

Variants of the H1J/H1J diplotype

Locus	Genotype	Ref	Observe	Type	Genes	Length	% Frequer	Exon	Transcript	Coding	Amino Acid Char
chr17:44061025	T/T	C	T	SNV	MAPT	1	99.77	6	NM_001123(c.855C>T		p.(=)
chr17:44067382	C/C	T	C	SNV	MAPT	1	100.00	8	NM_001123(c.1321T>C		p.Tyr441His
chr17:44104612	TG/TG	T	TG	INDEL	MAPT	1	100.00	15	NM_001123(c.5406_5407insC		p.?
chr17:44105395	G/G	A	G	SNV	MAPT	1	99.98	15	NM_001123(c.6189A>G		p.?

Variant Effect	dbSNP	ClinVar	Coverage	MAF
synonymous	rs63750222	Benign	3998	0.11
missense	rs2258689	Benign	1676	0.313
unknown	rs151340107,rs	Benign	3972	0.205
unknown	rs7521	Benign	3996	0.386 (ref)