Only Motif Sites	Moti	if Sites+Scanned Sites ? Motif Location ?	All Sequences <table-cell></table-cell>										
BOVIN- KRTAP1-1.CDS	1.13e-4	41 +						1					
KRTAP1-2.CDS	7.27e-4	44 -						_					
KRIAPI-3.CDS		•											
KRTAP1-4.CDS	4.65e-4	42 -											
CANFA- KRTAP1-1.CDS CANFA-	3.89e-4	44 - 45 ⁺											
CANFA- KRTAP1-2.CDS CANFA- KRTAP1-3.CDS	2.20e-4	44 +											
KRTAP1-4.CDS	5.38e-4	45 +											
KRTAP1-1 CDS	1.62e-3	39 +											
HORSE-	1.08e-4	42 +									L		
KRTAP1-2.CDS HORSE- KRTAP1-3.CDS HORSE- KRTAP1-4.CDS	2.37e-4	42 +											
KRTAP1-4.CDS HUMAN-	2.40e-4	42 -				_						_	
KRTAP1-1.CDS	1.908-4	44 _											
HUMAN- KRTAP1-3.CDS HUMAN- KRTAP1-4.CDS	2.30e	44 + _											
KRTAP1-4.CDS HUMAN- KRTAP1-5.CDS	1.43e-4	47 +											
KRTAP1-1.CDS	2.73e-3	37 +											
KRTAP1-2.CDS	7.07e-4	40 -			_								
LOXAF- KRTAP1-3.CDS	2.23e-4	40 +											
LOXAF- KRTAP1-4.CDS MACMU-	4.09e-4	40 -											
KRTAP1-1.CDS													
KR IAP1-2.CD3		•											
MACMU- KRTAP1-3.CDS MACMU- KRTAP1-4.CDS MOUSE-		•											
KRIAPI-I.CDS		•											
KRTAP1-2.CDS	6.68e-4	42 -											
KRTAP1-3.CDS	1.22e-3	33 +											
KRTAP1-4.CDS	2.25e-3	38 _											
KRTAP1-1.CDS RABIT-													_
KRTAP1-2.CDS RABIT-													
KABII- KRTAP1-3.CDS RABIT- KRTAP1-4.CDS RAT- KRTAP1-1.CDS RAT- KRTAP1-2.CDS	1.36e-4	40 +							1				
RAT- KRTAP1-1.CDS	2.33e-4	43 +											
KR IAP1-2.003		•											
KRTAP1-3.CDS	0.040												
KRIAP1-4.CDS													
KRTAP1-1.CDS													
SHEEP- KRTAP1-2.CDS SHEEP- KRTAP1-3.CDS	1.32e-4	40 +											
KRTAP1-3.CDS SHEEP- KRTAP1-4.CDS	2.39e-4	41 +											

Figure S2. MEME identifies copies of the 30 bp intragenic *KRTAP1* repeat at both ends of the gene.

MEME output showing the positions of 30 bp repeat motifs amongst all *KRTAP1-n* copies from all ten mammalian species. The red boxes represent the previously identified 30 bp repeat that is present at the 5' and 3' ends of the gene and varies in copy number between repeat copies within and between species. Other colored boxes are other motifs detected by MEME, and are predominantly motifs shared between rather than within genes.