

Supplementary Table 2.

Experiment 1 : Putative mutations reported based on the sequencing run on the IonTorrent PGM

Segment	Relative position	RA	AA	Cov. WT	AA Freq. WT (%)	Cov. DLD1-M	AA Freq. DLD1-M (%)	P	Adj. P
APC7	1	G	T	7871	11.43	7897	7.48	0	0
APC7	233	G	A	7818	10.42	7517	14.52	0	0
APC7 (*)	94	G	-C	7897	0.05	7856	0.54	0	0
KRAS	63	G	C	7868	0.69	7929	0.13	0	2e-06
APC7	221	T	A	7298	15.42	6802	11.73	0	3e-06
TP53_exon7	239	A	+A	7766	6.10	7758	8.62	0	3e-06
TP53_exon7	25	C	A	6797	17.44	6905	13.42	0	3e-06
TP53_exon7	50	C	T	6679	11.09	6644	8.24	1e-06	5.6e-05
APC7	186	C	-G	5354	4.42	5268	2.65	2e-06	0.0007
APC7	97	T	A	7933	0.01	7916	0.26	1.1e-05	0.0037
APC7	31	G	T	7958	3.69	7955	12.46	1.3e-05	0.0043
TP53_exon7	114	T	-G	7787	852	7734	8.8	5.8e-05	0.0192
TP53_exon7(*)	161	C	T	7770	10.94	7779	0.26	0.0001	0.0496
KRAS (**)	214	G	A	5590	0.19	5204	0.36	0.1032	34.0272

Note: (*) True positive. (**) False Negative. RA: Reference allele. AA: Alternative allele. WT: wild type. DLD1-M: DLD1 – mixed sample.