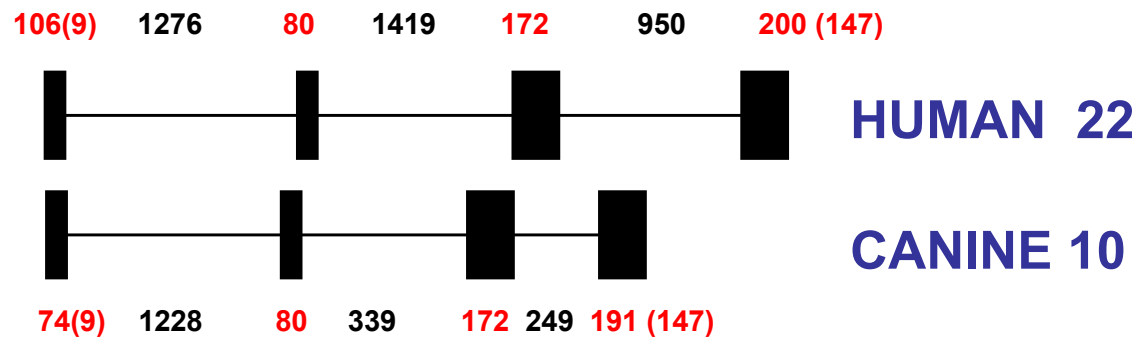


SUPPLEMENTAL FIGURE 1. Galectin-1 (Prototypical) The cloned cDNA has the same nucleotide and amino acid sequence as that predicted by the canine genome data base. A model of the gene structure is shown for human and dog with exons as black boxes. The numbers represent base pairs for exons (red) and introns (black). The numbers in parentheses for N-terminal and C-terminal encoding exons are base pairs within the coding sequence. The underlined residues are within the carbohydrate recognition domain (CRD). The symbols under the aligned sequences note identity (*), conserved residues (colon), semi-conserved residues (period) or non-conserved residues (blank spaces).

Chromosome #



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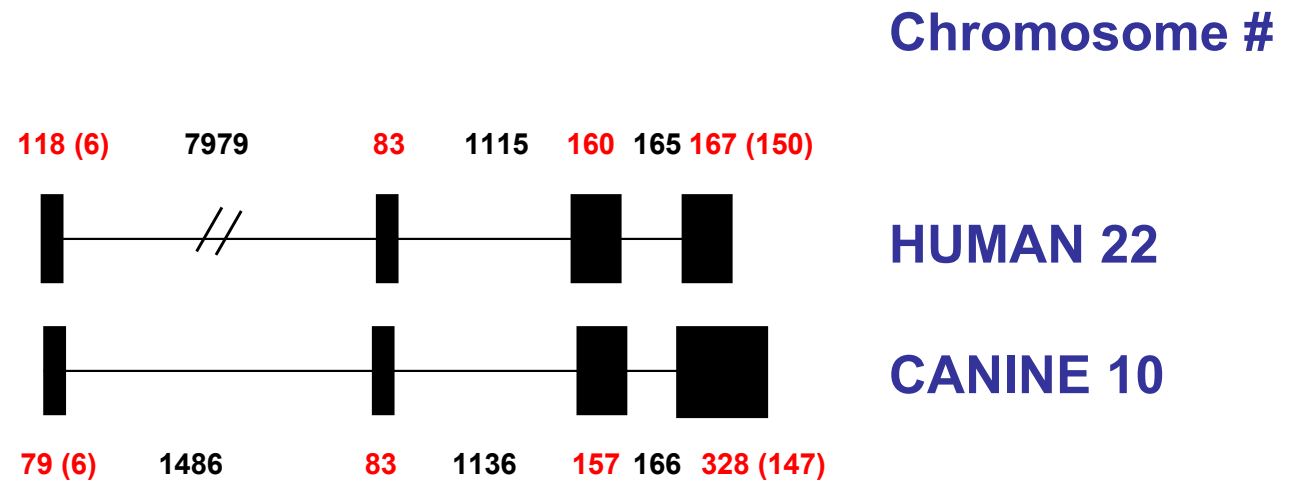
dog_G1 MACGLVASNLSLKPGQCLRVQCEVVPEAKSFVLNLGKDGDNLCLHFNPRFEAHGDVNTIV 60
hum_G1 MACGLVASNLNLPGECLRVGEVAPDAKSFVLNLGKDSNNLCLHFNPRFNAHGDANTIV 60
***** . ****:****: **.*:*****. :*****:****. ****

dog_G1 CNSKDGGAWGEELRESAFPFPQGTVTEVCISFDQADLTIKLPDGYTFKFPNRLNLEAISY 120
hum_G1 CNSKDGGAWGTEQREAVFPFQGSVAEVCITFDQANLTVKLPDGYEFKFPNRLNLEAINY 120
***** * **: .*****:*:****:****:***:***** ***** . *

dog_G1 LAADGDMKIKCLAFD 135
hum_G1 MAADGDFKIKCVAFD 135
:*****:****:***

```

SUPPLEMENTAL FIGURE 2. Galectin-2 (Prototypical) Cloned cDNA has the same nucleotide and amino acid sequence as that predicted by the canine genome data base except that we found Val124 is Leu124 in our clone (in red). Details of drawing are described above.



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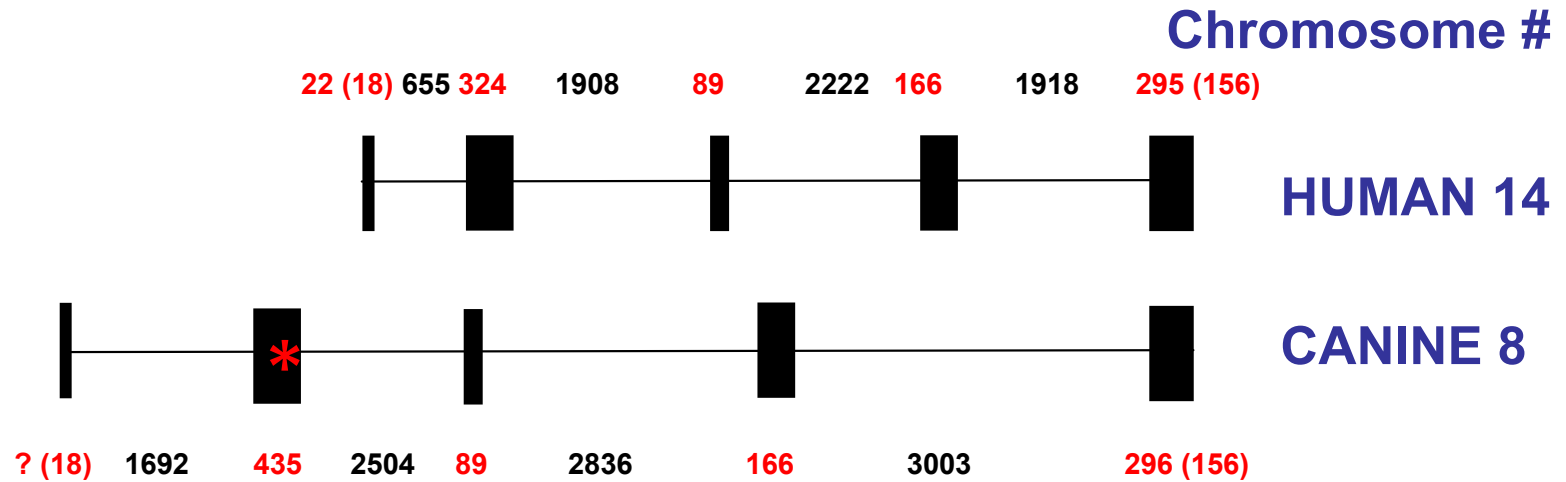
dog_G2  MSGKFEVMNMDMKLGGTLKIKGKIAGDADGFVINLGQSDKLNLFNPRFHESVIVCNSR 60
hum_G2  MTGELEVKNMDMKPGSTLKITGSIADGTDGFVINLGQGTDKLNLFNPRFSESTIVCNSL 60
*:*:;* ***** *.*****.*.**..:*****:***** **.******

dog_G2  DG-NWGQEQRDKHMCFSPGSEVKFTVTFENDGFVKVLPDGHOLTFPNRLGHSHLSYLGVQ 119
hum_G2  DGSNWGQEQREDHLCFSPGSEVKFTVTFESDKFKVLPDGHELTFPNRLGHSHLSYLSVR 120
** *****:.*:*****.* *****:*****.*:

dog_G2  GGLKLSSFKIE- 130
hum_G2  GGFNMSSFKLKE 132
**:::****:

```

SUPPLEMENTAL FIGURE 3. Galectin-3 (Chimeric) The cloned cDNA has the same nucleotide and amino acid sequence as that predicted from the canine genome data base, including the six 9-mer repeats as indicated* (also see box). Details of drawing are described above.



9-mer repeat:	
Q-A/G-P-P-G-G/A/P/T-Y-P-G	
Dog	6
Cow	4
Mouse, Pig	3
Human, Rat	2
Rabbit	1

```

Dog_G3  MADSFSLNDALSGSGNPNPQGWPWPWGNQPAGAGGYPGASYPGAYPGQAPPGGYPGQAPP 60
Human  MADNFSLHDALSGSGNPNPQGAWGNQPAGAGGYPGASYPGAYPGQAPPGAYPGQAPP 60
      ***.***:*****.*****.*****
Dog G3  GGYPGQAPPGGYPGQAPPGGYPGQAPPGTYPGPTAPAYPGPTAPGTQPGQP 120
Human  GAYPG-----APGAYPGAPAPGVYPPG-----P 83
      *.***          .**.* ** .**.* ** *
Dog G3  SGPGAYPPPGQPSAPGAYPAAGPFGIPAGPLTVPYDLPLGGVKPRMLITILGTVRPSAN 180
Human  SGPGAYPSSGQPSAPGAYPATGPYGAAGPLIVPYNLPLGGVVPRLITILGTVKPNAN 143
      *****.*****:***:***** *****:***** *****:*. **
Dog G3  RLALDFKRGNDVAFHFNPRFNEDNKRIVICNTKLDNIWGKEEROAAPPFESGKPFKIQVL 240
Human  RIALDFQRGNDVAFHFNPRFNENRRVIVICNTKLDNNWGREERQSVFPFESGKPFKIQVL 203
      *:***:*****:*.***** **:* **:*:*****
Dog G3  VESDHFQVAVNDAHLLQYNHRMKNLPEISKLGISGDIDLTSASYAMI 287
human  VEPDHFQVAVNDAHLLQYNHRVKKLNEISKLGISGDIDLTSASYNMI 250
      **.*****:*. ***** **

```

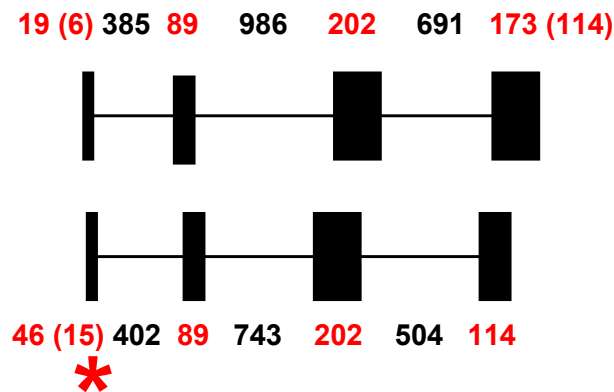

SUPPLEMENTAL FIGURE 5. Galectin-7 (Prototypical) The cloned cDNA is very different than that predicted by the canine genome data base where it is fused with Galectin-4 and predicted to have an additional exon between coding exons #3 and #4. The cloned canine cDNA is similar to all other mammalian galectin-7 sequences, although there are variations in the first coding exon as noted in the box*. Details of drawing are described above.

Chromosome #

HUMAN 19

CANINE 1

1 st coding exon * :	
Mouse	2 aa
Dog, cow	5aa
Horse	6aa

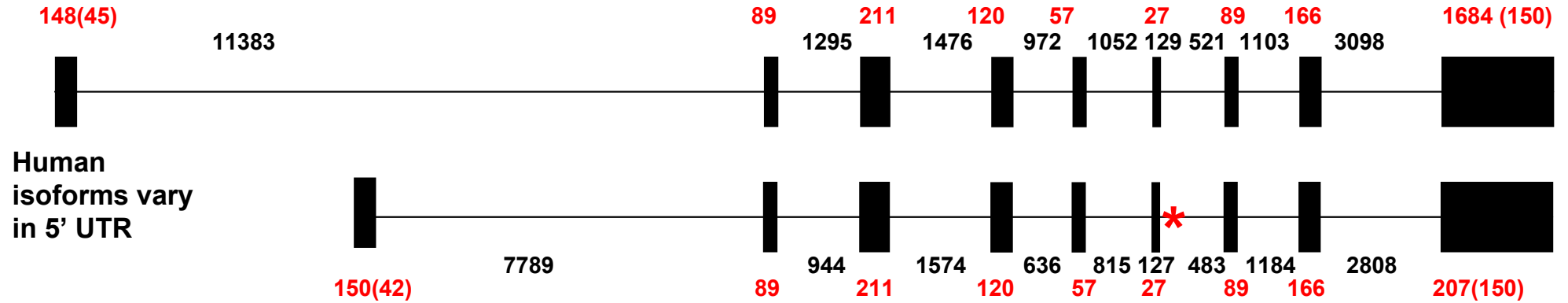


dogLGALS7	<u>MAGSSNVPHKTS</u> <u>LPEGIRVGTVMRIRGVV</u> <u>PNKAGRFYVNLLCGEAPGSE</u> <u>AALHFN</u> <u>PRLDE</u>	60
humLGALS7	--- <u>MSNVPHKSS</u> <u>LPEGIRPGTVLRIRGLVPP</u> <u>NASRFHVNLLCGEEQ</u> <u>GSDAALHFN</u> <u>PRLDT</u>	57
	*****:***** **:*:**:* *:*:**:***** **:******	
dogLGALS7	<u>STVVFNTLEQ</u> <u>AWGREERG</u> <u>TGIPFORGQ</u> <u>FDVLLIATDEG</u> <u>FKAVVGDSEY</u> <u>HHFRYRIPPA</u>	120
humLGALS7	<u>SEVVFNSKEQ</u> <u>GSWGREERG</u> <u>PGVPPFORGQ</u> <u>PFEVLI</u> <u>IASDDG</u> <u>FKAVVGD</u> <u>AQYHHFRHRLPLA</u>	117
	* ****: ***:*****.*:******:*:**:*:*:**:*****:*****:*:* *	
dogLGALS7	<u>RVRLLE</u> <u>VGGDLQ</u> <u>LESVS</u> <u>VF</u>	139
humLGALS7	<u>RVRLV</u> <u>EGGDV</u> <u>QLD</u> <u>SVRI</u> <u>F</u>	136
	****:*****:**:* * :*	

SUPPLEMENTAL FIGURE 6. Galectin-8 (Tandem repeat) The cloned cDNA has the same nucleotide and amino acid sequence as that predicted by the canine genome data base, except that it lacks the seventh coding exon of 123 bp within the linker region* consistent with the short isoforms. Details of drawing are described above.

HUMAN 1

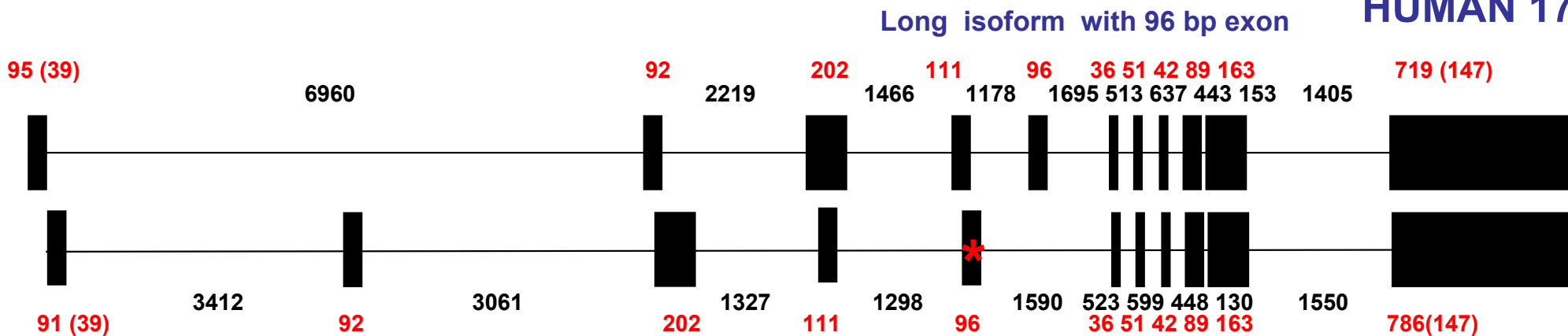
Short version of isoform B



Human isoforms vary in 5' UTR

CANINE 4

dogLGALS8	<u>-MLSLKNLQNI IYNPVI PYVGTIPGQLEPGTLIVIRGHVPCDSDRFQVDLQCGSSVKPRA</u>	59
humLGALS8	<u>MMLSLNNLQNI IYNPVI PFVGTIPDQLDPGTLIVIRGHVPSDADRQVDLQNGSSMKPRA</u>	60
	****:*****:*****.**:*****.*:***** ***:****	
dogLGALS8	<u>DVAFHFNPRFKWSDCIVCNTLKNKKGWEEITYDTPFKKEKSFEIVIMVLKDKFQVAVNG</u>	119
humLGALS8	<u>DVAFHFNPRFKRAGCIVCNTLINEKKGREEITYDTPFKREKSFEIVIMVLKDKFQVAVNG</u>	120
	***** :.***** ***** *****:*****:*****	
dogLGALS8	<u>NHILLYAHRITPGKIDTLGIYGVNVHSIGYSFSSDFRSTQASTLELTEISKENVLKPD</u>	179
humLGALS8	<u>KHTLLYGHRIPEKIDTLGIYGVNIHSIGFSFSSDLQSTQASSLELTEISRENVKSGT</u>	180
	:* ***.*** * *****:****:*****:*****:*****:*** *..*	
dogLGALS8	<u>PHFTLPFTARLNSSMGPGRTVVVKGVEVNTAKGFNVDLVSGKSKDIALHLNPRLNKAFV</u>	239
humLGALS8	<u>PQLRLPFAARLNTPMGPGRTVVVKGVEVNAKSFNVDLLAGKSKDIALHLNPRLNKAFV</u>	240
	*: : ***:****:*****:***** ***.*****:*****:*****	
dogLGALS8	<u>RNSFLHESWGEEERNITCFPFSPGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKELSN</u>	299
humLGALS8	<u>RNSFLQESWGEEERNITSFPFSPGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKELSSI</u>	300
	*****:*****.*****:*****:*****:*****:*****.*	
dogLGALS8	<u>DTLEIDGDIHLLEVRSW</u>	316
humLGALS8	<u>DTLEINGDIHLLEVRSW</u>	317
	*****:***** *	

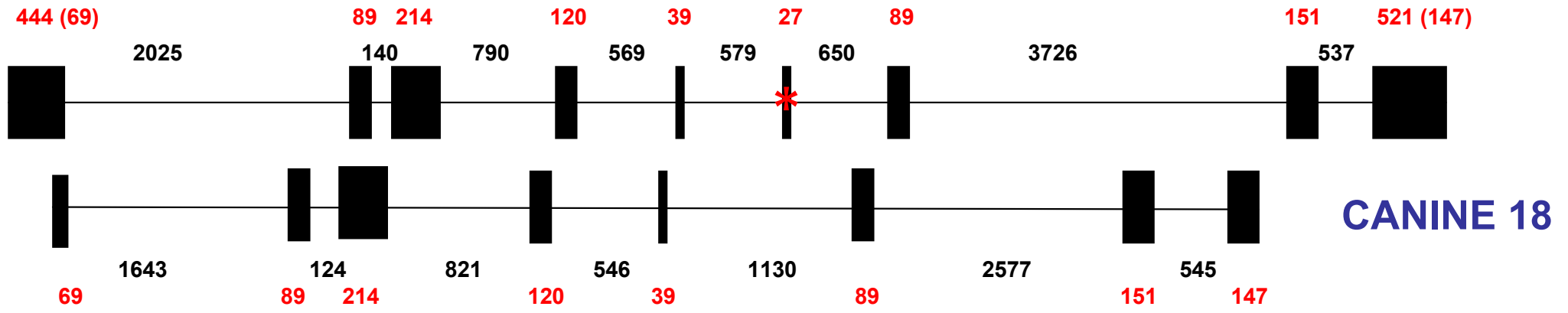


SUPPLEMENTAL FIGURE 7. Galectin-9 (Tandem repeat)

The cloned cDNA has the same nucleotide and amino acid sequence as that predicted by the canine genome data base, except that it includes the fifth coding exon of 96 bp within the linker region* consistent with the long isoform, and Met216 is Thr216 and Thr281 is Met281 (in red). Details of drawing are described above.

dogLGALS9	<u>MAFSSSQPPYLSPGVPFSGKIQGGLQDGLKITINGTILYCNGTRFAVNFHSGHSDSDIAF</u>	60
humLGALS9	<u>MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF</u>	60
	****. *. *****. *****. *****: **: ***: * . *****: : * . * . ****	
dogLGALS9	<u>HFNPRFEEGGYVVCNTKQKGSWGSEERKMOMPFQMGNPFELCFMVNSCDFKVTVNGSHFT</u>	120
humLGALS9	<u>HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMFDFLCFLVQSSDFKVMVNGILFV</u>	120
	*****: *****: *: *****. ***** : ***** * **: ***: *: * . ***** *** *	
dogLGALS9	<u>QYSHRVPFHYVDTLSITGAVQLSYISFQNTTRVTITQPAFSTMQFPQTACFPPRPKGRKPK</u>	180
humLGALS9	<u>QYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPFRPRGRRQK</u>	180
	** ***** ** *: *: *****. * . . *****: * . * . *****: **: *	
dogLGALS9	<u>SPGVWQSSSAPITQTVIHTVQTPPGQFPNPPIIPP</u> T <u>AYPTPTYMPFFETSIPGGLYPSKS</u>	240
humLGALS9	<u>PPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITLGGLYPSKS</u>	240
	. **** : . *****: : *** * . * ***: ** *: *****: *: * *****	
dogLGALS9	<u>IIVSGTVLPGAKRFHINLRSGNDIAFHLNPRFNENTVVRN</u> M <u>QINNSWGSEERSLPRKMPF</u>	300
humLGALS9	<u>ILLSGTVLPQAQRFHINLCSGNHIAFHLNPRFDENAVRNTQIDNSWGSEERSLPRKMPF</u>	300
	* : : *****. *: ***** ** . *****: **: *****: **: *****: *****	
dogLGALS9	<u>VQGQSFVWIMCEGHCFKVAVDGEHLFEYYHRLKNLLAINNMEVAGDVQLTHVQT</u>	355
humLGALS9	<u>VRGQSFVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT</u>	355
	* : *****: ** . **: *****: *****: ** : ** . : ** . ** : *****	

Chromosome HUMAN 11



SUPPLEMENTAL FIGURE 8. Galectin-12 (Tandem repeat)
 The cloned cDNA has the same nucleotide and amino acid sequence as that predicted from the canine genome data base, except that Val 300 is Leu 300 (in red), and it lacks the sixth coding exon of 27 bp within the linker region* consistent with the short isoform. Details of drawing are described above.

```

canine -----MSPGEKLDPLPDIFILQPPVFHPVVPYVTTIFGGLRAG 38
human  MSQPSGGRAPGTRIYSWSCPTVMSPGEKLDPIPDSFILQPPVFHPVVPYVTTIFGGLHAG 60
          *****:** *****:*****:**
canine  KMVMLQGMVPEDAHRFQVDFQCGLSLHPRPDIAIHFNPRFHHTTKPHVICNTLOHGRWQAE 98
human   KMVMLQGVVPLDAHRFQVDFQCGLSLCPRPDIAHFHFNPRFHHTTKPHVICNTLHGGRWQRE 120
          *****:** *****:*****:*****:**** *
canine  ARWPHLTLORGASFLILFLFGNEEMKVSVNGQHFLHYHYRLPLSRVDTLGIFGNILVEAI 158
human   ARWPHLALRRGSSFLILFLFGNEEVKVSVNGQHFLHFRYRLPLSHVDTLGIFGDILVEAV 180
          *****:***:*****:*****:*****:*****:*****:
canine  GFLNINPFAEGGIEYPIGYKVPCSCALPRGLWPGQVIVLRALVLSEPKDFTLSLSDEAAH 218
human   GFLNINPFVEGSREYPAGHEVPCSHALPQGLSPGQVIVRGLVLQEPKHFTVSLRDQAAH 240
          *****.**. *** *:**** **:** *****:*.***.***.**:** **:*
canine  VPVTLRASFADRTLAWISPWGCKKLISAPFIFYPORFFEVLLLCOEGLKLALNGOGLGA 278
human   APVTLRASFADRTLAWISRWGQKKLISAPFLFYPORFFEVLLLFQEGGLKLALNGOGLGA 300
          .***** ** *****:***** *****
canine  ISLHQQALEQLRELRIISGSVQLYCVHY 305
human   TSMNQQALEQLRELRIISGSVQLYCVHS 327
          *.:*****
  
```