

Supplementary information

Table S1: Primer list

Primer name	Sequence
mmKalnc1_RP	CACAAAGGCCACTTTCTCCT
mmKalnc1_FP	CTCCCCCAGTCATGAACC
mmKalnc2_FP	TCGGGAGAAATCAAAGATGG
mmKalnc2_RP	GGATCCATTCTCCATCCTCA
mmKalnc3_FP	TGGGTCAGATGAACAGAGCA
mmKalnc3_RP	GAGGAGGGGCTTGATGAGAT
mmKalnc4.1_FP	GTCAACGCCAGCTCTTTGTC
mmKalnc4.1_FP	CCTGGCTTCTGATGCTGTACTA
mmKalnc4.2_RP	TGTTACAGTGGGAGTCTGATGG
mmKalnc4.2_FP	ATGCTTGAATGGAACTGTCT
mmKalnc5_FP	AAGCTGGACATCTTCCTACAGC
mmKalnc5_RP	GAACGACTCAGGTTCCATTGTC
mmKalnc6_FP	GTGGAGAACTCGGGTAAAAATG
mmKalnc6_RP	AGTGATTTTCATTGTCCAAGG
mmKalnc7_FP	TGTGTTGCAATACCAAGCTTTA
mmKalnc7_RP	GAGCTTCACTCGAGGCACTG
mouse Kalirin-7(Kal7)_FP	GATACCATATCCATTGCCTCCAGGACC
mouse Kalirin-7(Kal7)_RP	CCAGGCTGCGCGCTAAACGTAAG
mouse Kalirin-9(Kal9)_FP	GCCCCTCGCCAAAGCCACAGC
mouse Kalirin-9(Kal9)_RP	CCAGTGAGTCCCGTGGTGGGC
mouse Kalirin-12(Kal12)_FP	CAGCAGCCACGTGCCTGCAGC
mouse Kalirin-12(Kal2)_RP	TCTTGACATTGGGAATGGGCCGCAC
mouse full-length Kalirin_FP	GCCTTTCTCAGCAAACACACTGGGG
mouse full-length Kalirin_RP	ATTCCCCAGTCTGAGCCAGCTGC
mmGapdh_FP	CTACACTGAGGACCAGGTTGTCT

mmGapdh_FP	TCATACCAGGAAATGAGCTTGAC
mmMalat1_FP	GGCGGAATTGCTGGTAGTTT
mmMalat1_RP	AGCATAGCAGTACACGCCTT
mm_circ_000686_FP	AGTGGGATTTATACCTGCATAGC
mm_circ_000686_RP	GGAGGAGATGGTGTATGTTGC
huKALNC2_FP	GTGTGGTCCTGGTGAGGATG
huKALNC2RP	CCCATGATGGAGATGACACC
human Kalirin_FP	CATGGTGAGGCCTTTCTCAGCAAAC
human Kalirin RP	CAGGTGTCGAGCTGCCTTGTAGAT
huGAPDH_FP	GGGAGCCAAAAGGGTCATCA
huGAPDH_RP	TAAGCAGTTGGTGGTGCAGG
humalat1_FP	CGCTTGAGATTTGGGCTTTA
humalat1_RP	CTTCCTGTGGCAGGAGAGAC
hu18SrRNA_FP	GTAACCCGTTGAACCCCAT
hu18SrRNA_RP	CCATCCAATCGGTAGTAGCG
hu45SrRNA_FP	TCGCTGCGATCTATTGAAAG
hu45SrRNA_RP	AGGAAGACGAACGGAAGGAC
huTUBB3_FP	GCTCAGGGGCCTTTGGACATCTCTT
huTUBB3_RP	TTTTCACACTCCTTCCGCACCACATC
huGFAP_FP	CCTCTCCCTGGCTCGAATGC
huGFAP_RP	GGAAGCGAACCTTCTCGATGTA
huSOX2_FP	CATGTCCCAGCACTACCAGA
huSOX2_RP	TACCGGGTTTTCTCCATGCT
huNESTIN_FP	TCTTTGCTCCCAGTCCTGAG
huNESTIN_RP	GGGCTCTGATCTCTGCATCT
huMAP2_FP	CTGCTTTACAGGGTAGCACAA
huMAP2_RP	TTGAGTATGGCAAACGGTCTG

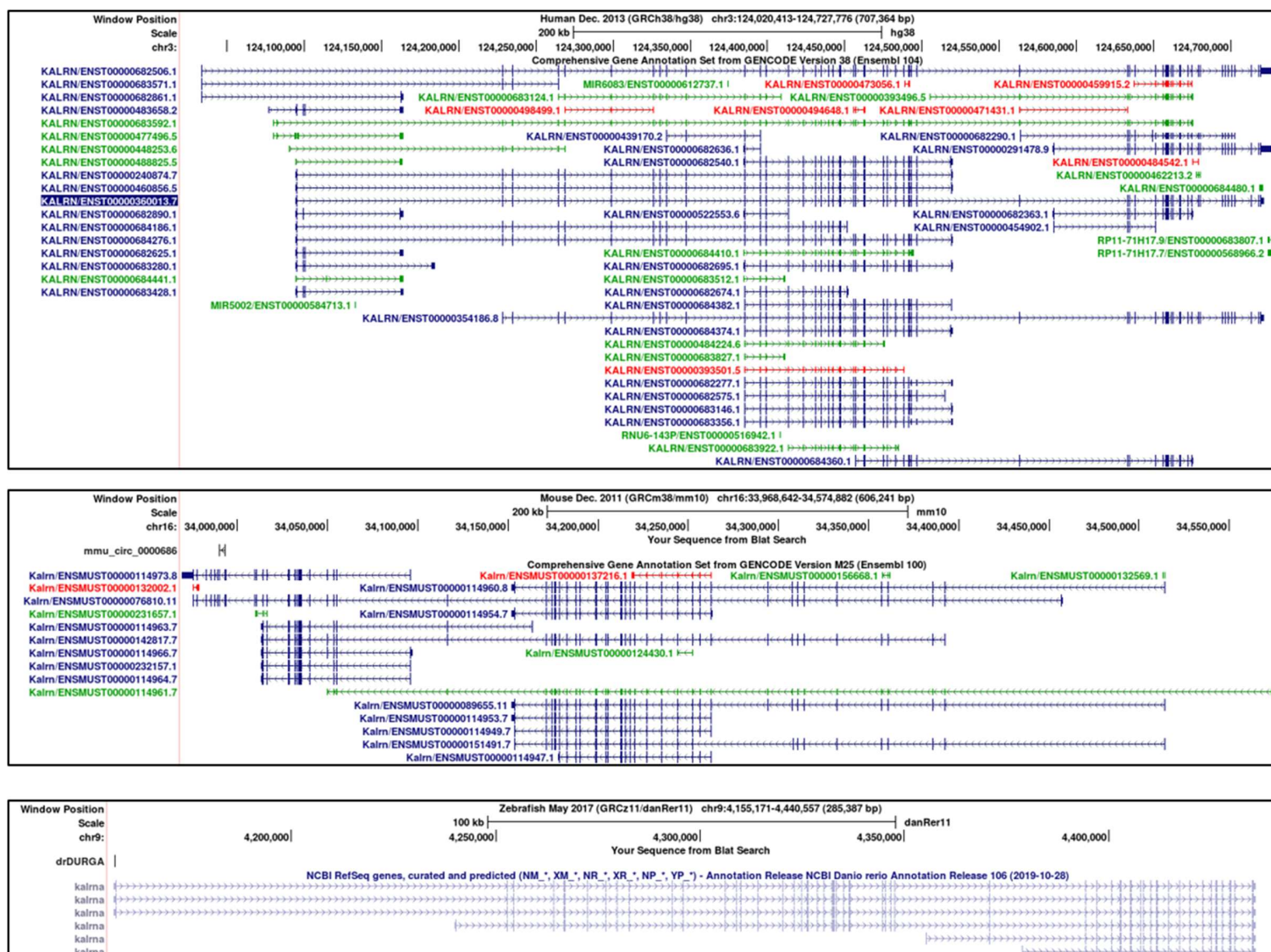


Figure S1. View of the *Kalrn* gene locus of human, mouse and zebrafish, taken from UCSC genome browser.



hsKALNC2(ENST00000488825.5)

Sequence ID: Query_45089 Length: 1344 Number of Matches: 1

Range 1: 49 to 247 [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
210 bits(132)	7e-58	178/206(86%)	8/206(3%)	Plus/Plus
Query 1	AGGCAGGCATTTGCTTAGAGCAGGCTGCGTGTGAGCCCAACATC -CGAGAATCTGGCCTC	59		
Sbjct 49	AGGCAGGCATTTGCTTAGAGCAGGCTGTGTGCGAGCCAGCGTCAAGTGATTCCGGCCTC	108		
Query 60	CTCGAGTCGGTTGGTGGTGGCGGGATGAGGCTGTGCCCTGGAGACTGACTGTGAAGG	119		
Sbjct 109	CTCGAGTC-----AGCGGTGGTGGGATGAGGCTCTGCCGAGGGGACTGGCTGTGAAGG	161		
Query 120	ATGAGTTCAGGGTGGGATGACGGACCGCTTCTGGGACCACTGGTATCTTTGGTATCTCCG	179		
Sbjct 162	ATGAGTTCAGGGTGGGATGACGGACCGCTTCTGGGACCACTGGTATCTCTGGTATCTCCG	221		
Query 180	CTTGCTTCGGCTTCTGGATCGAGCTT	205		
Sbjct 222	CTTGCTCCGGCTGCTGGATCGAGGTT	247		

hsKALNC2(ENST00000684441.1)

Sequence ID: Query_45088 Length: 2520 Number of Matches: 1

Range 1: 1 to 90 [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
134 bits(84)	5e-35	87/90(97%)	0/90(0%)	Plus/Plus
Query 113	GTGAAGGATGAGTTACAGGGTGGGATGACGGACCGCTTCTGGGACCACTGGTATCTTTGGT	172		
Sbjct 1	GTGAAGGATGAGTTACAGGGTGGGATGACGGACCGCTTCTGGGACCACTGGTATCTCTGGT	60		
Query 173	ATCTCCGCTTGCTTCGGCTTCTGGATCGAG	202		
Sbjct 61	ATCTCCGCTTGCTTCGGCTTCTGGATCGAG	90		

Figure S2. Sequence alignment of *mmKalnc2* and *hsKALNC2*. NCBI blast was used for the alignment, *mmKalnc2* was the subject and *hsKALNC2* was the query.