Supplemental data

Supplemental Table 1 The primer sequences used in the real-time PCR experiment

	Primer pairs	Length of products	Efficiency
SP1	F: 5'-GCCGCTCCCAACTTACAGAA-3' R: 5'-CCCATCAACGGTCTGGAACT-3'	102	102.3
USF1	F: 5'-TTGGATGAGTGACTGCTGACGC-3' R: 5'-CATCTTGGCGCAGGGCGTCTT-3'	115	101.2
CREB1	F: 5'-CCGGGCCGTGAACGAAAGCA-3' R: 5'-TGGCAATCTGTGGCTGGGCT-3'	155	93.7
CDX2	F: 5'-CAGGACGAAAGACAAATATC-3' R: 5'-GATGTAGCGACTGTAGTG-3'	85	101.3
MUC3A	F: 5'-CCGGACCTCAATGACAACACT-3' R: 5'-ACCACGATGCTGCCATTCCT-3'	146	100.6
GAPDH	F: 5'-GTAGAGGCAGGGATGATGTTCT-3' R: 5'-CTTTGGTATCGTGGAAGGACTC-3'	132	101
β-actin	F: 5'-GTGATCTCCTTCTGCATCCTGT-3' R: 5'-CCACGAAACTACCTTCAACTCC-3'	132	97.5

Supplemental Table 2 The primer sequences used in the each MUC3 promoter fragment

	Forward	Reverse
MUC3-M5	5'-CCGCTCGAGAGTCTAGTCTCGAACCCCTGACCT-3'	5'-CCCAAGCTTGGGCCCAGCGGGCAGGGGG-3'
MUC3-M4	5'-CCGCTCGAGGCTCTTGGCTCACTGCACCCTCCA-3'	5'-CCCAAGCTTGGGCCCAGCGGGCAGGGGG-3'
MUC3-M3	5'-CCGCTCGAGGGAATACAGGCGTGAGCCACCGC-3'	5'-CCCAAGCTTGGGCCCAGCGGGCAGGGGG-3'
MUC3-M2	5'-CCGCTCGAGCAGGCAGGCTGTGGGGCTGAGCC-3'	5'-CCCAAGCTTGGGCCCAGCGGGCAGGGGG-3'
MUC3-M1	5'-CCGCTCGAGCTGACGCTCAGCAAAACCGATA-3'	5'-CCCAAGCTTGGGCCCAGCGGGCAGGGGG-3'

Supplemental Table 3 The primer sequences used in the ChIP experiment

ChIP	Primer pairs	Length of products
ChIP1	Forward: 5'-CACTATGTTGGCCAGTCTAGTCTCGA-3'	156 bp
	Reverse: 5'-CAGCACATTGTTTGACCTATCCAGTT-3'	
ChIP2	Forward: 5'-GGGAATACAGGCGTGAGCCAC-3'	163 bp
	Reverse: 5'-GCCAGAAAAAACCGTGGGAGTAAT-3'	
ChIP3	Forward: 5'-CCTGGACTTGTCCTATCTTTTTCCC-3'	144 bp
	Reverse: 5'-TGCTGAGCGTCAGGGCTGAG-3'	
ChIP4	Forward: 5'-CCTGGACTTGTCCTATCTTTTTCCC-3'	144 bp
	Reverse: 5'-TGCTGAGCGTCAGGGCTGAG-3'	
Internal control	Forward: 5'-TACTAGCGGTTTTACGGGCG-3'	166 bp
(GAPDH)	Reverse: 5'-TCGAACAGGAGGAGCAGAGAGCGA-3'	

Supplemental Table 4 2.0 fold up-regulated transcription factors of TFLK-containing 10-mer-BP treated HT-29-Gal cells versus untreated HT-29-Gal cells

Row	Column	Position	Transcription Factor	Initial Values (untreated)	Initial Values (treated)	Standardised Values (untreated)	Standardised Values (treated)	Fold change (treated/untreated)
1	1	1	AP-1	25702	55423	0.022268	0.870609	39.09653
1	2	2	GAS/ISRE	26113	53329	0.033957	0.813418	23.95448
1	3	3	Pbx1	27200	51980	0.064871	0.776575	11.97113
1	4	4	Stat5/Stat6	31950	59423	0.199959	0.979855	4.900288
1	22	22	PREB	29412	46848	0.127779	0.636413	4.980574
1	23	23	T3R	26251	35690	0.037882	0.331671	8.755483
2	1	24	AP-2	25238	54253	0.009072	0.838654	92.44199
2	2	25	GATA	25794	51871	0.024885	0.773598	31.0874
2	3	26	Pit 1	34002	56814	0.258317	0.908599	3.517385
2	4	27	TFIID	28705	40470	0.107672	0.46222	4.292843
2	5	28	CREB	26008	34899	0.030971	0.310067	10.01164
2	23	46	Tat	29138	37148	0.119987	0.371491	3.096106
3	4	50	TR	27374	30830	0.069819	0.198937	2.849319
3	9	55	RREB (1)	27712	30762	0.079432	0.19708	2.481122
3	14	60	Pur-1	31330	42970	0.182326	0.530499	2.909615
4	1	70	Brn-3	26090	31425	0.033303	0.215187	6.461551
4	3	72	PRE	31922	48252	0.199162	0.674758	3.38798
4	4	73	TR(DR-4)	33670	60404	0.248875	1.006647	4.044796
4	5	74	CETP-CRE	32859	49675	0.22581	0.713622	3.160275
4	16	85	ATF-adelta	29984		0.144046	0.58067	4.03113
4	20	89	myc-CF1	29592	37199	0.132898	0.372884	2.805788
5	1	93	C/EBP	27132	36591	0.062937	0.356278	5.660897
5	4	96	USF-1	26400	54524	0.042119	0.846056	20.08727
5	7	99	HNF-3 b	26038	26617	0.031824	0.083874	2.635556
5	8	100	Nkx-2.5	35079	49528	0.288946	0.709607	2.455848
5	10	102	ATF2	26747	27527	0.051988	0.108727	2.091407
5	19	111	LF-A2	27254	36897	0.066406	0.364636	5.490975
5	21	113	p53(2)	29655	54769	0.13469	0.852747	6.331192
6	4	119	VDR(DR-3)	29352	58836	0.126073	0.963823	7.644983
6	13	128	MZF1(2)	36146	54578	0.319291	0.84753	2.654414
6	16	131	beta M-globin factor B1	30443	36723	0.1571	0.359884	2.290791
7	4	142	HSE	33579	57538	0.246287	0.928372	3.76948
7	9	147	SRY	27890	34142	0.084494	0.289393	3.42501
7	14	152	RIPE3a1	26934	53233	0.057306	0.810796	14.14861
7	20	158	NF-1(2)	30252	53018	0.151668	0.804924	5.307141

7	22	160	RORE	29546	34744	0.13159	0.305834	2.324147
8	1	162	c-Myb	33771	55087	0.251747	0.861432	3.421816
8	3	164	Smad SBE	32341	42251	0.211078	0.510862	2.420245
8	21	182	Pax5(2)	31014	55107	0.173339	0.861978	4.972784
9	7	191	IRF-1, IRF-2	30666	57283	0.163442	0.921408	5.637517
9	16	200	C/EBPalpha(1)	28690	33494	0.107246	0.271695	2.533389
9	18	202	HiNF-A	31903	41500	0.198622	0.490351	2.468764
9	19	203	LXRE1	27402	33704	0.070615	0.27743	3.928747
10	7	214	ISRE (1)	35238	59008	0.293468	0.96852	3.30026
11	6	236	GATA-4	31954	49561	0.200072	0.710509	3.551259
11	10	240	Cdx2	39728	59986	0.421162	0.995231	2.363063
11	12	242	LyF	26935	28115	0.057334	0.124786	2.176473
11	17	247	EBP-80	38720	52829	0.392494	0.799763	2.037641
11	18	248	HiNF-D3	39445	57936	0.413113	0.939242	2.273572
11	21	251	PCF	27843	42434	0.083157	0.51586	6.20342
11	22	252	SRF(2)	28223	34590	0.093964	0.301628	3.210029
12	8	261	Pax3	25374	36564	0.01294	0.355541	27.47612
12	15	268	ABF-1	39818	56032	0.423721	0.887241	2.093928
12	16	269	CBFB	27720	31198	0.079659	0.208988	2.62352
12	18	271	HNF1a/b/c	33091	48327	0.232408	0.676806	2.912145
12	19	272	MDBP(1)	31609	45075	0.190261	0.587989	3.09044
12	22	275	SSAP	36876	50597	0.340052	0.738803	2.172619
13	2	278	oct-1	26413	27350	0.042489	0.103893	2.445189
13	9	285	AF1, ARP1., NF-BA	28346	54147	0.097462	0.835759	8.575197
13	10	286	CP1, CTF, CBTF	26302	29549	0.039332	0.163951	4.168394
13	12	288	LyF-1	32159	55728	0.205902	0.878939	4.268714
13	13	289	p55	25819	25899	0.025596	0.064264	2.510741
13	14	290	TCE	28502	49701	0.101899	0.714332	7.010201
13	15	291	ACF	29081	38103	0.118365	0.397573	3.358864
13	18	294	HNF-4alpha2/1	30428	49831	0.156674	0.717883	4.582028
13	20	296	NF-E2(2)	39205	54834	0.406288	0.854522	2.103244
13	22	298	Sp1	26449	46243	0.043513	0.619889	14.24622
14	1	300	Ets-1/PEA3	28701	34079	0.107558	0.287672	2.674565
14	16	315	c-Ets-1	28263	30758	0.095102	0.196971	2.071152
14	18	317	HOXA4	27212	36973	0.065212	0.366711	5.623381
14	19	318	MEF-2a	25800	26785	0.025055	0.088462	3.530674
14	20	319	NFE-6/CP1	33680	55565	0.249159	0.874487	3.509754
14	21	320	PRDI-BFc	26334	43296	0.040242	0.539402	13.40396
14	22	321	Stat5b	25681	27974	0.021671	0.120935	5.580527

15	15	337	ALF1B	35429	48977	0.2989	0.694559	2.323717
15	17	339	EIL1/2/3	26017	28142	0.031227	0.125524	4.019761
15	18	340	IL-6 RE-BP	31199	46753	0.1786	0.633818	3.548803
15	19	341	Mfh-1	26332	34127	0.040185	0.288983	7.191295
15	20	342	NFkB	28515	58385	0.102269	0.951505	9.303976
15	21	343	PRDII-BF1	26107	46037	0.033786	0.614263	18.18088
15	23	345	YB1	29022	53182	0.116688	0.809404	6.936504

Supplemental Table 5 2.0 fold down-regulated transcription factors of TFLK-containing 10-mer-BP treated HT-29-Gal cells versus untreated HT-29-Gal cells

Row	Column	Position	Transcription Factor	Initial Values (untreated)	Initial Values (treated)	Standardised Values (untreated)	Standardised Values (treated)	Fold change (treated/untreated)
1	11	11	CSBP	27730	24887	0.0799436	0.0366247	0.4581319
1	14	14	PPUR(1)	56963	25920	0.9113174	0.0648375	0.071147
1	15	15	TGT3	51055	27686	0.7432965	0.1130696	0.1521191
1	19	19	ISGF	54232	29895	0.833649	0.1734007	0.2080021
2	18	41	Fra-1/JUN	30296	25019	0.1529195	0.0402298	0.2630785
3	18	64	GATA1(2)	30745	26177	0.1656889	0.0718566	0.4336835
3	22	68	PTF1	38241	28263	0.3788719	0.1288283	0.3400314
4	12	81	ICSBP	28333	24631	0.0970927	0.029633	0.305203
7	11	149	Elf-1	27750	24098	0.0805124	0.0150759	0.18725
9	10	194	CD28RC	27350	24224	0.0691366	0.0185172	0.267835
10	17	224	E2	27520	24812	0.0739713	0.0345764	0.4674293
12	23	276	v-rel 50-55K	27042	24583	0.0603772	0.028322	0.4690848

Legend of Supplementary Figure 1. Sequence of the promoter of MUC3 and potential transcriptional factor binding sites. The potential transcriptional factor binding sites were predicted using the TFSEARCH: Searching Transcription Factor Binding Sites (ver 1.3) (http://mbs.cbrc.jp/research/db/TFSEARCH.html). The start site in the MUC3 cDNA clone is indicated with an arrow; the possible transcription factor binding sites are underlined and the identity of the transcription factors are indicated above the binding sites. The truncated sites used to generate the human MUC3 promoter luciferase constructs, including -999, -775, -623, -242 and -62, are marked with '*'.

Supplementary Figure 1