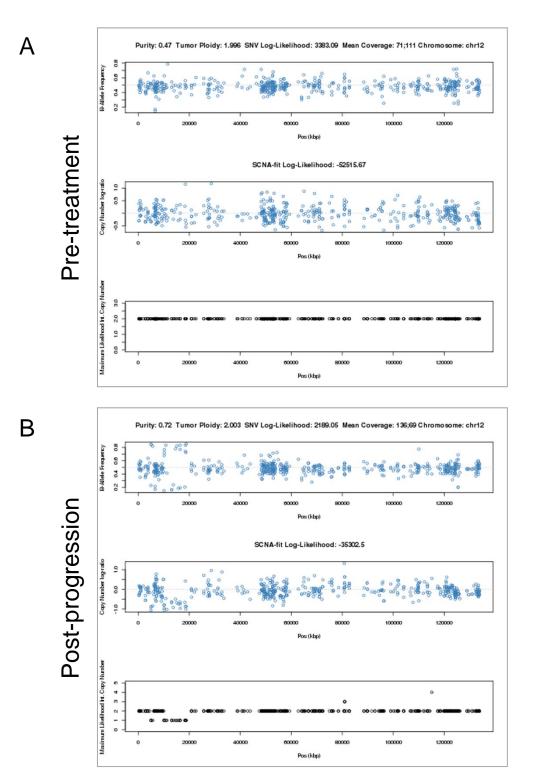
Supplemental Figure 1



Supplemental Figure 1: LOH at chromosome 12p in post-treatment sample. A). Germline allelic fractions (top), copy numbers (log2 ratio, normalized with matched blood sample, middle) and maximum likelihood tumor copy numbers (bottom) for all heterozygous germline variants in the pre-treatment sample on chromosome 12. Chromosome 12 is diploid with no evidence of LOH. B) The same plot for the post treatment sample. LOH at chr12:10,074,776-18,800,953 supported by both copy number and germline allelic fractions. In the LOH region, germline allelic fractions of about 0.22 represent variants lost in tumor and which are present in the normal contamination only; variants with allelic fraction of about 0.78 are present in tumor and normal.

Supplemental Table 1

	KI-67	рМАРК				pEGFR				рМЕК			
Block	% positive	1+	2+	3+	H-score	1+	2+	3+	H-score	1+	2+	3+	H-score
Pre-treatment	13%	20%	5%	0%	35	0%	0%	0%	0	50%	0%	0%	50
Post-progression	16%	10%	20%	0%	50	30%	0%	0%	30	70%	0%	0%	70

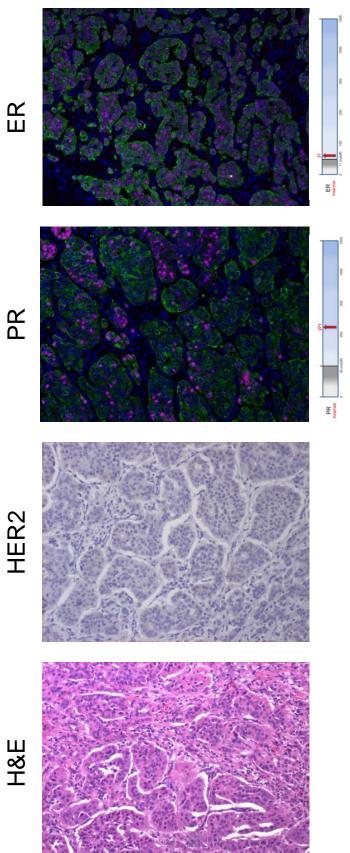
	рАКТ			pS6-235/236				pS6-240/244				
Block ID#	1+	2+	3+	H-score	1+	2+	3+	H-score	1+	2+	3+	H-score
Pre-treatment	0%	0%	0%	0	40%	0%	0%	40	20%	30%	20%	140
Post-progression	5%	5%	0%	15	10%	0%	0%	10	30%	10%	30%	140

	PTEN				E	ER	PR		
Block ID#	1+	2+	3+	H-score	Status	AQUA Score	Status	AQUA Score	
Pre-treatment	70%	30%	0%	130	Positive	31	Positive	271	
Post-progression	80%	0%	0%	80	Positive	312	Positive	1305	

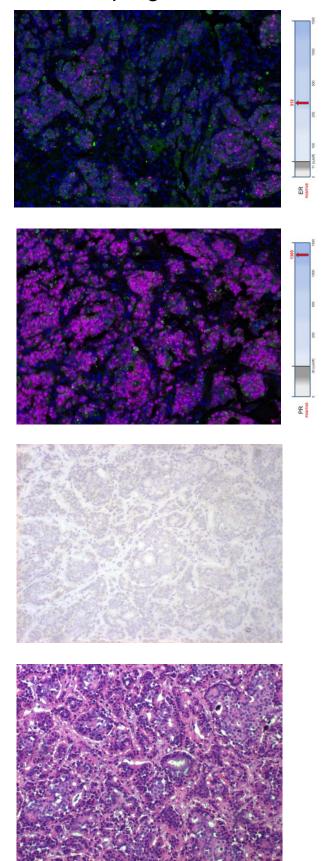
Supplemental Table 1. Immunohistochemical analysis of tumor samples.

Supplemental Figure 2

Pre-treatment



Post-progression



РР