Supplementary Material

A universal cell-free DNA approach for response prediction to preoperative chemoradiation in rectal cancer

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Content:

Supplementary Table 1. Additional clinicopathological characteristics of study population

	No pathCR (n = 30)	PathCR (n = 7)	*P*
Total mesorectal excision (%)	100%	100%	*ns*
Low anterior resection/ Abdominoperineal resection/unknown (%)	67%/30%/3%	56%/0/44%	*ns*
Distal surgical margins involvement[#]	14%		
Circumferential margins involvement[#]	10%		
Lymph node harvest (mean)[$]	19.6	19	*ns*
Lymphovascular \ perineural invasion (%)[$]	27%	0%	*P < 0.05*
Mismatch repair deficiency (%)[^]	9.5%		

ns – not significant

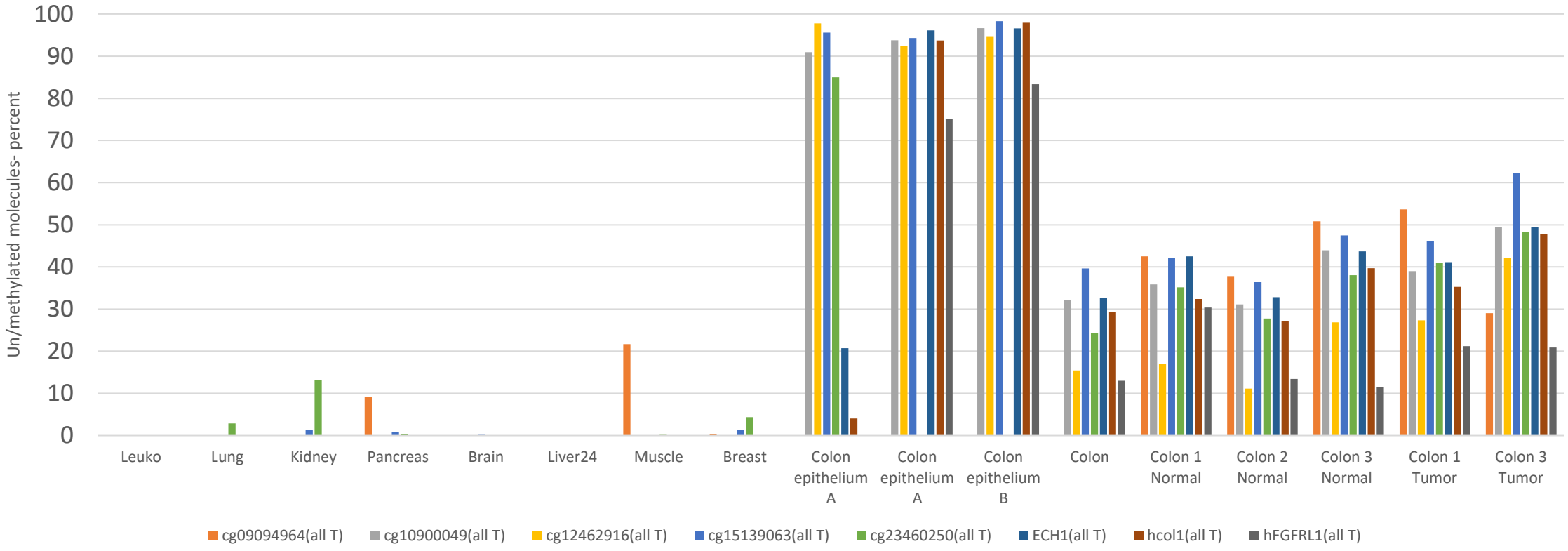
[#] Data not available for 1 patient

[$] Data not available for 2 patients in non-pathCR group and 3 in pathCR group

^ Data available for 21 patients (70%)

Supplementary Figure 1: Tissue panel of eight colon-specific methylation markers.

The percentage of molecules with colon-specific methylation in genomic DNA was obtained from different cell types and tissues. In these experiments, we determined the fraction of molecules that were largely unmethylated across amplified CpG sites.


Un/methylated molecules- percent
100
90
80
70
60
50
40
30
20
10
0
Leuko
Lung
Kidney
Pancreas
Brain
Liver24
Muscle
Breast
Colon epithelium A
Colon epithelium A
Colon epithelium B
Colon
Colon 1 Normal
Colon 2 Normal
Colon 3 Normal
Colon 1 Tumor
Colon 3 Tumor
cg09094964(all T)
cg10900049(all T)
cg12462916(all T)
cg15139063(all T)
cg23460250(all T)
ECH1(all T)
hcol1(all T)
hFGFRL1(all T)