

Figure S1. Representative H&E staining of tumors with high (80%; left) and low (20%; right) cellularity (x400).

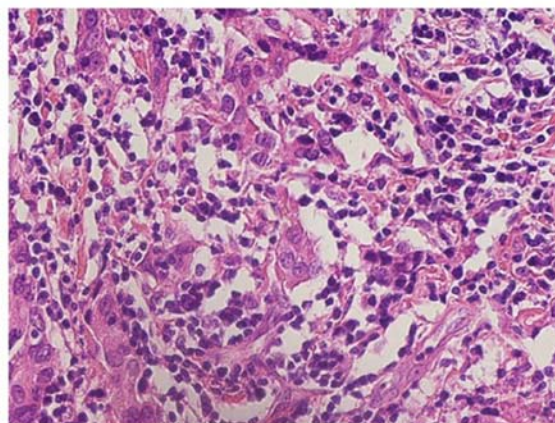
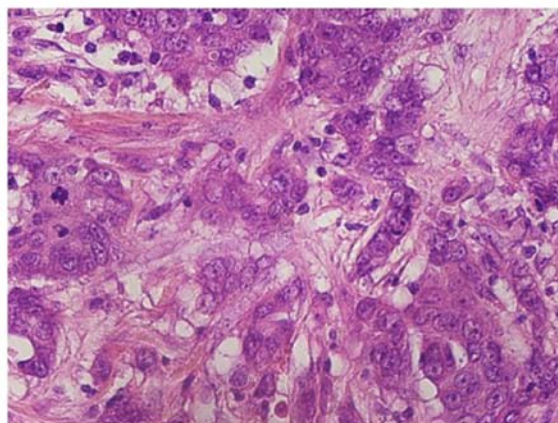


Table SI. List of the 20 genes included in multigene panel test.

A. Genes selected with high frequency of amplification

Gene	Cytoband	Region size, bp	Region, number	Coverage, %
<i>MDM4</i>	1q32	1,925	14	100.00
<i>MYC</i>	8q24.21	1,425	3	100.00
<i>PARP1</i>	1q41-42	3,748	24	99.87
<i>MUC1</i>	1q21	1,744	10	97.19
<i>CCND1</i>	11q13	988	5	100.00
<i>ERBB2</i>	17q12	4,545	29	96.99
<i>FGFR1</i>	8p11.23-22	3,321	21	100.00
<i>RPS6KB1</i>	17q23.1	1,971	17	97.77
<i>ZNF217</i>	20q13.2	3,396	5	100.00
<i>CDKN2A</i>	9p21	1,248	6	100.00

B. Genes selected with a high frequency of mutation

Gene	Cytoband	Region size, bp	Region, number	Coverage, %
<i>PIK3CA</i>	3q26.3	3,609	20	100.00
<i>TP53</i>	17p13.1	1,658	14	96.44
<i>GATA3</i>	10p15	1,435	5	100.00
<i>MAP3K1</i>	5q11.2	4,939	20	100.00
<i>CDH1</i>	16q22.1	3,036	16	100.00
<i>AKT1</i>	14q32.32	1,764	14	100.00
<i>NCOR1</i>	17p11.2	8,688	47	98.12
<i>MAP2K4</i>	17p12	1,473	12	99.86
<i>RB1</i>	13q14.2	3,327	27	99.79
<i>ESR1</i>	6q25.1	2,243	10	100.00

Table SII. Contingency table for the McNemar's test to analyze the concordance of the amplification of the four genes between MPT and OncoScan™ in Fig. 2.

A. All tumors				
Gene	MPT	OncoScan™		P-value ^a
		Amp+	Amp-	
HER2	Amp+	10	4	0.134
	Amp-	0	31	
MYC	Amp+	3	4	>0.999
	Amp-	3	35	
FGFR1	Amp+	3	2	0.480
	Amp-	0	40	
GATA3	Amp+	0	1	0.221
	Amp-	5	39	
B. High cellularity				
Gene	MPT	OncoScan™		P-value ^a
		Amp+	Amp-	
HER2	Amp+	8	0	>0.999
	Amp-	1	18	
MYC	Amp+	2	0	0.480
	Amp-	2	23	
FGFR1	Amp+	2	0	>0.999
	Amp-	0	25	
GATA3	Amp+	0	0	>0.999
	Amp-	0	27	
C. Low cellularity				
Gene	MPT	OncoScan™		P-value ^a
		Amp+	Amp-	
HER2	Amp+	2	3	0.248
	Amp-	0	13	
MYC	Amp+	1	4	0.371
	Amp-	1	12	
FGFR1	Amp+	1	2	0.480
	Amp-	0	15	
GATA3	Amp+	0	5	0.221
	Amp-	1	12	
^aMcNemar's test. Amp; amplification; MPT, multigene test.				