

Supplementary Table 1.

Experiment 1 : Putative mutations reported based on the sequencing run on the Illumina MiSeq

Segment	Relative position	RA	AA	Cov. WT	AA Freq. WT (%)	Cov. DLD1-M	AA Freq. DLD1-M (%)	P	Adj. P
APC3	147	A	G	8033	0.49	8014	1.9	0	0
APC7	147	A	C	8004	0.07	8003	1.49	0	0
APC7 (*)	94	G	-C	7999	0.03	7999	8.25	0	0
KRAS (*)	214	G	A	8043	0.08	8047	1.43	0	0
TP53_exon8	39	T	C	8019	3.49	8016	1.53	0	0
APC8	39	C	T	8012	3.95	8017	5.96	0	9.00E-06
TP53_exon7	196	A	C	5059	11.09	4767	14.98	1.00E-06	1.60E-04
TP53_exon7	147	C	A	6627	6.41	6822	8.50	2.10E-05	0.0066
Beta_Catenin	91	G	A	8019	0.07	8015	0.37	6.80E-05	0.0225
APC2	198	G	T	8007	0.03	8003	0.28	8.70E-05	0.0297
<i>TP53_exon7 (**)</i>	<i>161</i>	<i>C</i>	<i>A</i>	<i>6058</i>	<i>5.28</i>	<i>6331</i>	<i>0.72</i>	<i>0.1741</i>	<i>57.6516</i>

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