

Supplemental Table 7 - Statistical analyses of associations between *EGFR* polymorphisms and tumoral *EGFR* genetic alterations (*EGFR* a

	<i>EGFR</i> -216G/T				<i>EGFR</i> -191C/A				<i>EGFR</i> (CA)	
	GG	GT	TT	<i>p</i> -value	CC	CA	AA	<i>p</i> -value	SL	LL
<i>EGFR</i> Amplification¹										
Absent (n=18)	12	5	1		11	6	1		5	5
Present (n=16)	12	3	1	0.825	9	4	3	0.475	2	5
<i>EGFRvIII</i> Mutation¹										
Absent (n=32)	21	9	2		19	10	3		8	7
Present (n=8)	6	1	1	0.594	6	1	1	0.568	0	3
<i>EGFR</i> Genetic Alterations²										
Absent (n=17)	11	5	1		10	6	1		5	5
Present (n=17)	13	3	1	0.717	10	4	3	0.497	2	5

¹ *EGFR* amplification and *EGFRvIII* mutation were previously reported (13).

² Genetic alterations defined as presence of either *EGFR* amplication, *EGFRvIII* mutation, or both.

amplification or *EGFRvIII* mutation).

<i>EGFR</i> (CA)n repeat (17≤n<17)		<i>EGFR</i> (CA)n repeat (16≤n<16)				<i>EGFR</i> (CA)n repeat (18≤n<18)				<i>EGFR</i> (CA)n repeat (
SS	<i>p</i> -value	SL	LL	SS	<i>p</i> -value	SL	LL	SS	<i>p</i> -value	S	L
8		6	7	5		11	6	1		11	7
9	0.540	3	7	6	0.614	9	4	3	0.475	11	5
17		10	10	12		6	3	23		22	10
5	0.256	0	4	4	0.183	0	2	6	0.252	5	3
7		6	7	4		4	2	11		10	7
10	0.404	3	7	7	0.403	1	3	13	0.338	12	5

(36≤sum<36)

p -value

0.642

0.736

0.473
