

Supplemental Table 1: Patients and histopathology of the resected colorectal carcinomas which underwent microdessection and proteome analysis

		Stage UICC II	Stage UICC III
<b>Number</b>		9	10
<b>Gender</b>	m/f	5/4	5/5
<b>Age (range)</b>		74 (60-83)	70 (58-84)
<b>Local tumor invasion</b>			
<b>pT</b>	1	0	1
	2	0	3
	3 a	3	1
	3 b	3	3
	3 c	2	0
	3 d	0	0
	4 a	0	0
	4 b	0	1
	4 c	1	1
<b>Nodal status</b>			
<b>pN</b>	0	9	0
	1	0	6
	2	0	4
<b>Lymphatic vessel invasion</b>			
<b>pL</b>	0	8	5
	1	1	5
<b>Venous vessel invasion</b>			
<b>pV</b>	0	9	10
	1	0	0
<b>Distant metastases</b>			
<b>M</b>	0	9	10
	1	0	0
<b>Grading</b>			

<b>G</b>	Low grade (1, 2)	8	8
	High grade (3, 4)	1	2
<b>Residual tumor</b>			
<b>R</b>	R0	9	10
	R1	0	0
	R2	0	0
<b>UICC stage</b>			
	IIA	8	0
	IIB	1	0
	IIC	0	0
	IIIA	0	4
	IIIB	0	6
	IIIC	0	0
<b>Tumor side</b>			
	Coecum	0	1
	Sigmoid colon	4	5
	Rectum	5	4

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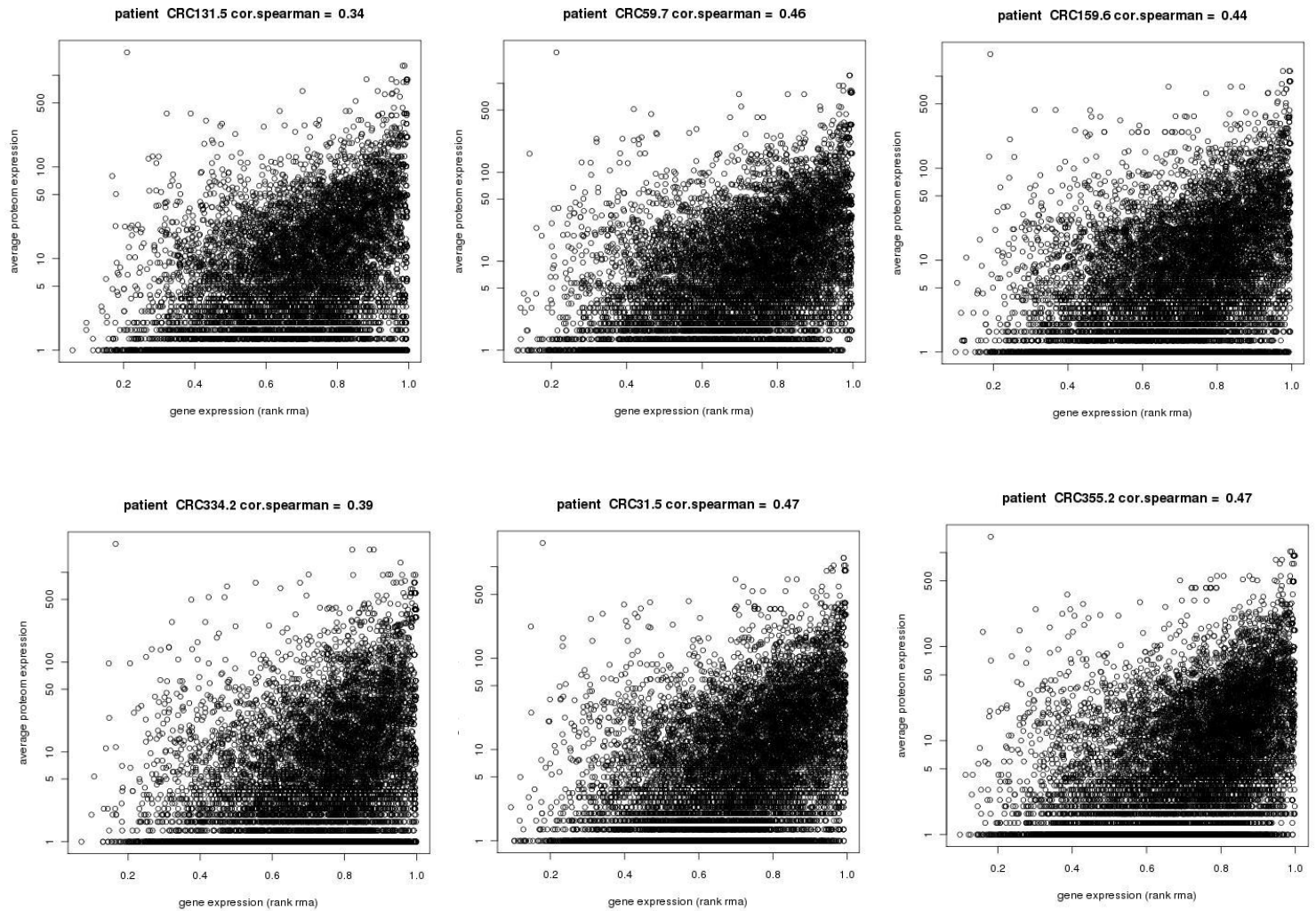
Supplemental Table 2: Genome-scale analysis of protein expression analysis in 19 individually dissected colorectal carcinomas. Proteins identified at 1% FDR at both, peptide and protein level are counted.

<b>Metrics</b>	<b>Stage UICC III tumors</b>	<b>Stage UICC II tumors</b>
Average total number of MS/MS spectra assigned per tumor	212,321 ± 39,634	220,754 ± 49,283
Average total Number of proteins identified per tumor	5,040 ± 577	5,167±1,034
Total number of proteins for all tumors in the group	8,346	8,543

Supplemental Table 3: Patient and tumor characteristics of lymph node negative (stage UICC II) and lymph node positive (stage UICC III) colon carcinomas of the validation cohort for immunohistochemistry.

	UICC II	UICC III
	mean	mean
n	20	20
Male	11	12
Female	9	8
Age	66 (range 52-88)	66 (range 51-80)
<b>Local tumor invasion</b>		
T1	0	0
T2	0	5
T3	17	14
T4	3	1
<b>Nodal status</b>		
N0	20	0
N1	0	14
N2	0	6
<b>Lymphatic vessel invasion</b>		
L0	16	12
L1	4	8
<b>Venous vessel invasion</b>		
V0	18	20
V1	2	0
<b>Distant metastasis</b>		
M0	20	20
M1	0	0
<b>Grading</b>		
Low grade	16	13
High grade	4	7

**Supplemental Figure 2.** Scatter plots comparing spectral count data for about 6,400 proteins and the microarray data for the corresponding genes in 6 colorectal tumors. The Spearman correlation coefficients are indicated in the plots.



Mean  $r = 0.43 \pm 0.05$