Figure S1. *ETV1* mRNA levels are significantly associated with reduced survival at (A) 1 and 3 years after colorectal cancer diagnosis and also associated with (B) increased disease stage; microarray data were analyzed using the Oncomine database. Similar, *JMJD2A* mRNA levels and their association with (C) survival and (D) disease stage. All data were derived from microarray experiments published by in the study by Smith *et al* (1). JMJD, Jumonji C domain-containing protein.

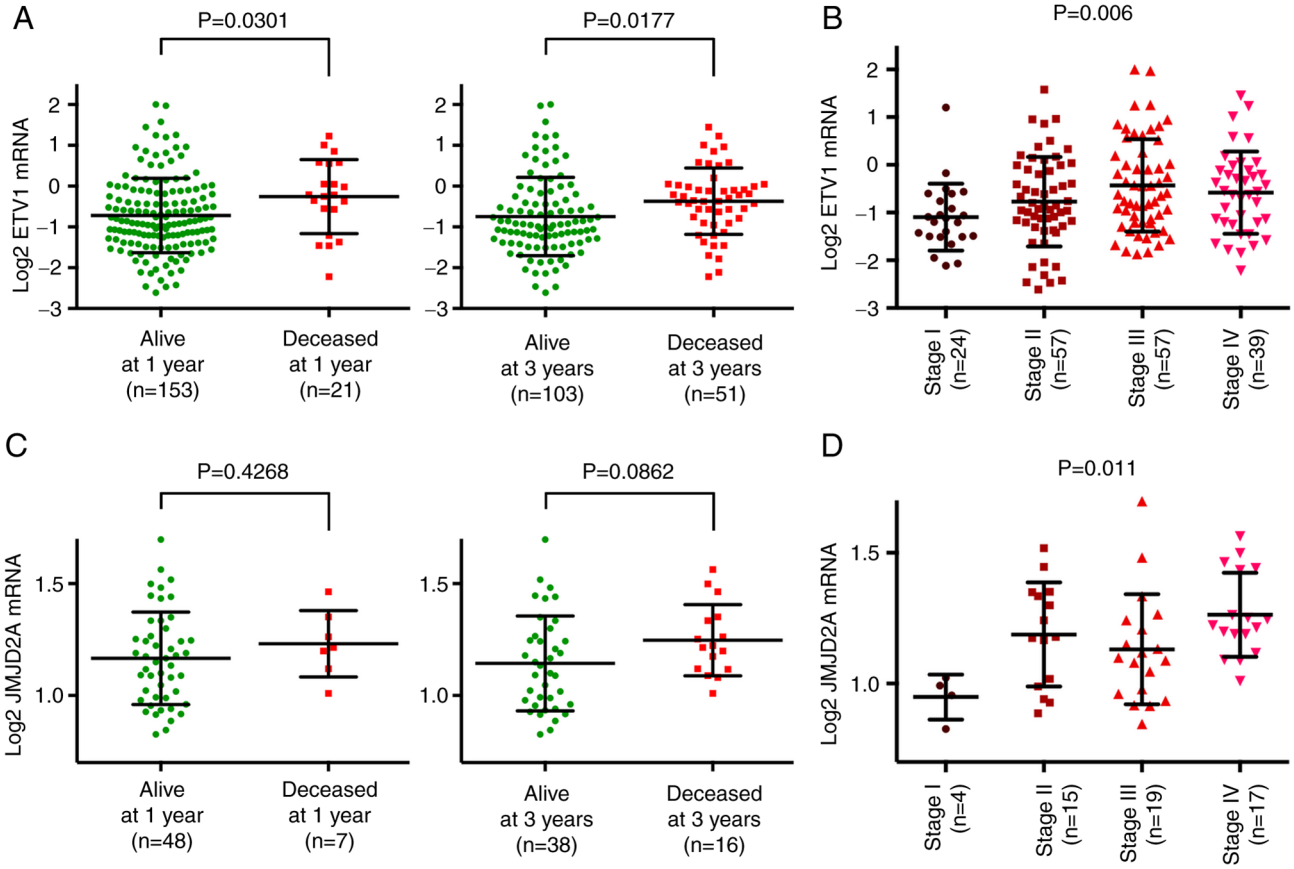

Figure S2. (A) Comparable ectopic expression of JMJD1A and JMJD2A in HCT116 cells as determined by western blotting. Further, ectopic ETV1 expression was unaffected by JMJD1A or JMJD2A co-expression. Asterisk indicates an unspecific band. (B) Activation of the *MMP1* gene promoter by ETV1, JMJD1A and JMJD2A in LNCaP prostate cancer cells. Cells were grown on poly-*L*-lysine coated 6-wells and transfected with 1 μg *MMP1* luciferase reporter plasmid, 1 μg pBluescript KS^{+}, 10 ng ETV1 expression vector or empty vector pEV3S, and 100 ng JMJD expression vector or empty vector pEV3S utilizing 6 μg polyethylenimine. Catalytically inactive JMJD proteins (H1120A/D1122G in case of JMJD1A and H188A in case of JMJD2A) are indicated by the suffix 'mut'. ANOVA (Tukey's multiple comparisons test; n=3). NS, not significant; ***P<0.001; ****P<0.0001. JMJD, Jumonji C domain-containing protein.

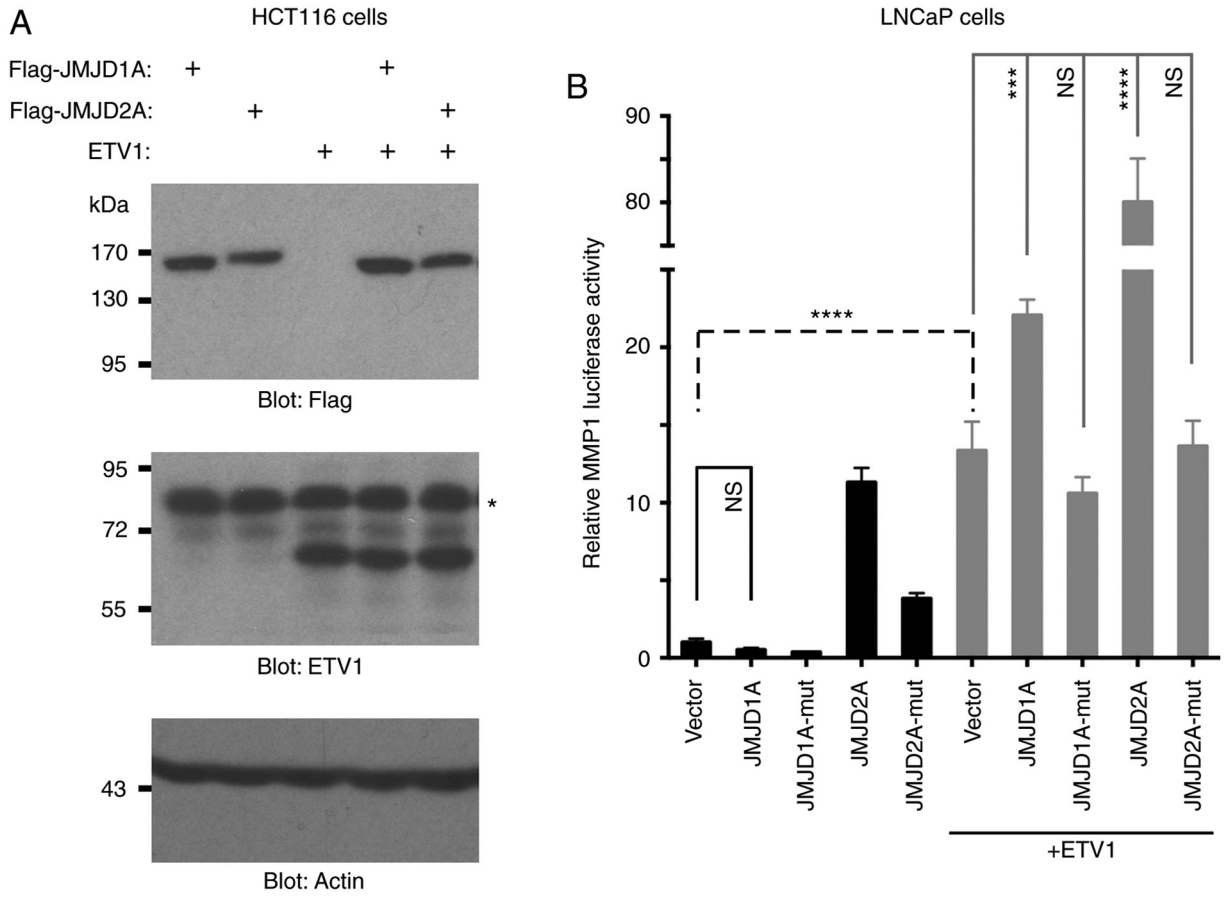

Figure S3. *FOXQ1* and *TBX6* mRNA levels in colorectal cancer. (A) Comparison of normal colorectal tissue to various cancerous samples with regard to *FOXQ1* mRNA levels. Microarray data were derived from the study by Kaiser *et al* (2). ANOVA (Dunnett's multiple comparisons test); ***P<0.001; ****P<0.0001. (B and C) Analogous, *FOXQ1* mRNA expression in microarray data published in the study by Skrzypczak *et al* (3) and TCGA (4), respectively. (D-F) Similar, *TBX6* mRNA levels in microarray datasets from TCGA (4), and the studies by Kaiser *et al* (2) and Hong *et al* (5), respectively. Data were analyzed by an unpaired, two-tailed Student's t-test.

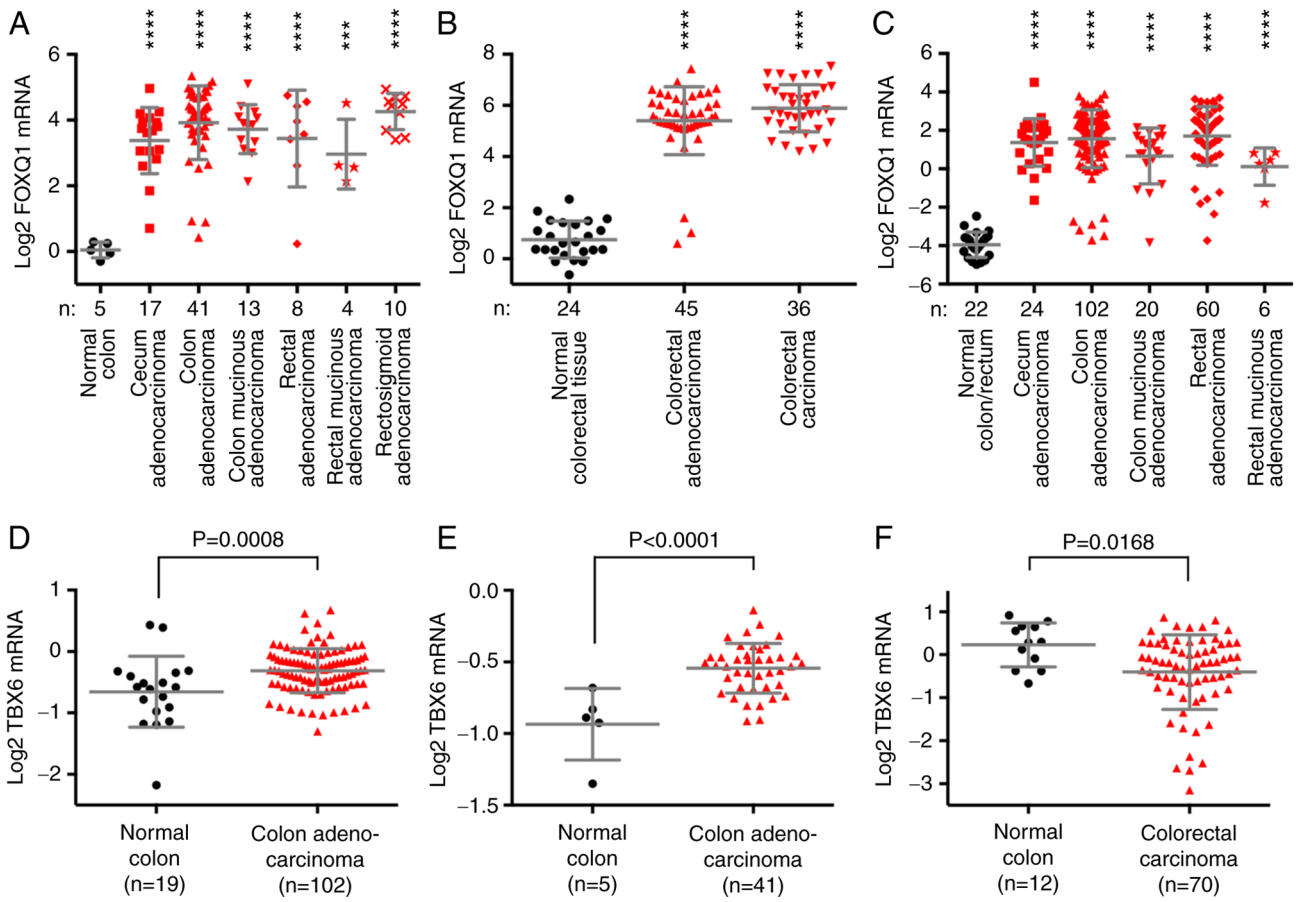

Figure S4. No effect of JMJD2A on *FOXQ1* and *TBX6* mRNA levels in HCT116 colorectal cancer cells is observed. (A) Downregulation of JMJD2A with two different shRNAs. Shown are respective western blots. Rabbit polyclonal antibodies against JMJD2A (A300-861A; Bethyl Laboratories) were utilized. Sequences of the used shRNAs have been described in the study by Kim *et al* (6). (B) *FOXQ1* and *TBX6* expression upon JMJD2A downregulation was determined by RT-qPCR. All mRNA levels were normalized to those of *GAPDH*. Statistical significance was assessed with one-way ANOVA with post hoc Dunnett's multiple comparisons test (n=3). JMJD, Jumonji C domain-containing protein.

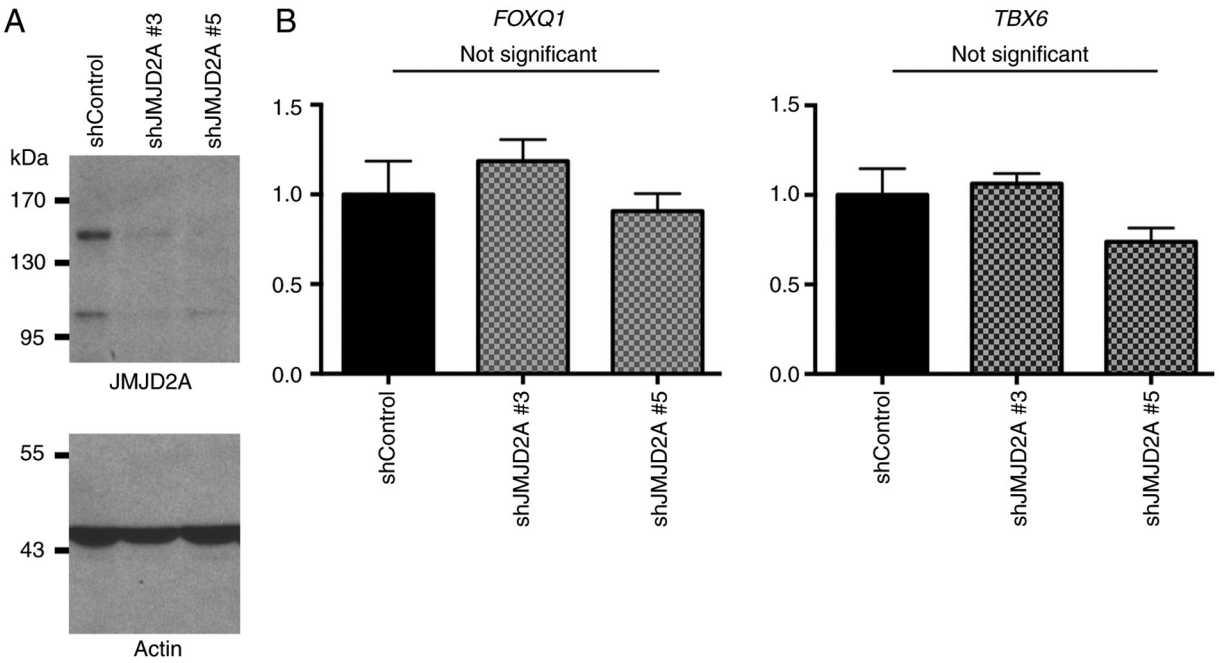

Figure S5. Upstream promoter sequence (2,000 bp) and the first 124 transcribed nucleotides (highlighted by underlining/italics) of the monoexonic human *FOXQ1* gene (NCBI Reference Sequence NM_033260.4). 5'-GGA$^{A}/_{T}$-3' (or $^{A}/_{T}$TCC in reverse) ETS core binding sequences, to which any ETS transcription factor may or may not bind, are highlighted in yellow color. The consensus binding sequence for human ETV1 is 5'-$^{A}/_{G}$ $^{C}/_{G}$ $^{C}/_{A}$ GGA$^{A}/_{T}$ $^{G}/_{A}$ $^{T}/_{C}$-3' (7).

TAGACATAAAAGGTGGGGCAGGTCCTTGCCCCCCTTGCCCCAAATGAAATCAGGGTAAGGAGAGGATCCC
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GTGCCCTCCTGCCCTGCCCAACCCCAGAGTTCAAGAGAGAAAAACATTCATTACGAACGCCTTTTATCCC
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CAAAAAGCAGCCATTCCCCACCTGGCTCCCGAGGCGCATACTTAATAAAGTCAGTCTAATCTCCGAACGC
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GACTTTGCCGCCGCGCTGCAGTGTGGCCTCCGCCTGGTGCGCGCCCGTTGGGGAGCTGGGGAACTGGGGA
GCCGCCACCACCTCGGCCACCTCGTTCCCCCCACCCCTTGCCGTCCGCGCTCAGGCCCCGCCCCCGCGGAG
CCGCCGCAGGGTTATATTGGGCCGGCCCGAAGGTGGAGGC*GAGACGCAGCCGCGGCAGGCCAGCGGGGAG*
ATGCTGCCCCGGAGGCTGGGAGCGGGAAGGCGGCTGCGGGCGCAGCGGCCTCGGGGACTCGCCTCCGCGG
GTGCTCAAGGCTGAAGGCGCCGGA

Figure S6. *JMJD1A* mRNA levels in prostate cancer. (A) Comparison of normal prostate gland to carcinoma in three different microarray data sets derived from the studies by Singh *et al* (8), Yu *et al* (9) and Lapointe *et al* (10). (B) Increased *JMJD1A* mRNA expression at metastatic sites compared to the primary tumor site. Microarray data sets were derived from Chandran *et al* (11), Yu *et al* (9) and LaTulippe *et al* (12). Data were analyzed by an unpaired, two-tailed Student's t-test.

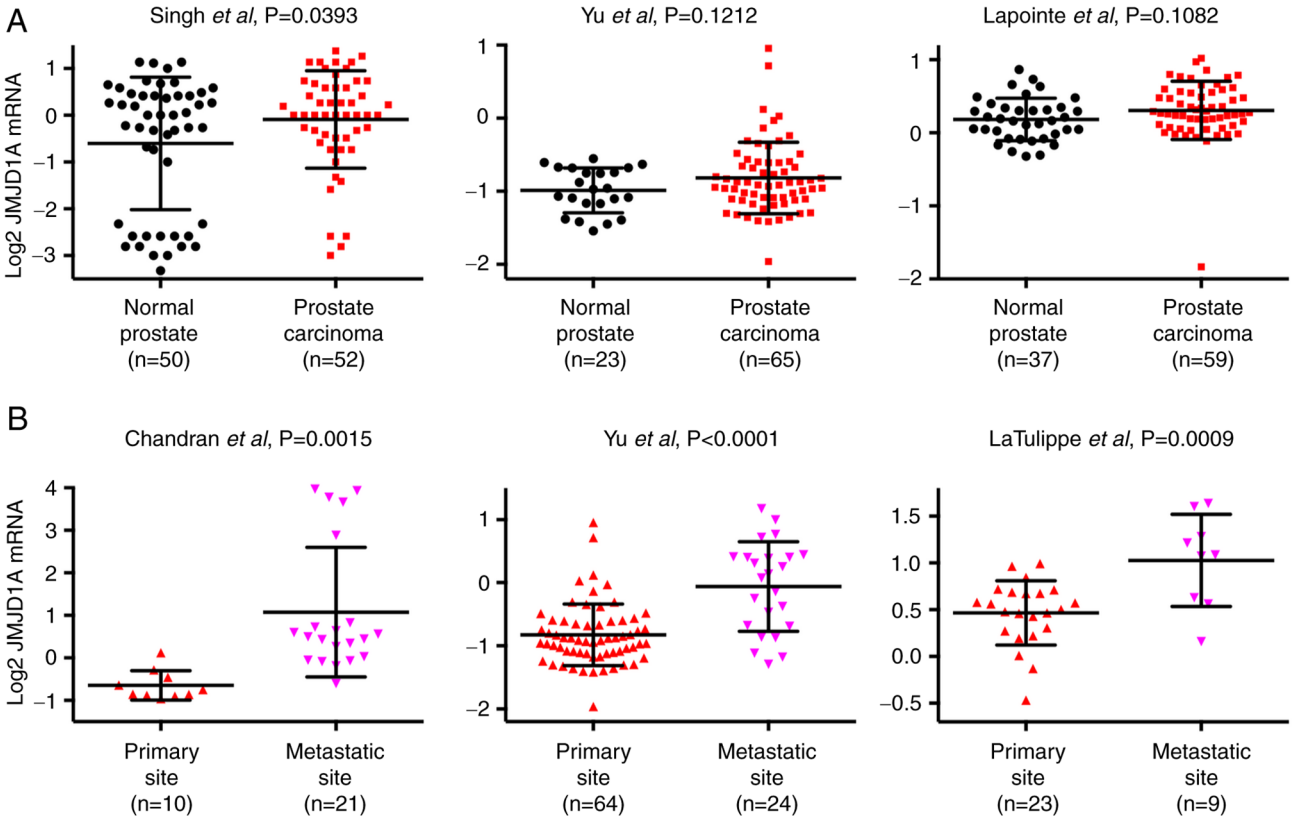

Figure S7. *FOXQ1* mRNA levels in prostate cancer. (A-D) Comparison of normal prostate gland to carcinoma at the primary site in four different microarray data sets derived from the studies by Arredouani *et al* (13), Grasso *et al* (14), Taylor *et al* (15) and Vanaja *et al* (16). Data were analyzed by an unpaired, two-tailed Student's t-test. (E and F) Decreased *FOXQ1* mRNA expression at metastatic sites compared to the primary tumor site. Microarray data sets were derived from the studies by Tamura *et al* (17) and Varambally *et al* (18).

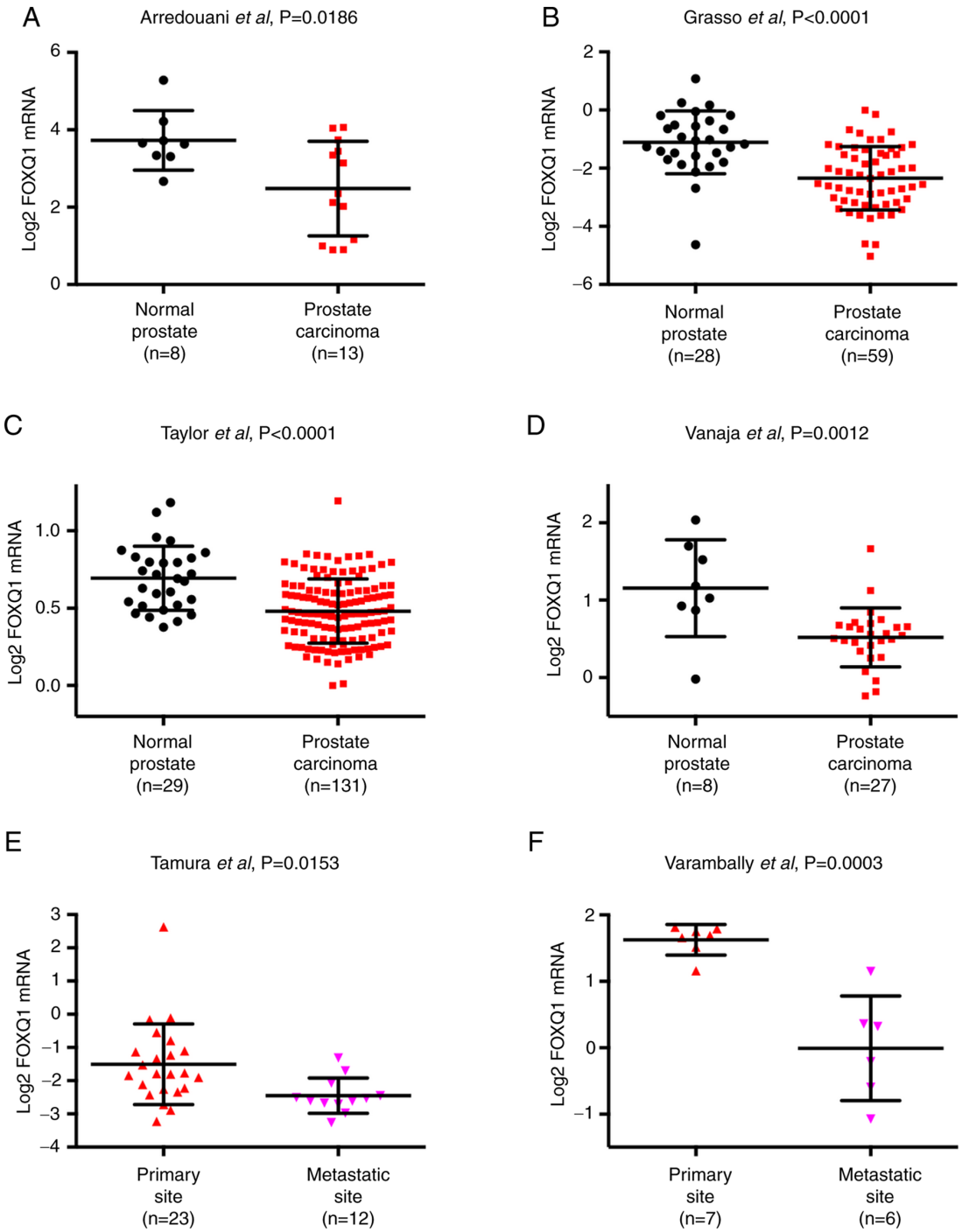

Figure S8. *MYCL* mRNA levels in colorectal and prostate cancer. (A) Comparison of normal colon to colon adenocarcinoma with regard to *MYCL* mRNA levels. Microarray data were derived from TCGA (4). Data were analyzed by an unpaired, two-tailed Student's t-test. (B and C) analogous, *MYCL* mRNA expression in colorectal tissue derived from microarray data published in the studies by Skrzypczak *et al* (3) and Gaedcke *et al* (19), respectively. (D-F) Likewise, *MYCL* upregulation in prostate carcinoma. Data are from the studies by Lapointe *et al* (10), Tomlins *et al* (20) and Yu *et al* (9), respectively.

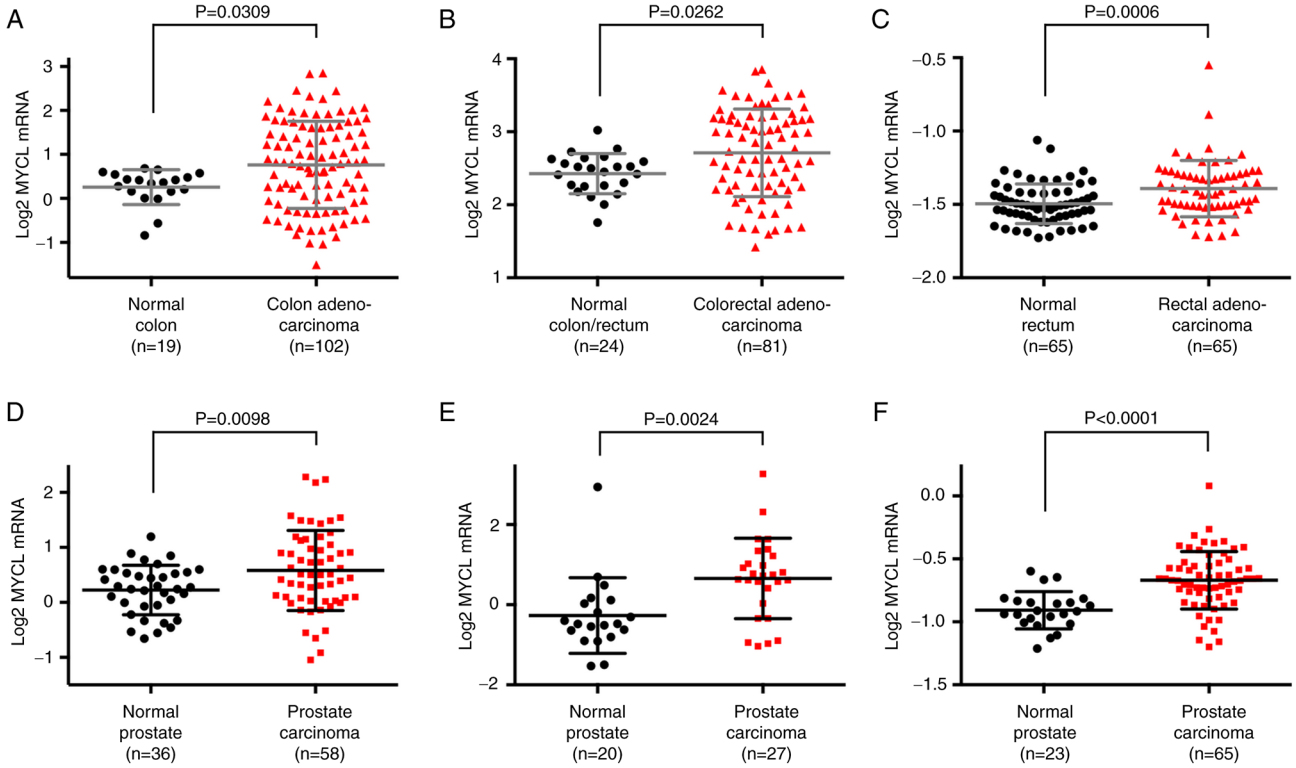

Table SI. Primer sequences used for RT-qPCR.

Gene	Forward primer (5'→3')	Reverse primer (5'→3')	Size (bp)
ETV1	CCAGCTTTCTGAACCCTGTAACTC	CATATGCAAAATCTCTGGGTTCCTG	233
GAPDH	GAGCCACATCGCTCAGACACC	TGACAAGCTTCCCGTTCTCAGC	226
WNT7A	CCATCACAGCTGCCTGTACCCAG	GTACTTGTCCTTGAGCACGTAGC	344
WNT11	GTTTTCCGATGCTCCTATGAAGGTGA	CAGCTGTCGCTTCCGTTGGATGTC	417
BHLHE40	GGATCTCCTACCCGAACATCTCA	GAGCGAAAGTCCGCTGGATGACTG	458
FOXQ1	GGACTTTGCACTTTGAATCCAGAG	GCCCAGAAACCCCAAACAGTAGTC	353
KLF7	GAGTGGACAGAGCGACAGTGAC	CCTTTAGACACTAGCCGATGCCATG	372
MYCL	TCGAAAGGCTGGGGCAGGAACTACG	CAGCATAGTTGTGCTGTTGCTGATGG	412
NFATC4	CTGCCCAGCCAATATGAGCAGCTG	AAGCTCAATGTCTGAATTCCGAAG	381
TBX6	GATCACACAACTGAAGATTGCAGC	CTCCAGAAATGCAGCCGAGTAGG	397
FAS	GGACCCAGAATACCAAGTGCAGATG	GTCATGACTCCAGCAATAGTGGTG	361
TP53I3	GCACAGCTGCTATCCAACTCACC	GACCTCAGCAAACTGGTGATCAGAC	343

Table SII. Primer sequences used for ChIP assays.

Region	Forward primer	Reverse primer
*A (1*st *PCR)*	1-for (5'-TAGACATAAAAGGTGGGGCAGGTC-3')	569-rev (5'-GGAAGGATCGCGTTCGGAGATTAGACTG-3')
*A (2*nd *PCR)*	46-for (5'-GAAATCAGGGTAAGGAGAGGATCCC-3')	532-rev (5'-AGTATGCGCCTCGGGAGCCAGGTG-3')
*B (1*st *PCR)*	508-for (5'-CCACCTGGCTCCCGAGGCGCATAC-3')	1052-rev (5'-GGATCTGACAGTCAACAGGAACGACG-3')
*B (2*nd *PCR)*	544-for (5'-GTCTAATCTCCGAACGCGATCCTTCC-3')	946-rev (5'-GCTGTGACCTCACTGGCACCAGTGT-3')
*C (1*st *PCR)*	1533-for (5'-CTAGACCCAGTCCCTTCAGGTGTCC-3')	Rev-3' (5'-TCCGGCGCCTTCAGCCTTGAGCAC-3')
*C (2*nd *PCR)*	1595-for (5'-CACTCGCCTAAACTGCGTCCCCGAAC-3')	2010-rev (5'-GCTGCGTCTCGCCTCCACCTTC-3')

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