AVB-CG
CENTRE DE RÉFÉRENCE
ATRÉSIE DES VOIES BILIAIRES
ET CHOLESTASES GÉNÉTIQUES

Mutation sequence analysis			
Contributed by : CHU Lyon			
HGVS nomenclature (NM_000295.4)			
Nomenclarure including the signal peptide			
c.863A>T			
Type of variation	Mutation Location	Genetic background	ACMG classification
AAT variant	Exon 3	M1 Val	Pathogenic
Comments			

AAT variant and Q0 alleles			
Variant name	Also Known as	Pathogenicity	HGVS nomenclature protéine
S		Deficient	p.Glu288Val

3D position of aa affected	Mobility on polyacrylamide gel	Mobility on agarose gel
	S	S

AATserum level (g/L)		Anti-elastolytic activity (IU/L)	
Heterozygous	**Homozygous**	**Heterozygous**	**Homozygous**
0.85-1.75	0.56-1.2	16160	12690
Comments			
The Glu264Val mutation prevents the formation of a salt bridge, but the secretion of the protein is less impaired than in case of the Z mutation, and there is no accumulation in the liver despite a low polymerization rate.			
Occurrence			
Ethnic background without frequency range :			
Ethnic background and frequency			

Frequency range		Group tested	
from (%)	To (%)	Size	Description (who was tested)
5.00	10.00		

Occurrence comments
Prevalence in Caucasian populations

Overall comments

Occurrence comments
The S variant is only associated per se with a pulmonar injury. However, in association with the Z variant, it can form heteropolymers leading to hepatic injury.

References n°1		
Medline ID	**Authors**	**Title**
8901864	Elliott PR,Stein PE,Bilton D,Carrell RW,Lomas DA	Structural explanation for the deficiency of S alpha 1-antitrypsin.

Journal	Year	Volume	Num	Pp
Nature structural biology	1996	3	11	910-1

References n°2		
Medline ID	**Authors**	**Title**
15994391	Dahl M,Hersh CP,Ly NP,Berkey CS,Silverman EK,Nordestgaard BG	The protease inhibitor PI*S allele and COPD: a meta-analysis.

Journal	Year	Volume	Num	Pp
The European respiratory journal	2005	26	1	67-76

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