

**S2 Table.** Genomic characteristics based on recurrence status (n=105).

<b>Characteristic</b>	<b>Total (n=105)</b>	<b>Recurrence (n=50)</b>	<b>No recurrence (n=55)</b>	<b>p-value</b>
<i>EGFR</i> mutation				< 0.001
E19del	40 (38.1)	22 (44.0)	17 (30.9)	
L858R	56 (53.3)	19 (38.0)	38 (69.1)	
Others	9 (8.6)	9 (18.0)	0 =	
<i>TP53</i> mutation				0.123
Mutant	17 (16.2)	11 (22.0)	6 (10.9)	
Wild type	88 (83.8)	39 (78.0)	49 (89.1)	
<i>RPS6KB1</i> amplification				< 0.001
Amplified	25 (23.8)	21 (42.0)	4 (7.3)	
Wild type	80 (76.2)	29 (58.0)	51 (92.7)	
<i>EGFR</i> amplification				0.038
Amplified	17 (16.2)	12 (24.0)	5 (9.1)	
Wild type	88 (83.8)	38 (76.0)	50 (90.9)	
<i>MDM2</i> amplification				0.160
Amplified	12 (11.4)	8 (16.0)	4 (7.3)	
Wild type	93 (88.6)	42 (84.0)	51 (92.7)	
p53 pathway				0.001
Altered	39 (37.1)	27 (54.0)	12 (21.8)	
Wild type	66 (62.9)	23 (46.0)	43 (78.2)	
PI3K pathway				<0.001
Altered	29 (27.6)	23 (46.0)	6 (10.9)	
Wild type	76 (72.4)	27 (54.0)	49 (89.1)	
Cell cycle pathway				0.008
Altered	22 (21.0)	16 (32.0)	6 (10.9)	
Wild type	83 (79.0)	34 (68.0)	49 (89.1)	
NPA				< 0.001
1	40 (38.1)	10 (20.0)	30 (54.5)	
2	32 (30.5)	14 (28.0)	18 (32.7)	
3	24 (22.9)	17 (34.0)	7 (12.7)	
4	9 (8.6)	9 (18.0)	0 =	
TMB				0.001
Low (< 4.7)	49 (46.7)	15 (30.0)	34 (61.8)	

High ( $\geq 4.7$ )	56 (53.3)	35 (70.0)	21 (38.2)
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Values are presented as number (%). *EGFR*, epidermal growth factor receptor; E19del, exon 19 deletion; NPA, number of pathway alterations; TMB, tumor mutational burden.