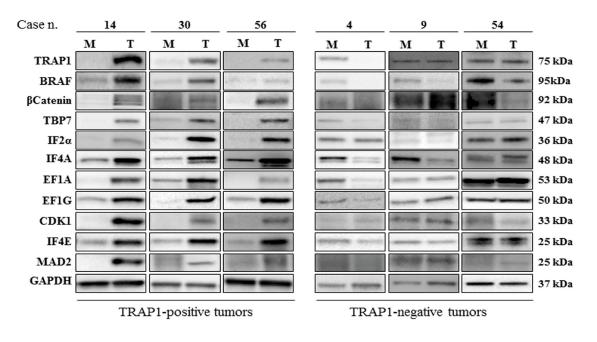
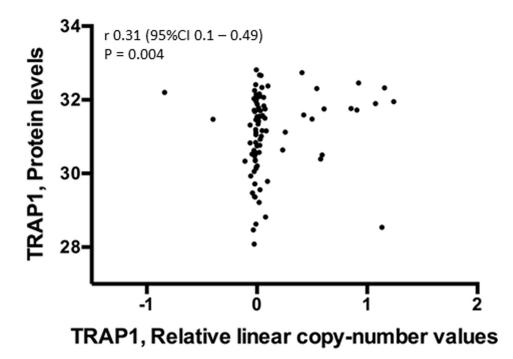
TRAP1 protein signature predicts outcome in human metastatic colorectal carcinoma



SUPPLEMENTARY FIGURES AND TABLE

Supplementary Figure 1: Co-expression of TRAP1 and its client protein network. Immunoblot analysis of TRAP1 and its client protein network in 6 representative cases of the study cohort.



Supplementary Figure 2: TRAP1 protein expression correlates with its gene copy number. Correlation between TRAP1 protein expression and its copy number linear level in TCGA Cohort_2.

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	FLA	Pase Sort	in 18 AK	BRA	s Bere	Caterin OK	, wao	2 18	1F2	alpha EF1	r _{let} i	3 Fat	
IF4A	0.3	0.19	0.17	0.12	0.07	0.19	0.18	0.26	0.45	0.14	0.28	0.29	
F1-A	TPase	0.36	0.21	0.14	0.32	-0.04	-0.35	0.09	0.01	-0.03	0.07	0.11	- (
	So	rcin 18	-0.17	0.07	0.16	0.06	0.07	0.03	0.07	-0.01	0.05	0.18	- (
			AKT	0.3	0.19	0.05	-0.09	0.04	0.05	0.18	0.16	0.06	- (
				BRAF	0.65	0.45	0.05	0.46	0.26	0.57	0.17	0.11	-
				Beta	Catenin	0.37	0.01	0.46	0.19	0.42	0.18	0.08	
						CDK1	0.39	0.38	0.32	0.38	0.25	0.3	
							MAD2	0.32	0.37	0.14	0.22	0.43	
								TBP7	0.51	0.49	0.43	0.47	
								IF2	2-alpha	0.6	0.49	0.56	
										EF1A	0.42	0.36	
											EF1G	0.44	

Supplementary Figure 3: Reciprocal correlation between TRAP1 client proteins. Correlation plot reporting Spearman r coefficients between TRAP1 network proteins.

Supplementary Table 1: TRAP1 expression in 60 human colorectal carcinomas and its distribution according to major pathological covariates

TRAP1 (60 cases)		
• Mean (±S.D.)	13.4 ± 22.23	
• Median (range)	3.15 (0.11 - 93.48)	
TNM	Median (range)	p-value
• I	2.4 (0.4 - 48.1)	
• II	3.7 (0.33 - 93.5)	
• III	4.005 (0.1 - 82.3)	0.83
• IV	2.44 (0.18 - 67.6)	
Grade		
• 1	9.33 (0.7 - 93.48)	
• 2	3.27 (0.11 - 82.24)	0.35
• 3	2.55 (0.9 - 67.6)	
Lymph nodes		
• N negative	3.72 (0.33 - 93.48)	
• N positive (1-3)	3.4 (0.16 - 79.6)	0.47
• N positive (>3)	2.44 (0.11 - 36.74)	