

A

Score	Expect	Identities	Gaps	Strand
42.1 bits(21)	6e-11	21/21(100%)	0/21(0%)	Plus/Plus

has-miR-151-5p	CGAGGAGCTCACAGTCTAGT	21
mmu-miR-151-5p	CGAGGAGCTCACAGTCTAGT	21

B

hsa-miR-151-5p/IL4R Alignment

3' ugAU-CUGACACUCGAGGAGCu 5' hsa-miR-151-5p :: :: :	mirSVR score: -0.0840 PhastCons score: 0.4808
681:5' ugUAUGGCUGGGGCUCCUCGu 3' IL4R	

IL4R Interleukin 4 receptor Display 150 bases per row

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1 GUGCAUGUCCUUGUUGCUGAGUCUGCAGAUGAGGACUAGGGCUUAUCCAUGCCUGGAAAUGCCACCUCCUGGAAGGCAGCCAGGCUGGCAGAUUCCAAGAAACUUGAAGAACCAUGGUUUGAAGGUGAUUGGCCCCACUGACGUUG 150
151 GCCUAACACUGGGCUGCAGAGACUGGACCCCGCCAGCAUUGGGCUGGGCUCGCCACAUCCAUGAGAGUAGAGGGCACUGGGUCGCCGUGCCCCACGGCAGGCCCCUGCAGGAAAACUGAGGCCCUUGGGCACCUCGACUUGUGAACGA 300
301 GUUGUUGGCUGUCUCCUCCACAGCUUCUGCAGCAGACUGUCCUGUUGUAACUGCCCAAGGCAUGUUUUGCCCACCAUGAUGGCCACGUGGAGGCCACCUGCCUCUGUCUCACUGAACUAGAAGCCGAGCCUAGAACAUAACACAG 450
451 CCAUCAAGGGAAUGACUUGGGCGGCCUUGGGAAAUCGAUGAGAAAUUGAACUUCAGGGAGGGUGGUCAUUUGCCUAGAGGUGUCUUAUUAUUAACAGAGCUUCCUAGGUUGAUGCUGGAGGCAGAAUCCCGGUGUCAAGGGGUGUUA 600
601 GUUAAGGGGAGCAACAGAGGACAUGAAAAUUGCUAUGACUAAAGCAGGGACAUUUUGCUGCCAACACCAUGCCAGCUGUAUGGCUGGGGCUCCUCGUUUGCAUGGAACCCCAAGAAUAAUUAUGCUCAGCCACCCUGUGGGCCGG 750
751 GCAAUCCAGACAGCAGGCAUAAGGCACCAGUUAUCCUUGCAUGUUGGCCAGACCUCAGGUGCUAGGGAAGGCGGGAACCUUGGGUUGAGUAAUGCUCGUCUGUGUUUAGUUUCAUCACCUGUUAUCUGUGUUUGCUGAGGAGAGUGG 900
901 AACAGAAGGGGUGGAGUUUUGUAAAAUAAAGUUUUCUUUGUCUCUUU 947
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Supplementary Figure 2. miR-151-5p characterization. (A) Human and mouse miR-151-5p have identical RNA sequences. (B) miR-151-5p was predicted to bind a site in the IL4R α RNA sequence.