

S14 Table. Variant allele frequency distribution of genes commutated with SETD2

Gene	Chr	Start	P1					P5	P8
			AAH1	MIA1	MIA2	ADC1	ADC2	MIA	AIS
<i>AMOT</i>	X	112,066,317	-	-	-	-	6%	-	-
<i>GPR149</i>	3	154,147,283	5%	-	-	-	-	-	-
<i>HLTF</i>	3	148,786,108	-	5%	-	-	-	-	-
<i>PRRG2</i>	19	50,086,960	-	-	-	-	-	5%	-
<i>PRRG2</i>	19	50,093,224	-	-	-	-	-	-	8%
<i>SPEG</i>	2	220,331,948	-	-	-	16%	20%	-	-
<i>TLL5</i>	14	76,173,966	7%	9%	5%	-	4%	-	-

The candidate gene list was from the top 20 in the Cancer Genome Atlas (TCGA) Pan-Lung Cancer (Nature genetic 2016). AAH, atypical adenomatous hyperplasia; ADC, adenocarcinoma; AIS, adenocarcinoma *in situ*; MIA, minimally invasive adenocarcinoma.

Reference

1. Bailey MH, Tokheim C, Porta-Pardo E, Sengupta S, Bertrand D, Weerasinghe A, et al. Comprehensive characterization of cancer driver genes and mutations. Cell 2018;173:371-85.