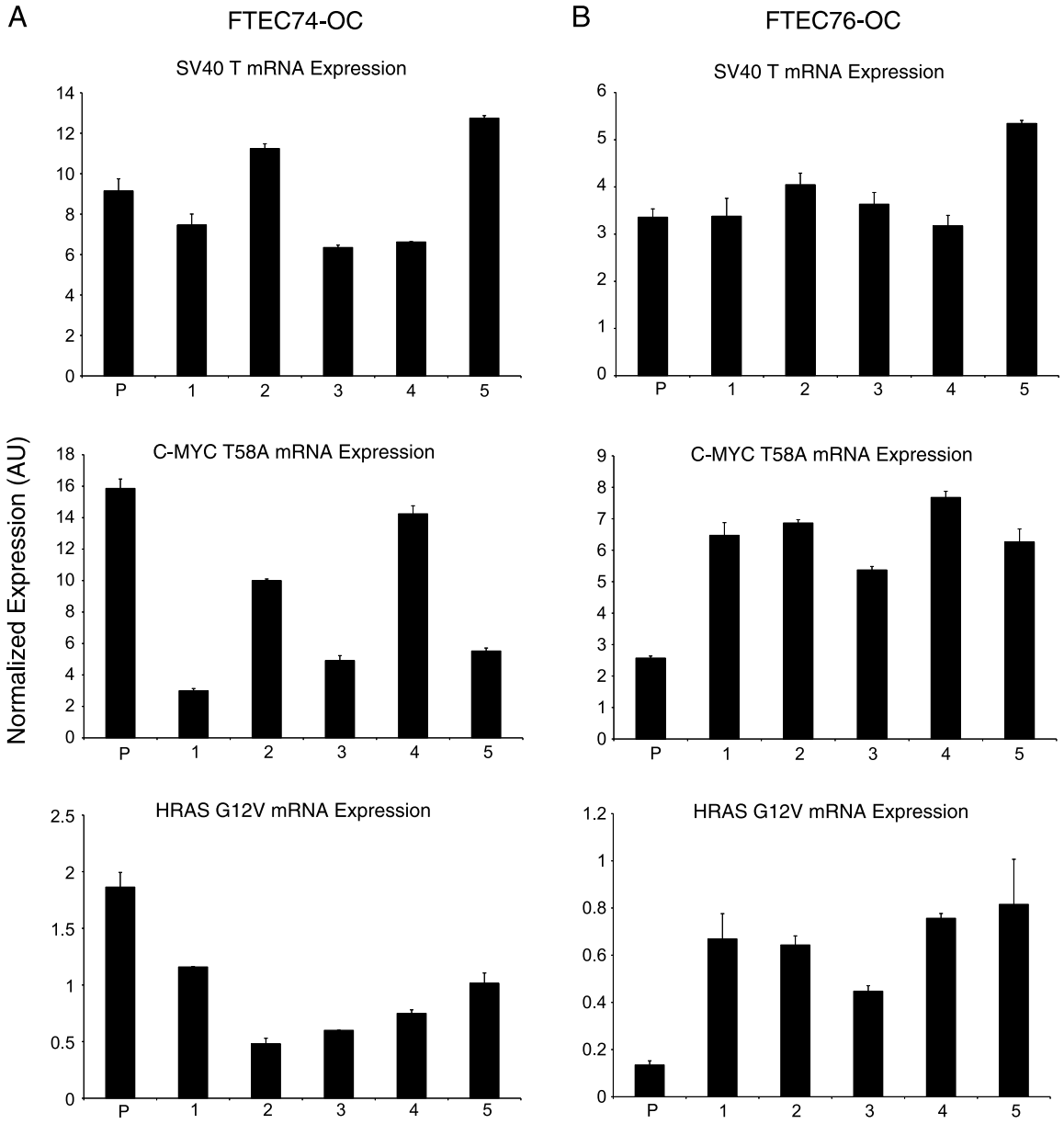

Figure W2. Clonal analysis of transformed FTEC lines. Expression levels of SV40 T, HRAS G12V, and C-MYC T58A in the parental (P) and five clonal sublines (numbered 1–5) of FTEC74-OC (A) and FTEC76-OC (B) using real-time RT-PCR. Error bars represent SD of replicates.