

Screening of histone modifier gene mutations in peripheral T-cell lymphomas, not otherwise specified (PTCL-NOS)



Tumor samples of 125 patients with PTCL-NOS



Targeted sequencing of histone modifier genes



91 somatic mutations identified in 48% (60/125) of patients with PTCL-NOS

Types of mutations

Missense mutations	n=72
Nonsense mutations	n=10
Frameshift	n=9

Single-nucleotide variation C>T/G>A

Categories

I	Histone methylation genes	KMT2D	→	H3K4 methyltransferase	20.0%
		SETD2	→	H3K36 methyltransferase	4.8%
		KMT2A	→	H3K4 methyltransferase	2.4%
		KDM6A	→	H3K27 demethylase	0.8%
		II	Histone acetylation genes	EP300	→
CREBBP	→	H3K18 acetyltransferase		4.0%	
III	DNA methylation genes	TET2		12.0%	
		TET1		3.2%	
		DNMT3A		3.2%	
IV	Chromatin remodeler genes	ARID1B		4%	
		ARID2		1.6%	

Histone modifier gene mutations, particularly those involved in histone methylation and acetylation, are significantly associated with tumor chemoresistance and disease progression of PTCL-NOS