

Supplementary Table 1: Primer pairs used to amplify the Fen1 5' flanking region

Position ^a	Orientation	Sequence ^b (5' → 3')	Constructs
-1821bp ~ 632 bp	Forward	GCGCGAGCTCGGGAGCTTTGTGGACCAGTGTCTATAGACACCAAGCTGAG	pGL4-FP1
	Reverse	GCGGGCTAGCCTAGGCAGGAAAGGGGCCTAAACAACCTCAAG	
352bp ~ 2662 bp	Forward	GCGCGAGCTCGTGAGACCCCATGGGAAGCGCCTCCGGGAGC	pGL4-FP2
	Reverse	GCGGGCTAGCCGGCAACACAGAGGAGGGATGACTAAAAAAG	
-1821bp ~ 352 bp	Forward	GCGCGAGCTCGGGAGCTTTGTGGACCAGTGTCTATAGACACCAAGCTGAG	pGL4-FP3
	Reverse	GCGGGCTAGCCGCTCCCGGAGGCGCTTCCCATGGGGTCTCA	
-1191bp ~ 632 bp	Forward	GCGCGAGCTCGCTTCTGACCTCCTGATCCGCTCGCC	pGL4-FP4
	Reverse	GCGGGCTAGCCTAGGCAGGAAAGGGGCCTAAACAACCTCAAG	
-701bp ~ 632 bp	Forward	GCGCGAGCTCGTTCCCCCAAATGATAAAGACAATC	pGL4-FP5
	Reverse	GCGGGCTAGCCTAGGCAGGAAAGGGGCCTAAACAACCTCAAG	
-421bp ~ 632 bp	Forward	GCGCGAGCTCGGCACGGGTTCGGCAGAAGAACTTTC	pGL4-FP6
	Reverse	GCGGGCTAGCCTAGGCAGGAAAGGGGCCTAAACAACCTCAAG	
-281bp ~ 632 bp	Forward	GCGCGAGCTCGGGCAAGGGGCTTCCCCCTCCCCAC	pGL4-FP7
	Reverse	GCGGGCTAGCCTAGGCAGGAAAGGGGCCTAAACAACCTCAAG	
70bp ~ 632 bp	Forward	GCGCGAGCTCGGCGGTGGAGAAGGGTACGCCAGGGT	pGL4-FP8
	Reverse	GCGGGCTAGCCTAGGCAGGAAAGGGGCCTAAACAACCTCAAG	
-458bp ~ 278 bp	Forward	GCGCGAGCTCGTCCACCAATAAACATTTGCCAGGGC	pGL4-FP9
	Reverse	GCGGGCTAGCCCGCTCTCCCTTCTCAGCTTAGCGGCGGGTG	

^aRelative to the transcription start site.

^bAll primer pairs with a *Sac* I (forward primers) and *Nhe* I (reverse primers) restriction site (underlined sequences).

Supplementary Table 2: Characteristics of the subjects used in methylation analysis

#	Age	Pathology	Stage	TNM	ER	PR	Her-2
1	47	infiltrating ductal carcinoma	II	110	+++	+++	-
2	44	infiltrating ductal carcinoma	II	210	-	-	+
3	50	infiltrating ductal carcinoma	II-III	110	+++	+++	-
4	45	infiltrating ductal carcinoma	II	110	+++	+++	-
5	58	infiltrating ductal carcinoma	IV	411	-	-	-
6	34	infiltrating ductal carcinoma	III	110	-	-	-

TNM: T = Primary tumour, N = Regional lymph nodes, M = Distant metastasis;

ER: estrogen receptor; **PR:** progesterone receptor; **Her-2:** human epidermal growth factor receptor 2

Supplementary Table 3: *FEN1* over-expression in matched normal/cancer tissues on cancer profiling array I

Cancer	Numbers of cancer samples with <i>FEN1</i> over-expression	Total numbers of paired normal/cancer tissues	Percentage of cancer samples with <i>FEN1</i> over-expression (%)
Breast ^a	47	50	94.00
Uterine ^a	33	42	78.57
Ovarian ^a	12	14	85.71
Cervical ^a	1	1	100.00
Lung ^a	17	21	80.95
Kidney ^a	14	20	70.00
Stomach ^a	19	29	65.52
Colon ^a	21	34	61.76
Rectum ^a	11	18	61.11
Small intestine ^a	1	2	-
Pancreas ^b	1	1	-
Prostate ^b	1	4	-
Breast ^b	1	3	-
Uterine ^b	1	2	-
Ovarian ^b	0	4	-
Colon ^b	1	2	-
Rectum ^b	1	1	-

^aPrimary cancer, ^bMetastatic cancer, - Percentage not calculated due to small number of samples