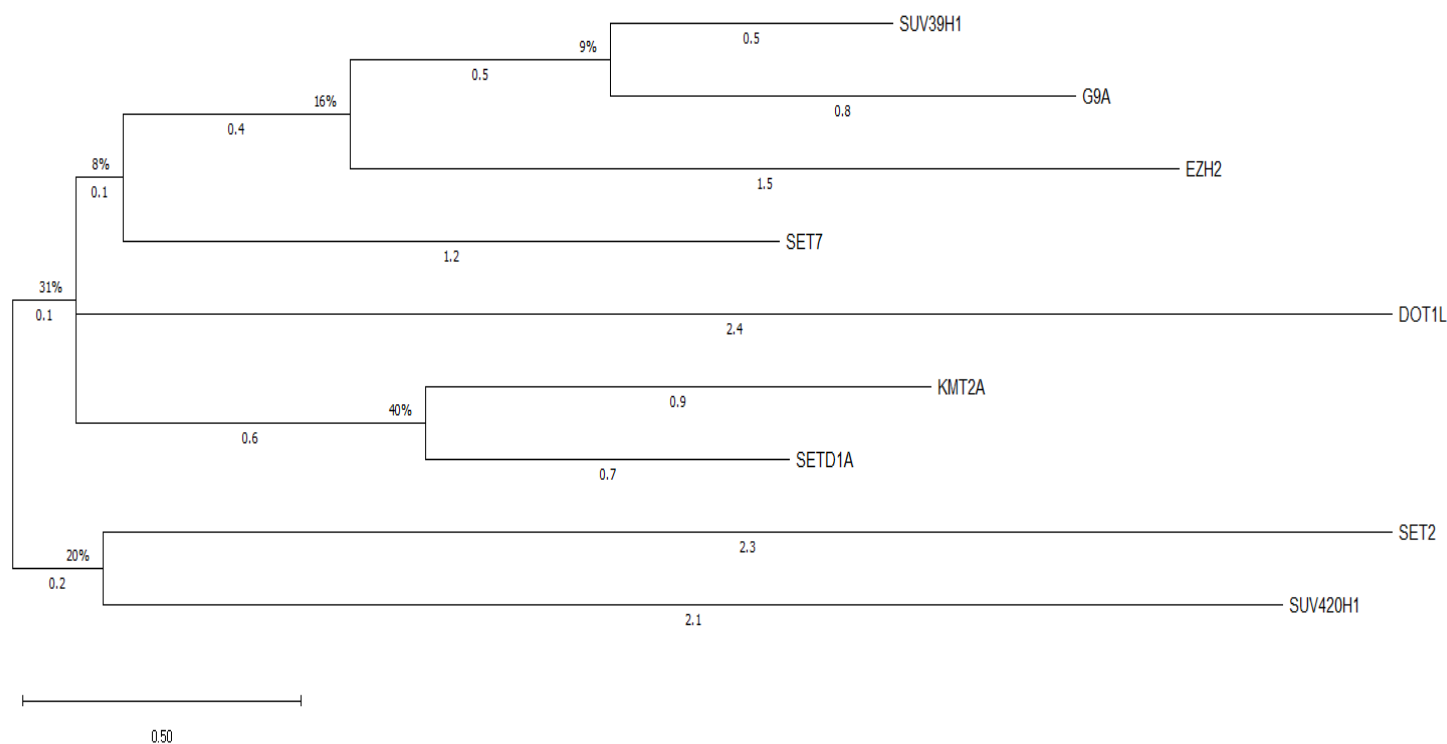


# Phylogenetic Analysis of *Homo Sapien* Histone Methyltransferases



**Figure:** Molecular Phylogenetic analysis of Histone Methyltransferases in *Homo Sapiens* using MEGAX software. Node roots of tree list different KMT genes all found in humans. Summary statistics of tree creation are provided in table below.

**Table:**

[General Info]		
No. of Taxa	=	9
No. of Sites	=	4229
[Analysis Settings]		
Initial Tree for ML	=	Make initial tree automatically (Default = NJ/BioNJ)
[Analysis Statistics]		
Execution Time	=	35.644 (seconds)
Peak Memory Used(Working Set)	=	349.402 (MB)
Sum of branch lengths	=	14.264
Model	=	Jones-Taylor-Thornton (1992) model
Num of params	=	15

Num of rates	= 1
AICc	= 74412.072
BIC	= 74524.643
LnL	= -37191.018
Invar	= n/a
Gamma	= n/a