

S2 Figure: Predicted amino acid sequences of the wildtype and mutant *MKLN1* proteins

Genetic variant:	Chr14:5,731,405T>G	(CanFam 3.1 assembly)
	<i>MKLN1</i> :c.400+3A>C	(XM_005628367.3)
	<i>MKLN1</i> :r.312_400del	(XM_005628367.3)
	<i>MKLN1</i> :p.(Gly105SerfsTer10)	(XP_005628424.1)

wildtype	maaggavaaa pecrllpyal hkwssfssty lpenilvdkp ndqssrwsse snyppqylil	60	1..160	discoidin domain
mutant	maaggavaaa pecrllpyal hkwssfssty lpenilvdkp ndqssrwsse snyppqylil	60		
wildtype	klerpaivqn itfgkyekth vcnlkkfkvf ggmneenmte llssglnkndy nketftlkhh	120		
mutant	klerpaivqn itfgkyekth vcnlkkfkvf ggmneenmte llsssalivg tql	113		
wildtype	ideqmfpcrf ikivpllswg psfnfsiywv elsgiddpdv vqpclnwysk yregeairlc	180	172..204	LisH domain
wildtype	lkhfrqhnyt eafeslqkkt kialehpmlt dlhdklvkkg dfdaceelxe kavndglnfnq	240	206..258	CTLH domain
wildtype	yisqqeykpr wsqiipkstk gdgednrpgm rgghqmvidv qte	300	284..330	Kelch 1
wildtype	waysvkenqw tcisrdteke ngpsarschk mcidiqrrqi ytlgryldss vrnsklsksd	360	339..391	Kelch 2
wildtype	fyrydidtnt wmlsedtaa dggpklyfdh qmcmdsekhn iytfggrilt cngsvddsra	420	408..458	Kelch 3
wildtype	sepqfsglfa fncqcqtwk1 lredscnagp ediqsrighc mlfhsknrcl yvfggxrskt	480	469..515	Kelch 4
wildtype	ylndffsydv dsdhvdiisd gtkkdsqmv mtgftqrati dpelneihvl sglskdkekr	540	526..578	Kelch 5
wildtype	eenvrnsfwi ydivrnsWSC vykndqaakd npskslqee pcpfrfahqlv ydelhkvhyl	600	597..651	Kelch 6
wildtype	fggnpgkscs pkmrlddfws lklcrpskdy llrhckylir khrfeekaqm dplsalkylq	660		
wildtype	ndlyitvdhs dpeetkefql lasalfksgs dftalgsdv dhyaqrtql fdtlvnffpd	720		
wildtype	smtppkgnlv dlitl	735		

An alignment of the canine wildtype *MKLN1* protein with the predicted translation product of the mutant transcript is shown. Skipping of exon 4 leads to a frameshift and an early premature stop codon. The predicted mutant protein lacks 630 amino acids (86%) of the wildtype protein. The wildtype canine *MKLN1* protein has the same length of 735 amino acids as the human *MKLN1* protein (NP_037387.2) and differs in only 6 amino acids from its human homolog, which corresponds to 99.2% sequence identity. Important functional domains of *MKLN1* are highlighted and annotated.