

ADDITIONAL MATERIAL

SUPPLEMENTARY FIGURES

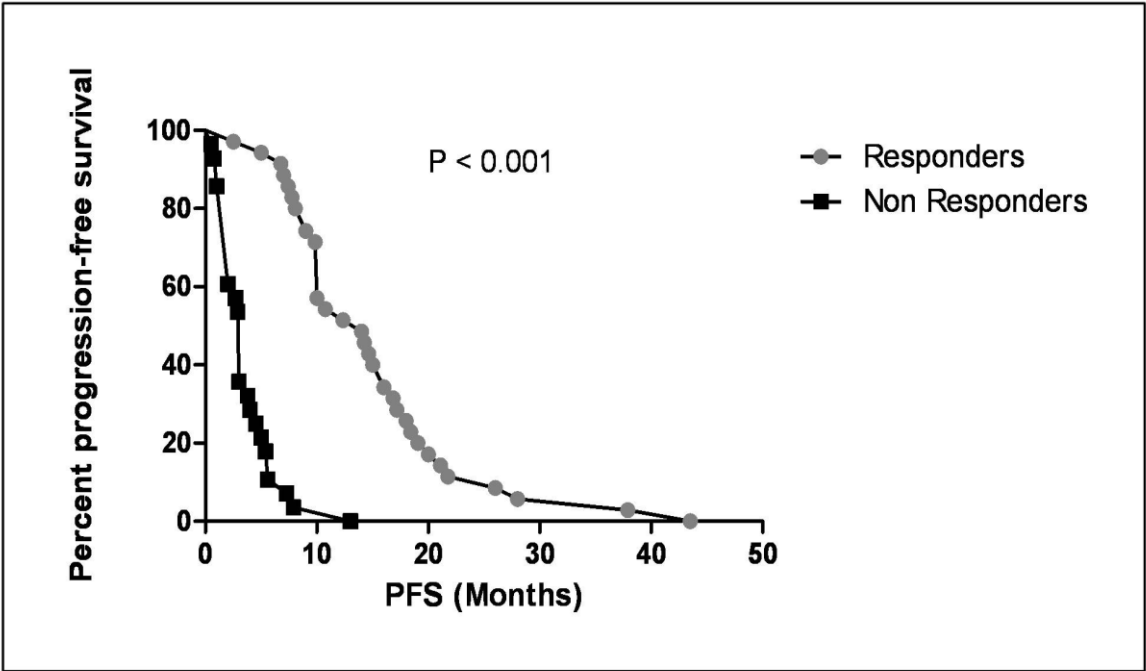


Figure S1. Kaplan Meier plots for progression-free survival (PFS) in the two cohorts (responders and non-responders) of CRC patients. The plots show a significantly different profile in responder versus non-responder patients.

	Sample	Genes						Mutations / Sample	
		KRAS ¹	NRAS	BRAF	PIK3CA	FBXW7	SMAD4		
Responders	CR	D_5427						0	
	CR	D_5442						0	
	CR	D_5058						0	
	CR	D_5033						0	
	CR	D_5038						0	
	CR	D_5031						0	
	CR	D_5032						0	
	PR	D_5449							1
		D_5426							0
		D_5432							0
		D_5434							0
		D_5444							2
		D_5050							0
		D_5048							0
		D_5056							0
		D_5272							0
		D_5071							0
		D_5039							0
		D_5065							0
		D_5066							0
		D_5041							0
		D_5040							0
	D_5450							0	
	D_5438							0	
	D_5453							1	
	D_5064							1	
	D_5063							0	
	D_5448							0	
	D_5409							0	
	D_5428							1	
D_5429							2		
D_5451							0		
D_5435							0		
D_5445							0		
D_5452							0		
D_5447							0		
D_5408							1		
Non Responders	PD	D_5070						0	
		D_5060						1	
		D_5061						2	
		D_5053						0	
		D_5034						0	
		D_5082						1	
		D_5051						0	
		D_5074						1	
		D_5035						2	
		D_5043						1	
		D_5052						1	
		D_5068						0	
		D_5037						2	
		D_5044						0	
		D_5425						1	
		D_5431						1	
		D_5433						1	
		D_5436						0	
		D_5437						0	
		D_5439						1	
		D_5443						3	
		D_5454						1	
		D_5455						1	
D_5407						3			
D_5430						1			
D_5440						0			
D_5446						1			
D_5441						1			

Mutations in Responders	3	1	1	2	1	1
Percent	8%	3%	3%	5%	3%	3%
Mutations in Non Responders	8	1	4	4	5	4
Percent	29%	4%	14%	14%	18%	14%
Total Mutations	11	2	5	6	6	5
Percent	17%	3%	8%	9%	9%	8%

KRAS ¹	NRAS	BRAF	PIK3CA	FBXW7	SMAD4
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¹ = previously undetected mutations

CR = Complete remission

PR = Partial response

SD = Stable disease

PD = Progressive disease

Figure S2. Frequencies of mutation in the six genes correlated with anti-EGFR moAb responsiveness. The figure shows the mutations detected in genes (*NRAS*, *BRAF*, *PIK3CA*, *FBXW7*, *SMAD4* and previously undetected variations at *KRAS*,) that display imbalanced frequencies in responder versus non-responder patients.

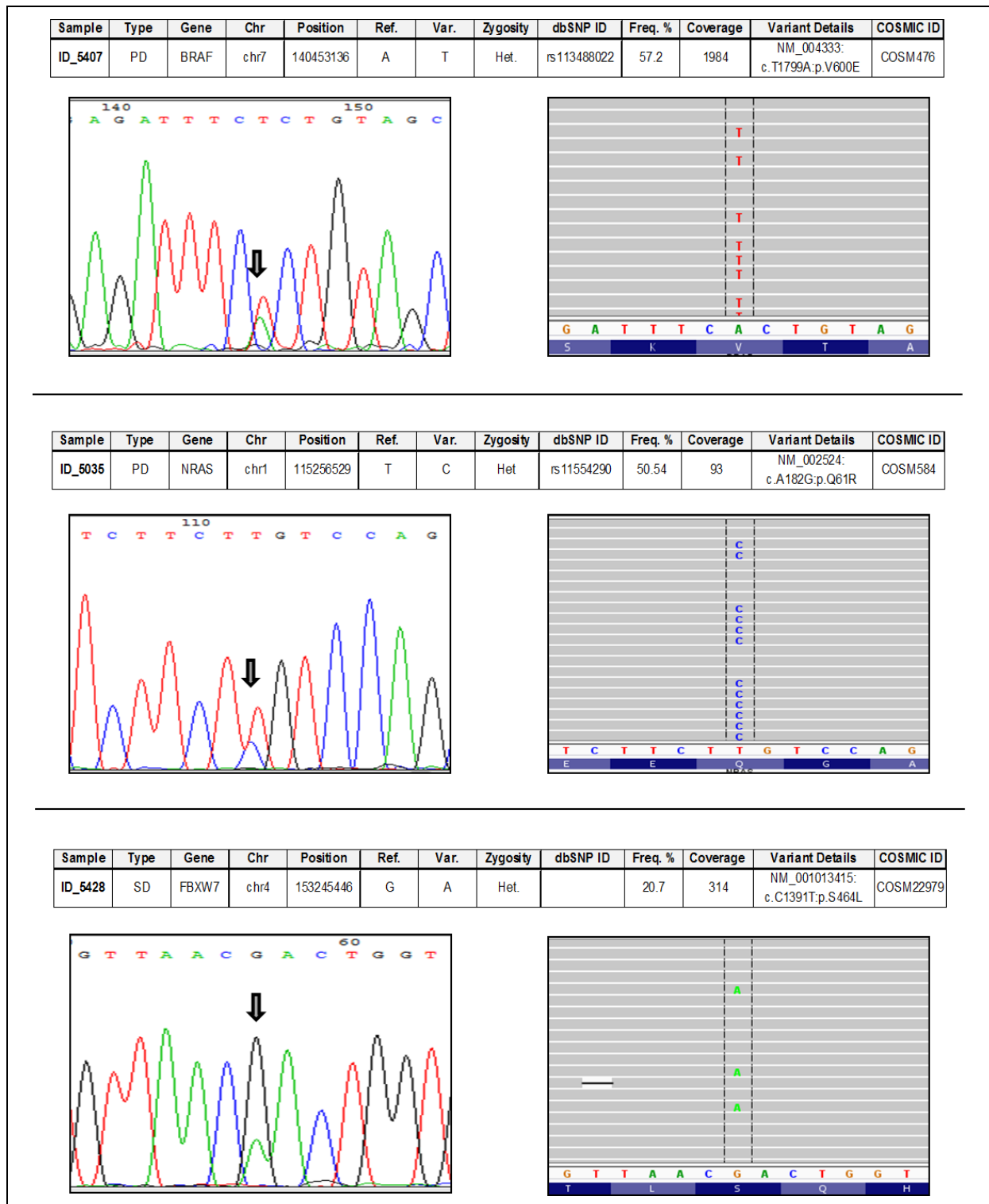


Figure S3. Sanger sequencing validation of *BRAF*, *NRAS*, and *FBXW7* mutations. All mutations found in *BRAF*, *NRAS*, and *FBXW7* were validated with Sanger sequencing. The figure shows one representative sample for each gene. On the left are displayed Sanger chromatograms, while results of NGS, showing read alignment to the reference genome, are on the right of the panel.