

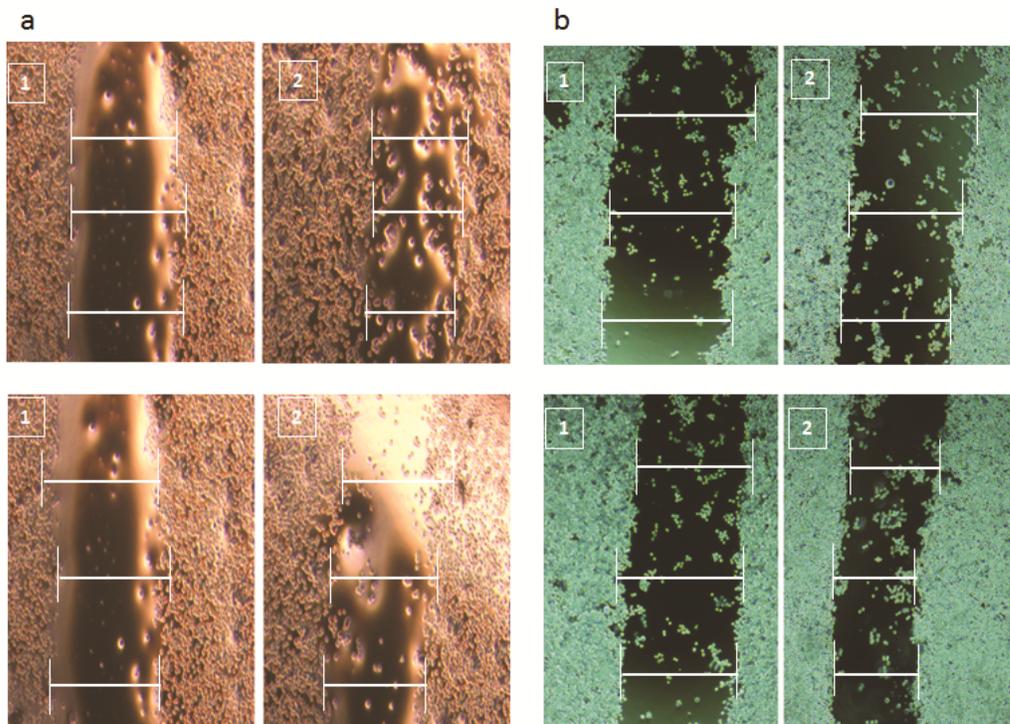
Supplementary Table 1

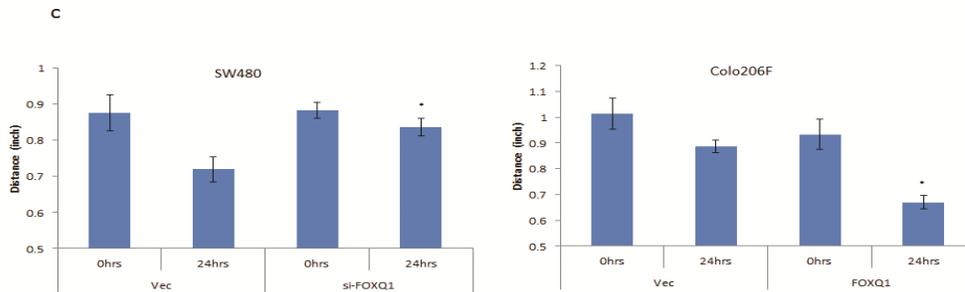
Gene symbol	Gene name	Fold change (T/N)
ASCL2	Achaete-scute complex-like 2 (Drosophila)	8
TGFB1	Transforming growth factor, beta-induced, 68KDa	8
TIMP1	TIMP metalloproteinase inhibitor 1	8
BCAP29	B-cell receptor-associated protein 29	7
GLIPR2	GLI pathogenesis-related 2	7
HNMT	Histamine <i>N</i> -methyltransferase	7
KIAA1199	Hypothetical protein IR215535	7
C9orf24	Chromosome 9 open reading frame 24	7
ADHFE1	Alcohol dehydrogenase, iron containing, 1	6
CA4	Carbonic anhydrase IV	6
CDH3	Cadherin 3, type 1, P-cadherin (placental)	6
HKDC1	Hexokinase domain containing 1	6
MAMDC2	MAM domain containing 2	6
TEAD4	TEA domain family member 4	6
TRIB3	Tribbles homolog 3 (Drosophila)	6
ABI3BP	ABI gene family, member 3 (NESH) binding protein	5
ETV4	ETS Variant gene 4 (e1A enhancer binding protein , E1AF)	5
GPT2	Glutamic pyruvate transaminase (alanine aminotransferase) 2	5
KLHL35	Kelch-like 35 (Drosophila)	5
PDK4	Pyruvate dehydrogenase kinase, isozyme 4	5
PHLDA1	Pleckstrin homology-like domain, family A, member 1	5
C2	Complement component 2	4
CLDN1	Claudin 1	4
CXCL16	Chemokine (C-X-C motif) ligand 16	4
HIG2	Hypoxia-inducible protein-2	4
IFITM1	Interferon induced transmembrane protein 1 (9-27)	4
PRPH	Peripherin	4
SMOX	Spermine oxidase	4
FOXQ1	Forkhead box q 1	3
ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	-4
PDE7B	Phosphodiesterase 7B	-4
PMEPA1	Transmembrane, prostate androgen induced RNA	-4
PPARGC1A	Peroxisome proliferative activated receptor, gamma, coactivator 1, alpha	-4
SLCO4A1	Solute carrier organic anion transporter family, member 4A1	-4
TESC	Tescalcin	-4
KRT17	Keratin 17	-5
MYH11	Myosin, heavy polypeptide 11, smooth muscle	-5
NOS3	Nitric oxide synthase 3 (endothelial cell)	-5
SCD	Stearoyl-coA desaturase (delta-9-desaturase)	-5
ADAMTS1	ADAM metalloproteinase with thrombospondin type 1, motif 1	-6
CKB	Creatine kinase, brain	-6
LPAR1	Lysophosphatidic acid receptor 1	-6
SNTB1	Syntrophin, beta 1 (dystrophin-associated protein A1, 59KDa, basic component 1)	-6
GSTM3	Glutathione S-transferase M3 (brain)	-8

Supplementary Table 1:

Common gene signature identified from a validated microarray analysis of whole and laser-capture microdissected colorectal cancer tissues in which epithelial, stromal and whole-tissue compartments were compared alongside each other. This gene signature contains a rich EMT undertone of several molecules already implicated in the process, as well as some novel molecules. Fold changes represent the expression in tumor compartments in comparison to the normal compartmentalized equivalents. The microarray data have already been deposited in NCBI's Gene Expression Omnibus and are accessible via the GEO Series accession number GSE31279. Details of the analysis are provided in our recent publication, Abba et. al; 2012).

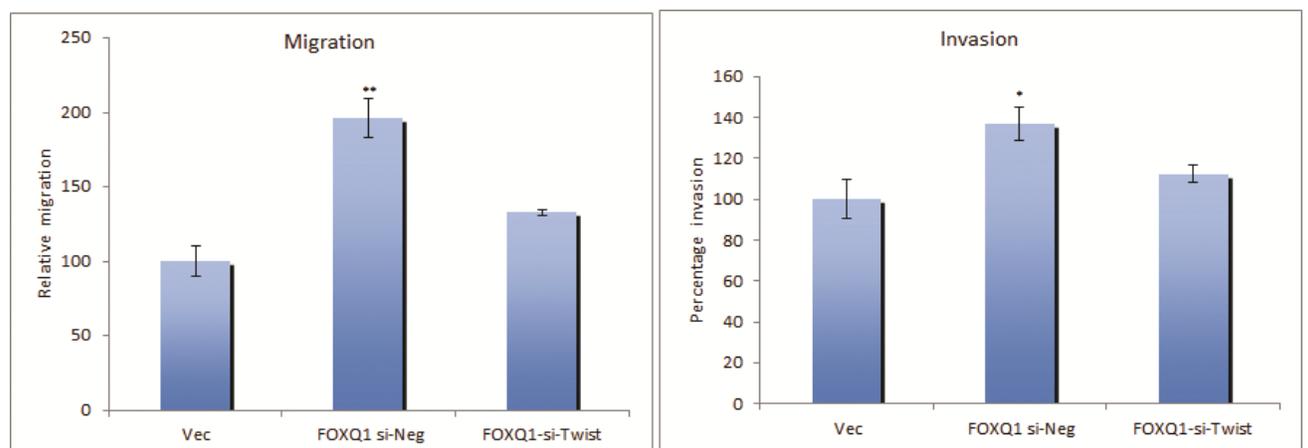
Supplementary Figure 1





Supplementary Figure 1: Wound healing assay in a) SW40 and b) Colo206f cell lines. In (a) the upper panel represents SW480 cells treated with negative control siRNA and the lower panel cells treated with si-RNA against FOXQ1; In (b) the upper panel represents stable EGFP expressing Colo206F cells and the lower panel FOXQ1-EGFP cells as described in the materials and methods section. Images were acquired on an Olympus CKX-41 microscope at 40X magnification. Migration was calculated by measuring wound closure at 24hrs and taking the average of 3 measurements. In all cases (1) is the initial scratch and (2), the scratch at 24hrs. The measured distances are graphically represented in (c). The results mirror that obtained with the Boyden-chamber assay.

Supplementary Figure 2



Supplementary Figure 2: Evaluation of Twist 1 knockdown on migration and invasion in stable FOXQ1 over-expressing Colo206f cell lines. A significant reduction in both migration and invasion in the Twist1 knockdown cell lines was observed as compared to the FOXQ1 stably expressing cells. Still, this knockdown did not completely eliminate the increase in migration and invasion associated with FOXQ1 overexpression (as compared to the vector group).