Supplemental Table 1. qRT-PCR Expression of 45 Genes : Mybl2 siRNA or Spontaneous Differentiation

Gene	Expression Relative to GAPDH (x100) NT siRNA	Mybl2 siRNA	Prolif	Spont. Day 2	Spont. Day 14
ALDH7	0.880	1.359	1.002	1.662	1.627
ALPi	0.072	0.056	0.065	0.183	0.762
E-cadherin	7.439	8.175	7.352	13.605	29.126
cathepsin B	1.131	1.161	1.133	2.536	9.626
cdk2	0.406	0.706	0.889	1.002	0.991
cdk4	2.381	2.429	5.145	6.819	4.546
cyclin A2	4.243	3.269	2.636	2.075	0.979
cyclin B1	0.101	0.069	0.226	0.239	0.046
cyclin B2	1.522	1.099	1.244	1.458	0.537
cyclin D1	2.309	3.177	4.179	3.335	2.997
cyclin D2	11.264	18.102	18.157	4.446	1.408
cyclin E1	0.004	0.004	0.003	0.003	0.002
cdc2	4.669	3.226	3.735	3.504	1.557
cdc25A	1.095	1.282	1.133	0.740	0.404
cdc25B	0.750	0.494	0.820	1.336	0.710
cdc25C	0.666	0.453	0.602	1.037	0.646
cycloph G	0.013	0.017	0.005	0.008	0.013
CYP1A1	1.675	1.504	1.790	1.218	0.552
DNA topo	0.338	0.372	0.289	0.213	0.321
DP-1	0.037	0.051	0.064	0.042	0.030
DPPIV	1.615	1.519	2.210	9.380	12.504
E2M	0.160	0.175	0.058	0.050	0.020

Gene	Expression Relative to GAPDH (x100) NT siRNA	Mybl2 siRNA	Prolif	Spont. Day 2	Spont. Day 14
endothelin	0.061	0.073	0.147	0.058	0.185
EPHX2	0.131	0.124	0.128	0.948	2.798
fibronectin	26.905	26.796	32.745	67.122	17.820
GSPT1	0.349	0.504	0.411	0.127	0.154
GSTA3	0.002	0.001	0.000	0.007	0.326
HAT1	0.169	0.214	0.097	0.091	0.077
HDAC2	1.043	1.375	0.647	0.848	0.501
eIF-4E	0.050	0.064	0.044	0.059	0.038
Id-2	2.149	2.056	2.540	2.763	14.940
α-5 integrin	0.003	0.003	0.007	0.014	0.109
KLF4	0.025	0.027	0.027	0.144	0.537
MEK2	0.269	0.325	0.488	0.635	1.129
Mybl2	3.189	0.537	5.484	4.924	1.998
c-myc	0.012	0.019	0.066	0.091	0.026
NAP1L1	24.987	29.340	30.119	66.704	28.832
Notch1	0.015	0.014	0.016	0.051	0.043
PCNA	9.654	11.627	13.505	13.143	6.295
PSMC3	0.622	0.773	0.700	0.597	0.765
Ran	1.644	1.785	0.378	0.568	0.267
TARS	0.076	0.068	0.172	0.108	0.063
TCF-4	0.182	0.158	0.148	0.418	1.179
TGF-b2	0.087	0.078	0.062	0.075	0.013
thy synth	1.526	1.798	1.514	1.470	1.256

Supplemental Table 2. Primers used for qRT-PCR

Gene	forward primer (5'→3')	reverse primer (5'→3')
ALDH7	GAGGCGACTGTTTATACATG	AAGAAACATGCTCACTGCCT
ALPi	GCAACCCTGCAACCCACCCAAGGAG	CCAGCATCCAGATGTCCCGGGAG
A-myb	ACCTTGTGCAGCTATGGATC	GTGACACATACTGATACCCA
E-cadherin	TGAAGGTGACAGAGCCTCTGGAT	TGGGTGAATTCGGGCTTGTT
cathepsin B	AGCACTACGGATACAATTCC	ACTTGTAGAGCAGGAAGTCC
cdk2	GCTAGCAGACTTTGGACTAGCCAG	AGCTCGGTACCACAGGGTCA
cdk4	ATGTTGTCCGGCTGATGGA	CACCAGGGTTACCTTGATCTCC
cycl A2	TGCTGCTATGCTGTTAGCCT	TGCTCCATTCTCAGAACTTG
cycl B1	TGCTGCCTGGTGAAGAGGAA	TGCCATGTTGATCTTCGCCT
cycl B2	CTTCTGTCAAACCAGTACAG	ATTTTGCAGAGCAAGGCATC
cycl D1	ATGCTGGAGGTCTGCGAGGA	AGGAAGCGGTCCAGGTAGTT
cycl D2	GAAGGACATCCAACCCTACA	AGGAGTTGCAGATGGGACTT
cycl E1	CTCCAGGAAGAGGAAGGCAA	TCGATTTTGGCCATTTCTTCA
cdc2	TCCTGGTCAGTACATGGATT	GTCTCTGTGAAGAACTCTTC
cdc25A	CTCCGAGTCAACAGATTCAG	CTACATCCCAACAGCTTCTG
cdc25B	TCGTCTGAATCCTCCGAATC	CATAGACTGGAAGCGTCTGA
cdc25C	TATCACTCAGATGCTGGAGG	TCTGGGTTGACATACTTCAG
cycloph G	CTTTGTACAGGTGAAAAGGG	CTTCACTGAAGTCACCACCT
CYP1A1	TACCCAACCCTTCCCTGAAT	AGTGCTCAATCAGGCTGTCT
DNA topo	GGAACCAGTATCGAGAAGAC	CTCCTTTTCATTGCCTGCTC
DP-1	TTCCGACTCCTCACCTTGGT	TAGGCCCTTGCCATTCTTCT
DPPIV	AGTCTTCAGTGCCTACTCTG	CAGTTGGATTCACAGCTCCT
E2M	CAGAAGGACATAAACGAGCT	TTGAAGTTGAGGAGGTCGTC
endothelin	AGCTCCAGAAACAGCAGTCT	TTATCCATCAGGGACGAGCA
EPHX2	CCACTACCCGGCTTATGAAA	TTAGCGGTCTCGGAGCACTT

Gene	forward primer (5'→3')	reverse primer (5'→3')
fibronectin	ACGCCTCCACTGCCATTGAT	AGACCCAGGCTTCTCATACT
GAPDH	CCATCAATGACCCCTTCATT	TTGATGACAAGCTTCCCGTT
GSPT1	TCAGGAAGAACGAGACAAGG	TGAGATTACCAGCACAGCCA
GSTA3	TTCAATGGACGGGGCAGAAT	CCAACTTCATCCCATCAATC
HAT1	GTAGGCTACATGACAGTCTA	CCTTGACCTTGAAATGGAGT
HDAC2	CGTGTAATGACGGTATCATTCC	CTGCCCATATGACTCATCATC
eIF-4E	GGTTGTGCGATCAGATCGAT	TTCTCCTCTTCTGTAGTCGG
Id-2	CATCCTGTCCTTGCAGGCTT	CACACAGTGCTTTGCTGTCA
α-5 integr	CTCCATTGGTTTCACAGTGG	ATTCTGGATGAGCAGGGTCT
KLF4	TGCTGATTGTCTATTTTTGCGTTTA	GAGAAGAAACGAAGCCAAAACC
MEK2	TGCTCACAAACCACACCTTCAT	ACACAACCAGCCGGCAAA
Mybl2	CTGACCAGCAATGCCAGTAC	TTCAGGTGCTTGGCAATCAG
c-myb	TCGCAAAGCTACTGCCTGGA	AAGACTCCTGCAGATAACCT
c-myc	TGCCAGGACCCGCTTCT	GAGGCTGCTGGTTTTCCACTA
NAP1L1	CACGTCAGCTAACTGTTCAG	ACCCTAGGCAGGCTTTCAAT
Notch1	CAGGCAATCCGAGGACTATG	CAGGCGTGTTGTTCTCACAG
PCNA	GACCGCAACCTGGCCAT	CCGCGTTATCTTCGGCC
PSMC3	GTACAGAAATACGTCGGTGA	GTCACCTCCAGCACCATCAT
Ran	TTATATCCAAGCCCAGTGTG	ACAATGGATTTCGCCTTCAC
TARS	CAGTCTATAGATGTGGCCCT	TCTCCATATCTGCTTTGCCT
TCF-4	CCGAAAGTTTCCGAGACAAA	AGTGGCCATTTCATCTGGAG
TGF-b2	AATAGACATGCCGCCCTTCT	TCTCCATTGCTGAGACGTCA
thy synth	ACTGCAAAGAGTGATTGACACCAT	CAGAGGAAGATCTCTTGGATTCCAA

Supplemental Table 2 (continued). Primers used for chromatin immunoprecipitation

Gene	forward primer (5'→3')	reverse primer (5'→3')
E-cadherin	AGTGGAATCAGAACCGTGCA	CTGCCGGCCACAGCCAATCA
cdk2	CACTCTCATCTTGATGCACT	CTGGTTTAATTCACTCTCCC
cdk4	CTCATGGTGGAGCGAAAAGG	CTGAAGGATTGTCTCACTAC
cdc25B	GTGGCTTTACAAGGACACTT	CTCTGCAAGACTGAATTTCC
c-myc	CACTTAACACTTGAACGCTG	GTGTATAGCATGTACGCTGT
cyclin B2	TCAGAGGCGTCCTACGTCTG	AGATGCACTCTCGCACTCTC
cyclin D2	CTACACCTACAGAATGAGTG	ACTACCGACTCCTATTTCTG
MEK2	GTGGATCTAACACAGCTACA	ATGAGTAGGATCACACAGGT

Supplemetary Experimental Procedures

Reporter plasmids

A plasmid containing –2.4 kbp of promoter region of the human *CDK2* gene up to nucleotide +58 bp cloned into pGL2 Basic (Promega) (1) was a gift of A. van Wijnen (University of Massachusetts Medical School, Worcester, MA). A 3.3kb fragment of the human c-myc promoter, containing residues -2328 bp to +936 bp relative to transcription initiation site P1, inserted upstream of a luciferase reporter (2) was a gift of D. Levins (Laboratory of Pathology, National Cancer Institute, Bethesda, MD). The upstream regions of cdk6, cyclin D2, cdc25B, and cyclin B2 were cloned by PCR from genomic DNA of Caco-2 cells as follows : ~250ng genomic DNA, isolated from ~$3x10^6$ Caco-2 cells using the Dneasy Blood and Tissue kit (Qiagen) as described by the manufacturer, was amplified by PCR using Phusion High Fidelity DNA polymerase (New England Biolabs) and the following primers : cdk6 (-1004bp to +172bp, relative to start site of longest transcript (3)) 5' **ggggtacc**ctttgttgtgcagagggctc, 3' *gaagatct*aatcagacagcccagaagcc ; cyclin D2 (-881bp to +147bp relative to start site of longest transcript (4)) 5' **ggggtacc**aagcgggtttttcctgcgtg, 3' *gaagatct*tgacctccttcctttggcta ; cdc25B (-1328bp to +559 relative to start site of longest transcript, Genbank accession NM_021873) 5' **ggggtacc**acatacaccctgtgcagatg, 3' *gaagatct*tctagttgcagctgccactt ; cyclin B2 (-797bp to +94 bp relative to transcriptional start site, Genbank accession NM_004701) 5' **ggggtacc**gattctggacactaggcctt, 3' *gaagatct*aaagggaggacactagcgta. Sequences in bold and italics represent, respectively, sites for cleavage by KpnI and BglII restriction endonucleases. Cycling conditions : 98^o for 30 s ; 30 cycles of 98^o for 10 s, 65^o (cdk6, cyclin D2, cyclin B2) or 72^o (cdc25B) for 30 s, 72^o for 45 s (cdk6, cyclin B2, cyclin D2) or 2 min (cdc25B); 72^o for 10 min. Appropriately-sized fragments were purified (Gel Extraction Kit, Qiagen) and digested overnight with KpnI and BglII, then ligated into similarly-digested pGL3 Basic (Promega).

Supplementary Experimental Procedures References

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