Supplementary Table 4. Number of homozygously deleted genes in lung cancer cell lines according to genetic alterations

Gene	Genetic alteration	No. of cell line	No. of genes homozygously deleted			*P* by t-test	
			Mean	±	SD	univariate analysis	multivariate analysis
Oncogene							
EGFR	+	4	14.5	±	9.1	0.14	-
	-	69	5.5	±	11.9		
KRAS	+	12	3.3	±	3.6	0.10	-
	-	61	6.5	±	12.8		
NRAS	+	4	6.0	±	9.4	1.00	-
	-	69	6.0	±	12.1		
PI3KCA	+	7	8.3	±	12.0	0.62	-
	-	66	5.8	±	11.9		
Tumor suppressor gene							
TP53	+	65	6.5	±	12.5	0.027	0.42
	-	9	2.0	±	3.6		
CDKN2A/p16	+	42	9.7	±	14.5	0.00041	0.018
	-	31	1.0	±	2.5		
LKB1	+	21	9.6	±	12.3	0.068	0.29
	-	53	3.7	±	6.4		
PTEN	+	8	0.6	±	1.2	0.00033	0.62
	-	66	6.6	±	12.4		