

Table S3. Distribution of concurrent genetic alterations

Type of concurrent genetic alterations identified	n	%
<i>EGFR</i> mutation + <i>NRAS</i> mutation	1	(0.8)
<i>EGFR</i> mutation + <i>EGFR</i> copy number gain	1	(0.8)
<i>EGFR</i> mutation + <i>PIK3CA</i> copy number gain	1	(0.8)
<i>KRAS</i> mutation + <i>PIK3CA</i> mutation	1	(0.8)
<i>PIK3CA</i> mutation + <i>PIK3CA</i> copy number gain	3	(2.4)
<i>PIK3CA</i> copy number gain + <i>EGFR</i> copy number gain	2	(1.6)
<i>PIK3CA</i> copy number gain + <i>FGFR1</i> copy number gain	2	(1.6)
<i>KRAS</i> mutation + <i>EGFR</i> copy number gain + <i>PIK3CA</i> copy number gain	1	(0.8)