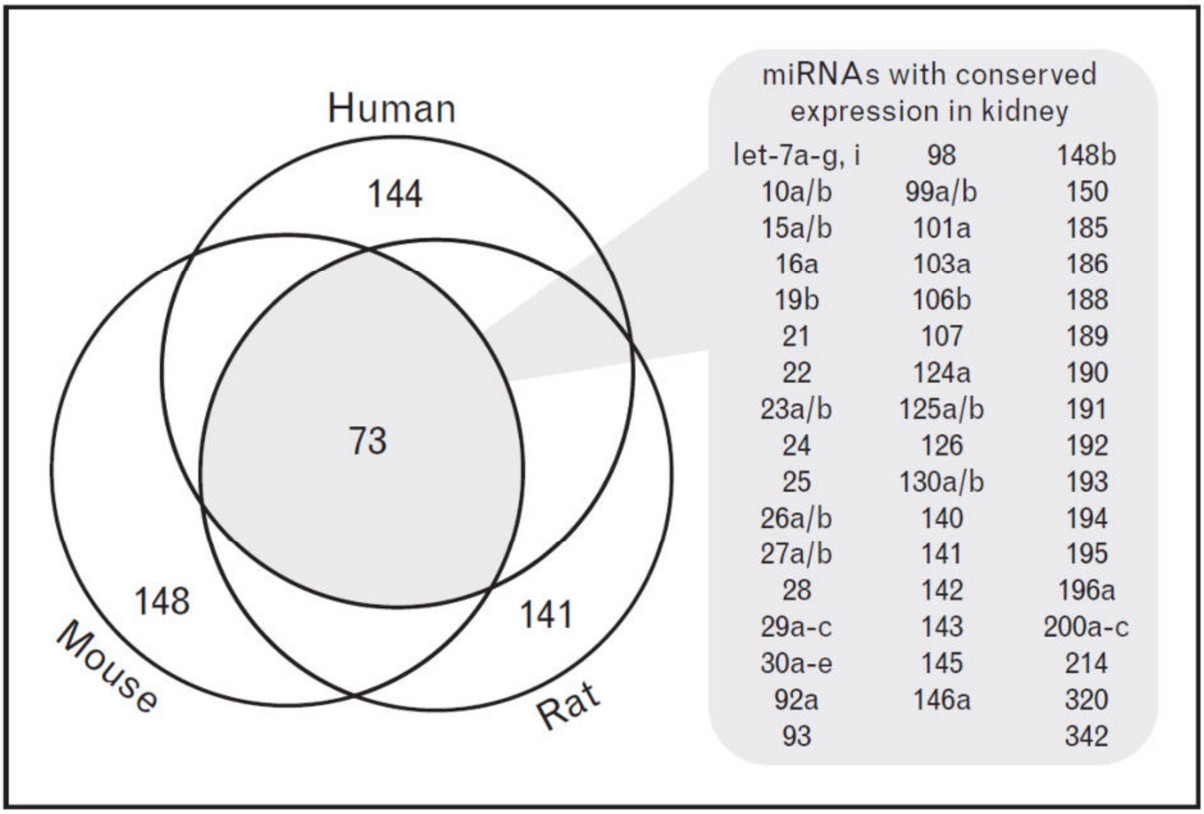
Supplementary Figure S1. Selection of 73 miRNA genes comprising 96 miRNAs with conserved expression in kidney.



miRNAs with conserved expression in kidney

let-7a-g, i
10a/b
15a/b
16a
19b
21
22
23a/b
24
25
26a/b
27a/b
28
29a-c
30a-e
92a
93
98
99a/b
101a
103a
106b
107
124a
125a/b
126
130a/b
140
141
142
143
145
146a
148b
150
185
186
188
189
190
191
192
193
194
195
196a
200a-c
214
320
342

Source: Saal S, Harvey SJ (2009) MicroRNAs and the kidney: coming of age. Curr Opin Nephrol Hypertens 18: 317-323

Supplementary Table S1. Targets, oligo nucleotides, and coverage statistics.

<u>88 stem-loop regions of miRNA genes were sufficiently covered:</u> *MIR1011, MIR1012, MIR103A1, MIR103A2, MIR106B, MIR107, MIR10B, MIR1242, MIR125A, MIR125B1, MIR125B2, MIR126, MIR130A, MIR130B, MIR140, MIR141, MIR142, MIR143, MIR145, MIR146A, MIR148B, MIR150, MIR15A, MIR15B, MIR185, MIR186, MIR188, MIR190B, MIR191, MIR192, MIR193A, MIR193B, MIR1941, MIR1942, MIR195, MIR196A1, MIR19B1, MIR19B2, MIR200A, MIR200C, MIR21, MIR214, MIR22, MIR23B, MIR241, MIR25, MIR26A1, MIR26A2, MIR26B, MIR27A, MIR27B, MIR28, MIR29A, MIR29B1, MIR29C, MIR30A, MIR30B, MIR30C1, MIR30C2, MIR30D, MIR30E, MIR320A, MIR320B1, MIR320B2, MIR320C2, MIR320D1, MIR320D2, MIR320E, MIR342, MIR516A1, MIR516A2, MIR92A1, MIR92A2, MIR93, MIR98, MIR99A, MIR99B, MIRLET7A1, MIRLET7A2, MIRLET7A3, MIRLET7B, MIRLET7C, MIRLET7D, MIRLET7E, MIRLET7F1, MIRLET7F2, MIRLET7G, MIRLET7I*

<u>8 target miRNAs were not sufficiently covered:</u> *MIR10A, MIR1241, MIR1243, MIR196A2, MIR200B, MIR23A, MIR242, MIR320C1*

HGNC Gene Symbol	Stem Loop Sequence	5' flanking Oligo	3' flanking Oligo	hg19 Position of Target	Target Size	Median Coverage
MIR1011	TGCCCTGGCTCAGTTATCACAGTGCTGATGCTGTCTATTCTAAAGGTACAGTACTGTGATAACTGAAGGATGGCA	ATTTCAGCCTCACCACTTGC	TTCTTCCTGGGTACGGTGAG	chr1:65524091-65524337	246	392,59
MIR1012	ACTGTCCTTTTTCGGTTATCATGGTACCGATGCTGTATATCTGAAAGGTACAGTACTGTGATAACTGAAGAATGGTGGT	GCGGAAAACAGCCTATTTGAG	CAAGCTCCTGGTTTTCATGC	chr9:4850182-4850442	260	574,36
MIR103A1	TACTGCCCTCGGCTTCTTTACAGTGCTGCCTTGTTGCATATGGATCAAGCAGCATTGTACAGGGCTATGAAGGCATTG	AAGGCAGCTATGCTCACCAC	TTCTCTTCCAAACAAAGAATCC	chr5:167987814-167988033	219	436,13
MIR103A2	TTGTGCTTTCAGCTTCTTTACAGTGCTGCCTTGTAGCATTCAGGTCAAGCAGCATTGTACAGGGCTATGAAAGAACCA	CCCTAGGGAGGAATCCAGAG	AAGCCATAAGCTGCACCAAC	chr20:3898061-3898257	196	1021,09
MIR106B	CCTGCCGGGGCTAAAGTGCTGACAGTGCAGATAGTGGTCCTCTCCGTGCTACCGCACTGTGGGTACTTGCTGCTCCAGCAGG	AAAGGGGTAGCTCCTTACCG	CAAGACGGGAGGACAGAAAG	chr7:99691501-99691733	232	221966,23
MIR107	CTCTCTGCTTTCAGCTTCTTTACAGTGTTGCCTTGTGGCATGGAGTTCAAGCAGCATTGTACAGGGCTATCAAAGCACAGA	AGGTCTGAGCATCCTTGCAC	GTTCCATGCCTCAACTCCTC	chr10:91352316-91352625	309	131,51
MIR10A	GATCTGTCTGTCTTCTGTATATACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCACAAATTCGTATCTAGGGGAATATGTAGTTGACATAAACACTCCGCTCT	AGACTCGCACTGCCTTTTTC	CCAGTCACCAGACTGTCCTC	chr17:46657145-46657423	278	1,65
MIR10B	CCAGAGGTTGTAACGTTGTCTATATATACCCTGTAGAACCGAATTTGTGTGGTATCCGTA	CAAGCCCATTAGGCTACCTG	CCGGCTGCTTCTAGTCTCC	chr2:177014932-177015177	245	444,56

	TAGTCACAGATTCGATTCTAGGGGAATATATGGTCGATGCAAAAACTTCA					
MIR1241	AGGCCTCTCTCTCCGTGTTCACAGCGGACCTTGATTTAAATGTCCATACAATTAAGGCACGCGGTGAATGCCAAGAATGGGGCTG	TACCCACCCCTCTTCCTTTC	TGCATCTCTAAGCCCCTGTC	chr8:9760722-9761027	305	0,00
MIR1242	ATCAAGATTAGAGGCTCTGCTCTCCGTGTTCACAGCGGACCTTGATTTAATGTCATACAATTAAGGCACGCGGTGAATGCCAAGAGCGGAGCCTACGGCTGCACTTGAA	AGACAGGAGCTGGGCTTATG	ATTTATGCGGCAAGAGATGG	chr8:65291613-65291887	274	232,45
MIR1243	TGAGGGCCCCTCTGCGTGTTCACAGCGGACCTTGATTTAATGTCTATACAATTAAGGCACGCGGTGAATGCCAAGAGAGGCGCCTCC	AAGACGCCTGAGCGTTCG	ATTGTTCGCCGGATTTGTC	chr20:61809774-61810039	265	0,00
MIR125A	TGCCAGTCTCTAGGTCCCTGAGACCCTTTAACCTGTGAGGACATCCAGGGTCACAGGTGAGGTTCTTGGGAGCCTGGCGTCTGGCC	CCCCTCCCGATATCTCTCTG	TGCTCTGGAGGAAGGGTATG	chr19:52196393-52196642	249	475,08
MIR125B1	TGCGCTCCTCTCAGTCCCTGAGACCCTAACTTGTGATGTTTACCGTTTAAATCCACGGGTTAGGCTCTTGGGAGCTGCGAGTCGTGCT	CCATACCACCTGTTTGTTGC	AGCTGCCACTCTCTGGTCAC	chr11:121970349-121970631	282	173,19
MIR125B2	ACCAGACTTTTCCTAGTCCCTGAGACCCTAACTTGTGAGGTATTTTAGTAACATCACAAGTCAGGCTCTTGGGACCTAGGCGGAGGGGA	TGAACCCAACTGTAATTTCTAAGC	GGATGGGTCATGGTGAAAAC	chr21:17962520-17962755	235	430,22
MIR126	CGCTGGCGACGGGACATTATTACTTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCCGTCCACGGCA	ATCAGCCAAGAAGGCAGAAG	GCAGAGCCAGAAGACTCAGG	chr9:139564995-139565299	304	76,28
MIR130A	TGCTGCTGGCCAGAGCTCTTTTCACATTGTGCTACTGTCTGCACCTGTCACTAGCAGTGCAATGTTAAAAGGGCATTGGCCGTGTAGTG	AGGGACTGGGAGAAGGAGTG	TCACAGTAACGGAGGCAGTG	chr11:57408648-57408913	265	508,75
MIR130B	GGCCTGCCCGACACTCTTTCCCTGTTGCACTACTATAGGCCGCTGGGAAGCAGTGCAATGATGAAAGGGCATCGGTCAGGTC	CTACCCAATTCGCTCCCTTC	GGCACCTCAACCTTCTCAAC	chr22:22007451-22007729	278	260,19
MIR140	TGTGTCTCTCTCTGTGTCCTGCCAGTGGTTTTACCCTATGGTAGGTTACGTCATGCTGTTCTACCACAGGGTAGAACCACGGACAGGATACCGGGGCACC	TTGGTGTTGGGTTAACTTGC	TAAACCAGCAAGGGGATGTC	chr16:69966857-69967152	295	119,14
MIR141	CGGCCGGCCCTGGGTCCATCTTCCAGTACAGTGTTGGATGGTCTAATTGTGAAGCTCCT	CACAGTCGACCTTGAGCTTG	TGTCTCCTTCCCATTGTTCC	chr12:7073170-7073458	288	310,76

	AACACTGTCTGGTAAAGATGGCTCCCGGGTGGGTTC					
MIR142	GACAGTGCAGTCACCCATAAAGTAGAAAGCACTACTAACAGCACTGGAGGGTGTAGTGTTTCCTACTTTATGGATGAGTGTACTGTG	GGATCTTAGGAAGCCACAAGG	GAGGCCTTTCAGGCATCTG	chr17:56408483-56408752	269	267,49
MIR143	GCGCAGCGCCCTGTCTCCCAGCCTGAGGTGCAGTGCTGCATCTCTGGTCAGTTGGGAGTCTGAGATGAAGCACTGTAGCTCAGGAAGAGAGAAGTTGTTCTGCAGC	AGGCCACAGACAGGAAACAC	TGGAGTCTGGAAACACTCTGTC	chr5:148808362-148808640	278	274,65
MIR145	CACCTTGTCCTCACGGTCCAGTTTTCCCAGGAATCCCTTAGATGCTAAGATGGGGATTCCTGGAAATACTGTTCTTGAGGTCATGGTT	GGCTGGATGCAGAAGAGAAC	CAGGGACAGCCTTCTTCTTG	chr5:148810156-148810373	217	898,88
MIR146A	CCGATGTGTATCCTCAGCTTTGAGAACTGAATTCCATGGGTTGTGTCAGTGTCAGACCTCTGAAATTCAGTTCTTCAGCTGGGATATCTCTGTCATCGT	GCAGCTGCATTGGATTTACC	TCTGTCTCCAGTCTTCCAAGC	chr5:159912280-159912513	233	605,62
MIR148B	CAAGCACGATTAGCATTTGAGGTGAAGTTCTGTTATACACTCAGGCTGTGGCTCTCTGAAAGTCAGTGCATCACAGAACTTTGTCTCGAAAGCTTTCTA	CACCCAATCTCCCACAAAAC	AAGTTTTTGCAAAGGGCAAG	chr12:54730979-54731269	290	144,44
MIR150	CTCCCCATGGCCCTGTCTCCCAACCCTTGTACCAGTGCTGGGCTCAGACCCTGGTACAGGCCTGGGGGACAGGGACCTGGGGAC	TGGGTATAAGGCAGGGACTG	ACTTTGCGCATCACACAGAG	chr19:50003876-50004176	300	58,29
MIR15A	CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAAAAGGTGCAGGCCATATTGTGCTGCCTCAAAAATACAAGG	ATATTCTTTAGGCGCGAATG	CAACCTTACTTCAGCAGCACAG	chr13:50623133-50623357	224	177,41
MIR15B	TTGAGGCCTTAAAGTACTGTAGCAGCACATCATGGTTTACATGCTACAGTCAAGATGCGAATCATTATTTGCTGCTCTAGAAATTTAAGGAAATTCAT	GCCATGGAATTGACTTGGAC	ACGTGCTGCTAGAGTGGAAC	chr3:160122269-160122532	263	151,49
MIR185	AGGGGGCGAGGGATTGGAGAGAAAGGCAGTTCCTGATGGTCCCCTCCCCAGGGGCTGGCTTTCCTCTGGTCCTTCCCTCCCA	AGACCTGCTGGCTAGAGCTG	CAAGGAAGGCCATAAACAG	chr22:20020626-20020816	190	1133,39
MIR186	TGCTTGTAACTTTCCAAAGAATTCTCCTTTTGGGCTTTCTGGTTTTATTTTAAGCCCAAAGGTGAATTTTTTGGGAAGTTTGAGCT	CCTTTGGGAACCATTATAATTAAG	TTGACATTCACATGCTTCAGG	chr1:71533243-71533442	199	200,79

MIR188	TGCTCCCTCTCTCACATCCCTTGCATGGTGGAGGGTGAGCTTTCTGAAAACCCCTCCCACATGCAGGGTTTGCAGGATGGCGAGCC	TTGCCTCCTAGAGCATACCC	GGAGAAAGGACATGGCTGAG	chrX:49768078-49768291	213	661,15
MIR190B	TGCTTCTGTGTGATATGTTTGATATTGGGTTGTTTAATTAGGAACCAACTAAATGTCAAACATATTCTTACAGCAGCAG	CAAAGGCCAGGAGCTTGTAG	AGGAGCCCCAGAGATTGAAG	chr1:154166115-154166411	296	164,66
MIR191	CGGCTGGACAGCGGGCAACGGAATCCCAAAAGCAGCTGTTGTCTCCAGAGCATTCCAGCTGCGCTTGGATTTCGTCCCCTGCTCTCCTGCCT	CAACCTACTCCCGGGTCTTC	CTCCCACGTCTACACCCATC	chr3:49057949-49058225	276	382,16
MIR192	GCCGAGACCGAGTGCACAGGGCTCTGACCTATGAATTGACAGCCAGTGCTCTCGTCTCCCCTCTGGCTGCCAATTCCATAGGTCACAGGTATGTTCGCCTCAATGCCAGC	TACCCACGAAGAAGGAGAGG	ATTCACGGGGAATGAGACAG	chr11:64658514-64658806	292	81371,75
MIR193A	CGAGGATGGGAGCTGAGGGCTGGGTCTTTGCGGGCGAGATGAGGGTGTCGGATCAACTGGCCTACAAAGTCCCAGTTCTCGGCCCCCG	GAGGGACACCCAGAGCTTC	GCACCTCACCACTCCTTCTC	chr17:29886937-29887194	257	257,82
MIR193B	GTGGTCTCAGAATCGGGGTTTTGAGGGCGAGATGAGTTTATGTTTTATCCAACTGGCCCTCAAAGTCCCGCTTTTGGGGTCAT	CCAAACTCTTGCCTCAAAGG	TGGTAGCTCTCTGCCCTCAC	chr16:14397756-14397947	191	923,61
MIR1941	ATGGTGTTATCAAGTGTAACAGCAACTCCATGTGGACTGTGTACCAATTTCCAGTGGAGATGCTGTTACTTTTGATGGTTACCAA	AAATCGAGACTTTCTTCTGTGAAAC	TCAAATGAGAGTCCAAGTGACC	chr1:220291455-220291646	191	423,69
MIR1942	TGGTTCCCGCCCCCTGTAACAGCAACTCCATGTGGAAGTGCCCACTGGTTCCAGTGGGGCTGCTGTTATCTGGGGCGAGGGCCAG	AAGAAGCCTCGGTGAAAAGAC	ACCGACAGCCCTCCACTAC	chr11:64658743-64659016	273	72166,90
MIR195	AGCTTCCCTGGCTCTAGCAGCACAGAAATATTGGCACAGGGAAGCGAGTCTGCCAATATTGGCTGTGCTGCTCCAGGCAGGGTGGTG	ATCTCCAGGGCAGTTTCAAG	GCCTGTTCCCTCTTCTCTCC	chr17:6920897-6921095	198	994,44
MIR196A1	GTGAATTAGGTAGTTTCATGTTGTTGGGCCTGGGTTTCTGAACACAACAACATTAAACCACCCGATTCAC	CTTCTGTTGGGGAAGAGGTG	ATCCTTGTTGCTCCTGGATG	chr17:46709750-46710021	271	161,96
MIR196A2	TGCTCGCTCAGCTGATCTGTGGCTTAGGTAGTTTCATGTTGTTGGGATTGAGTTTTGAACTCGGCAACAAGAAACTGCCTGAGTTACATCAGTCGGTTTTCGTCGAGGGC	AATTTCTTCCTTCCCCAACC	GAGAGGACGGCATAAAGCAG	chr12:54385476-54385762	286	8,04

MIR19B1	CACTGTTCTATGGTTAGTTTTGCAGGTTTGCATCCAGCTGTGTGATATTCTGCTGTGCAAATCCATGCAAAACTGACTGTGGTAGTG	GCTGTAGAACTCCAGCTTCG	CAATCCCCACCAAACTCAAC	chr13:92003412-92003634	222	12666087,22
MIR19B2	ACATTGCTACTTACAATTAGTTTTGCAGGTTTGCATTTCAGCGTATATATGTATATGTGGCTGTGCAAATCCATGCAAAACTGATTGTGATAATGT	AACAGATGGTGGGGACTGTG	TGCTGGAGATACGCATGAAG	chrX:133303674-133303948	274	14716,79
MIR200A	CCGGGCCCCTGTGAGCATCTTACCGGACAGTGCTGGATTTCCCAGCTTGACTCTAACACTGTCTGGTAACGATGTTCAAAGGTGACCCGC	GGCCTGTGTGCAGTCTCAG	CCCATCCCTGGAGTAGGAG	chr1:1103118-1103367	249	136,48
MIR200B	CCAGCTCGGGCAGCCGTGGCCATCTTACTGGGCAGCATTGGATGGAGTCAGGTCTCTAATACTGCCTGGTAATGATGACGGCGGAGCCCTGCACG	CCCCAGCTACTGAGCTTCC	ATTCCGGGGTCTCTGAGATG	chr1:1102443-1102745	302	0,00
MIR200C	CCCTCGTCTTACCCAGCAGTGTTTGGGTGCGGTTGGGAGTCTCTAATACTGCCGGGTAATGATGGAGG	AGGGATCTGCAGCTTTTCC	AACAAGAACCACCCCTTGTG	chr12:7072807-7073047	240	29,54
MIR21	TGTCGGGTAGCTTATCAGACTGATGTTGACTGTTGAATCTCATGGCAACACCAGTCGATGGGCTGTCTGACA	TTTATCAAATCCTGCCTGACTG	GCTGCATTATGGCACAAAAG	chr17:57918579-57918810	231	377,84
MIR214	GGCCTGGCTGGACAGAGTTGTCATGTGTCTGCCTGTCTACACTTGCTGTGCAGAACATCCGCTCACCTGTACAGCAGGCACAGACAGGCAGTCACATGACAACCCAGCCT	TCCCTTTCCCCTTACTCTCC	GCCCCTCATTTTGGTTGTAG	chr1:172107879-172108117	238	628,60
MIR22	GGCTGAGCCGCAGTAGTTCTTCAGTGGCAAGCTTTATGTCCTGACCCAGCTAAAGCTGCCAGTTGAAGAACTGTTGCCCTCTGCC	CAGCGAGGTTAACAGCTTCC	TGTCACCTTCCAGATGATGG	chr17:1617164-1617449	285	236,01
MIR23A	GGCCGGCTGGGGTTCCTGGGGATGGGATTTGCTTCCTGTCACAAATCACATTGCCAGGGATTTCCAACCGACC	TGATCAAAGGAAGCATCTGG	GTGAACACGACTTGGTGTGG	chr19:13947297-13947588	291	0,00
MIR23B	CTCAGGTGCTCTGGCTGCTTGGGTTCCTGGCATGCTGATTTGTGACTTAAGATTAAAATCACATTGCCAGGGATTACCACGCAACCACGACCTTGGC	GCTGCACTGGCATTTTTATG	TGCACCTGTTCTCCAATCTG	chr9:97847317-97847618	301	195,55
MIR241	CTCCGGTGCCTACTGAGCTGATATCAGTTCTCATTTTACACACTGGCTCAGTTCAGCAGGAACAGGAG	TGTGGTAGCTCATGGCTGTG	GGCACTTACAGACACGAAGG	chr9:97848139-97848390	251	363,25

MIR242	CTCTGCCTCCCGTGCCTACTGAGCTGAAACACAGTTGGTTTGTGTACACTGGCTCAGTTCAGCAGGAACAGGG	CCAAGTCGTGTTCACAGTGG	CATCCCTCCTCCAGACACAG	chr19:13947018-13947271	253	0,00
MIR25	GGCCAGTGTTGAGAGGCGGAGACTTGGGCAATTGCTGGACGCTGCCCTGGGCATTGCACTTGTCTCGGTCTGACAGTGCCGGCC	CTCTGCCAATTGTCTTCTTGG	GGGTCGCCTACTCACAAAAC	chr7:99691143-99691359	216	680914,55
MIR26A1	GTGGCCTCGTTCAAGTAATCCAGGATAGGCTGTGCAGGTCCCAATGGGCCTATTCTTGGTTACTTGCACGGGGACGC	CTCTCCCGAGGGAATGAAG	CTTTGCCCACAAGACTCCTC	chr3:38010851-38011137	286	398,18
MIR26A2	GGCTGTGGCTGGATTCAAGTAATCCAGGATAGGCTGTTTCCATCTGTGAGGCCTATTCTTGATTACTTGTTTCTGGAGGCAGCT	TGGTCATTGAGGGGAAAAAG	CAACCTGGCTCAGGAAGAAG	chr12:58218342-58218560	218	749,41
MIR26B	CCGGGACCCAGTTCAAGTAATTCAGGATAGGTTGTGTGCTGTCCAGCCTGTTCTCCATTACTTGGCTCGGGGACCGG	CTCGGATGGGAATTGGATAC	GCCTCAACCTCAGCCTAGTG	chr2:219267226-219267488	262	407,90
MIR27A	CTGAGGAGCAGGGCTTAGCTGCTTGTGAGCAGGGTCCACACCAAGTCGTGTTCACAGTGGCTAAGTTCCGCCCCCCAG	ATCACATTGCCAGGGATTTC	CCTGTTCCTGCTGAACTGAG	chr19:13947122-13947409	287	5838279,49
MIR27B	ACCTCTCTAACAAGGTGCAGAGCTTAGCTGATTGGTGAACAGTGATTGGTTTCCGCTTTGTTCACAGTGGCTAAGTTCTGCACCTGAAGAGAAGGTG	ACCAGCTGAGGAAGATGCTC	ATTCCCAGCAGGAGACAGTG	chr9:97847692-97847951	259	562,21
MIR28	GGTCCTTGCCCTCAAGGAGCTCACAGTCTATTGAGTTACCTTTCTGACTTTCCCACTAGATTGTGAGCTCCTGGAGGGCAGGCACT	GCCTTTTGCATGGTAGACAAC	GCTCCTGCTGTGTCAATCAC	chr3:188406532-188406813	281	134,25
MIR29A	ATGACTGATTTCTTTTGGTGTTCAGAGTCAATATAATTTTCTAGCACCATCTGAAATCGGTTAT	TTGTGCCTGGGTTAAAGAGC	CCACATGCAATTCAGGTCAG	chr7:130561359-130561639	280	103,55
MIR29B1	CTTCAGGAAGCTGGTTTCATATGGTGGTTTAGATTTAAATAGTGATTGTCTAGCACCATTTGAAATCAGTGTTCTTGGGGG	TGCCAAAGCTCTGTTTAGACC	TGTCCCATTCACTTCTTTTGC	chr7:130562192-130562397	205	545,27
MIR29C	ATCTCTTACACAGGCTGACCGATTTCTCCTGGTGTTCAGAGTCTGTTTTTGTCTAGCACCATTTGAAATCGGTTATGATGTAGGGGGA	GGAGTATTCGGCGTTGATTG	TCCATCTTCCAGGAAACCAC	chr1:207975149-207975352	203	1147,59
MIR30A	GCGACTGTAAACATCCTCGACTGGAAGCTGTGAAGCCACAGATGGGCTTTCAGTCGGATGTTTGCAGCTGC	TACAGAATCGTTGCCTGCAC	TGCTGAAGCCCTCTAAAAATG	chr6:72113112-72113405	293	113,02

MIR30B	ACCAAGTTTCAGTTCATGTAAACATCCTACACTCAGCTGTAATACATGGATTGGCTGGGAGGTGGATGTTTACTTCAGCTGACTTGGA	TGTGAATGCTGTGCCTGTTC	CCCTGCCAGCTAGACAATTAAC	chr8:135812631-135812917	286	85,27
MIR30C1	ACCATGCTGTAGTGTGTGTAAACATCCTACACTCTCAGCTGTGAGCTCAAGGTGGCTGGGAGAGGGTTGTTTACTCCTTCTGCCATGGA	TGCCCTGAATAAGGACATGAG	TGATTAGGGAGGTCGCATTC	chr1:41222791-41223090	299	122,84
MIR30C2	AGATACTGTAAACATCCTACACTCTCAGCTGTGGAAAGTAAGAAAGCTGGGAGAAGGCTGTTTACTCTTTCT	AAGAACTGAGCAGGCAGCAC	AACACGGGATAGGATCAATTC	chr6:72086612-72086920	308	55,43
MIR30D	GTTGTTGTAAACATCCCCGACTGGAAGCTGTAAGACACAGCTAAGCTTTCAGTCAGATGTTTGCTGCTAC	AGGAGAAATTGCACTTGGTG	TTTCTGAGGTTTTCCCACAC	chr8:135817053-135817349	296	37,21
MIR30E	GGGCAGTCTTTGCTACTGTAAACATCCTTGACTGGAAGCTGTAAGGTGTTCAGAGGAGCTTTCAGTCGGATGTTTACAGCGGCAGGCTGCCA	TTGGATTAGCAAGCCCTCTG	TCTGAGAGAGGAGGGAAGGAC	chr1:41219977-41220193	216	543,85
MIR320A	GCTTCGCTCCCCTCCGCCTTCTCTTCCCGGTTCTTCCCGGAGTCGGGAAAAGCTGGGTTGAGAGGGCGAAAAAGGATGAGGT	GTCACAACCTCACCTGCAAC	GTGGTGGCCGACAAAACC	chr8:22102390-22102689	299	84,79
MIR320B1	AATTAATCCCTCTCTTTCTAGTTCTTCCTAGAGTGAGGAAAAGCTGGGTTGAGAGGGCAAACAAATTAACTAATTAATT	AGAGCACAGCCTGAAAGAGC	CACTTGGCCATATCTTATCCAC	chr1:117214227-117214491	264	67,46
MIR320B2	TGTTATTTTTTGTCTTCTACCTAAGAATTCTGTCTCTTAGGCTTTCTCTTCCCAGATTTCCCAAAGTTGGGAAAAGCTGGGTTGAGAGGGCAAAAGGAAAAAAAAAAGAATTCTGTCTCTGACATAATTAGATAGGGAA	TCAGGCAACCATCTCATTTG	CTCAAACCACCACCACCTTG	chr1:224444674-224444911	237	286,73
MIR320C1	TTTGCATTAAAAATGAGGCCTTCTCTTCCCAGTTCTTCCCAGAGTCAGGAAAAGCTGGGTTGAGAGGGTAGAAAAAAAAATGATGTAGG	CTGGCAAACAGGCATGTGAC	TTCCCTTAGTCTGTGTTCATTCAG	chr18:19263369-19263671	302	0,00
MIR320C2	CTTCTCTTTCCAGTTCTTCCCAGAATTGGGAAAAGCTGGGTTGAGAGGGT	TCCTAGGCTCAAGCGATCTG	TGGCCACTCTGTATCTCTTCC	chr18:21901497-21901783	286	80,35
MIR320D1	TTCTCGTCCCAGTTCTTCCCAAAGTTGAGAAAAGCTGGGTTGAGAGGA	TCCACCATAACAACAGCCTTC	CCTCTTTGCTTCTCTCTGCTG	chr13:41301903-41302206	303	33,25
MIR320D2	TTCTCTTCCCAGTTCTTCTTGGAGTCAGGAAAAGCTGGGTTGAGAGGA	CACCTTTAAGCAAGTGGGAAC	TGCATTTTTCTCCAACAACC	chrX:140008211-140008445	234	126,62

MIR320E	GCCTTCTCTTCCCAGTTCTTCCTGGAGTCGGGGAAAAGCTGGGTTGAGAAGGT	TTGGTGGACGCCTGTAATTC	GCCAGGGTGGTCTCAATC	chr19:47212457-47212754	297	59,18
MIR342	GAAACTGGGCTCAAGGTGAGGGGTGCTATCTGTGATTGAGGGACATGGTTAATGGAATTGTCTCACACAGAAATCGCACCCGTCACCTTGGCCTACTTA	GCCCATGTCATATTGTGTGC	GTCCGAAGTTCCTTCCACAG	chr14:100575902-100576175	273	463,56
MIR516A1	TCTCAGGCTGTGACCTTCTCGAGGAAAGAAGCACTTTCTGTTGTCTGAAAGAAAAGAAAGTGCTTCCTTTCAGAGGGTTACGGTTTGAGA	CAAACAGGGCCAATAAATGC	CCCACCATTATCCACGTCTG	chr19:54259922-54260143	221	421,00
MIR516A2	TCTCAGGTTGTGACCTTCTCGAGGAAAGAAGCACTTTCTGTTGTCTGAAAGAAAAGAAAGTGCTTCCTTTCAGAGGGTTACGGTTTGAGA	CAAACAGGGCCAATAAATGC	CCTGGGCAACAGATACCTTG	chr19:54264309-54264587	278	190,55
MIR92A1	CTTTCTACACAGGTTGGGATCGGTTGCAATGCTGTGTTTCTGTATGGTATTGCACTTGTCCCGGCCTGTTGAGTTTGG	CCATGCAAAACTGACTGTGG	GCCAGAATTTATACTGCCAAATC	chr13:92003528-92003815	287	10591398,01
MIR92A2	TCATCCCTGGGTGGGGATTTGTTGCATTACTTGTGTTCTATATAAAGTATTGCACTTGTCCCGGCCTGTGGAAGA	TGTGCAAATCCATGCAAAAC	GGTCCTGCGGTTTACAGATG	chrX:133303420-133303715	295	13648,43
MIR93	CTGGGGGCTCCAAAGTGCTGTTCGTGCAGGTAGTGTGATTACCCAACCTACTGCTGAGCTAGCACTTCCCGAGCCCCCGG	GTGGTTGGGGTCTGTTTCAC	AGGGAGACCAGACCCTTTTG	chr7:99691312-99691534	222	150877866,18
MIR98	AGGATTCTGCTCATGCCAGGGTGAGGTAGTAAGTTGTATTGTTGTGGGGTAGGGATATTAGGCCCCAATTAGAAGATAACTATACAACTTACTACTTTCCCTGGTGTGTGGCATATTCA	GATTGTACCAAAGCCTGCAC	TCTGTCCCCTTCCATGTCTC	chrX:53583109-53583418	309	61,07
MIR99A	CCCATTGGCATAAACCCGTAGATCCGATCTTGTGGTGAAGTGGACCGCACAAGCTCGCTTCTATGGGTCTGTGTCAGTGTG	TTTATGAAGGCCTTTAATGGAG	GAACTATTGTTGAACGGCACTG	chr21:17911282-17911512	230	100,71
MIR99B	GGCACCCACCCGTAGAACCGACCTTGCGGGGCCTTCGCCGCACACAAGCTCGTGTCTGTGGGTCCGTGTC	TGGATTCCAGGAACATTTGG	AGACAGACAGGGACCAGGAG	chr19:52195680-52195988	308	99,66
MIRLET7A1	TGGGATGAGGTAGTAGGTTGTATAGTTTTAGGGTCACACCCACCACTGGGAGATAACTATACAATCTACTGTCTTTCCTA	CCTTCCTGTGGTGCTCAACT	CCAGGCCATAAACAAATGCT	chr9:96938197-96938415	218	629,57

MIRLET7A2	AGGTTGAGGTAGTAGGTTGTATAGTTTAGAATTACATCAAGGGAGATAACTGTACAGCCTCCTAGCTTTCCT	AATGGCCCAAATAGGTGACA	ATAGGGAGAAAAGGCCTGGA	chr11:122017187-122017385	198	700,75
MIRLET7A3	GGGTGAGGTAGTAGGTTGTATAGTTTGGGGCTCTGCCCTGCTATGGGATAACTATACAATCTACTGTCTTTCCT	CTCCTCAGCCCTCTTTCCTC	CCAAGGTCACACAGCAAGTG	chr22:46508562-46508840	278	190,64
MIRLET7B	CGGGGTGAGGTAGTAGGTTGTGTGGTTTCAGGGCAGTGATGTTGCCCCTCGGAAGATAACTATACAACCTACTGCCTTCCCTG	CCAGAGAGCCAGGGACTTC	GGTCGTGTCACTGAGGTAGG	chr22:46509400-46509685	285	58,92
MIRLET7C	GCATCCGGGTTGAGGTAGTAGGTTGTATGGTTTAGAGTTACACCCTGGGAGTTAACTGTACAACCTTCTAGCTTTCCTTGGAGC	GCCATATTTGGAGGAGCTGA	GCCCAAATCAATGATCCAAG	chr21:17912104-17912314	210	477,98
MIRLET7D	CCTAGGAAGAGGTAGTAGGTTGCATAGTTTTAGGGCAGGGATTTTGCCCACAAGGAGGTAACTATACGACCTGCTGCCTTTCTTAGG	TGCCAAGTAGAAGACCAGCA	TTATCAATGTCAGCACCATGC	chr9:96941098-96941341	243	292,94
MIRLET7E	CCCGGGCTGAGGTAGGAGGTTGTATAGTTGAGGAGGACACCCAAGGAGATCACTATACGGCCTCCTAGCTTTCCCCAGG	CTGTCTGTCTGTCGGGTCTG	GCAGGGACAAGGACAGAAAA	chr19:52196023-52196222	199	966,08
MIRLET7F1	TCAGAGTGAGGTAGTAGATTGTATAGTTGTGGGGTAGTGATTTTACCCTGTTCAGGAGATAACTATACAATCTATTGCCTTCCCTGA	GGGGAAACCTTTTGCTTCTT	ATGTCAAAATTAATTCTTCTGAGTTTT	chr9:96938507-96938759	252	51,25
MIRLET7F2	TGTGGGATGAGGTAGTAGATTGTATAGTTTTAGGGTCATACCCCATCTTGGAGATAACTATACAGTCTACTGTCTTTCCCACG	GAGTAGCTGGCCCACATAGG	AGGACCAGCCACTTCAAAGA	chrX:53584009-53584257	248	608,19
MIRLET7G	AGGCTGAGGTAGTAGTTTGTACAGTTTGAGGGTCTATGATACCACCCGGTACAGGAGATAACTGTACAGGCCACTGCCTTGCCA	AGCCTCTGCTGTGAGGATGT	GGTTTCCCAGAGATGAGCAG	chr3:52302247-52302444	197	1443,21
MIRLET7I	CTGGCTGAGGTAGTAGTTTGTGCTGTTGGTCGGGTTGTGACATTGCCCGCTGTGGAGATAACTGCGCAAGCTACTGCCTTGCTA	GAAGGCAAAGGAAAAGAAGG	AACTAACGGTTTCCGTGGTG	chr12:62997369-62997658	289	101,34

Supplementary Table S2. Evaluation workflow applied to Next Generation Sequencing-based mutation-analysis in 96 miRNA stem-loop regions in 1,213 individuals with CAKUT.

Filters applied	**# of remaining variants**
All variants detected	**116,431**
➢ Exclude variant if present in common dnSNP132 (MAF >1%)	**111,867**
➢ Exclude variant if variant frequency in NGS-reads ≤ 25%	**32,510**
➢ Exclude variant if present in ≥ 5% of subjects	**6,740**
➢ Exclude variant if coverage ≤ 10x	**1,440**
➢ Exclude variant if not located within miRNA stem-loop region	**300**
➢ Exclude if nucleotide conservation score (PhyloP) <2	**176**
➢ Inspection of NGS-alignment and Sanger Confirmation	**47**
Total number of variants considered (Shared variants among multiple individuals counted as one)	**18**
➢ Evolutionary conserved at least down to zebrafish, not present in public databases	**2**
Total number of potentially pathogenic variants detected	**2**

Supplementary Table S3. Unlikely pathogenic variants and benign variants detected in 96 miRNA stem-loop regions in 1,213 individuals with CAKUT.

Gene	Genomic variant	*Mm*	*Gg*	*Xt*	*Dr*	SNP ID	EVS	1000G	Family ID	Ind. ID	State	Origin	Phenotype
Unlikely pathogenic variants (known SNPs, bad evolutionary conservation)													
MIR30E	chr1:41220114T>C	T	T	T		n/a	unknown	unknown	UROGE340	-1	het	unknown	UPJO
MIR26B	chr2:219267373G>C	G	NA	G		n/a	unknown	unknown	A1402	-21	het	Egypt	Rt duplex
MIR141	chr12:7073282C>T	C	C			n/a	unknown	unknown	A1548	-21	het	Kuwait	UPJO
									A3903	-21	het	India	Lt hypoplastic kidney
MIR196A2	chr12:54385585G>T	G	A	G	A	n/a	unknown	unknown	A3957	-21	het	India	B hydronephrosis, anorect. MF
MIRLET7I	chr12:62997517G>A	G	G	G	A	n/a	unknown	unknown	A1549	-21	het	Kuwait	UPJO
MIR342	chr14:100576067G>A	G				n/a	unknown	unknown	A5120	-21	het	Macedonia	VUR, Renal agenesis L
MIR185	chr22:20020729G>A	G				n/a	unknown	unknown	A2246	-21	het	Kuwait	B hydronephrosis
MIR130B	chr22:22007595C>G	C				n/a	unknown	unknown	A2037	-22	het	Switzerland	Rt VUR, Lt renal agenesis
MIR190B	chr1:154166182A>G	A	A			rs376882956	G=7/A=10293	unknown	P43	-1	het	unknown	UPJO
MIR1941	chr1:220291556G>A	G	G	G		rs369094973	A=1/G=10283	unknown	UROGE045	-1	het	unknown	UPJO
MIR10B	chr2:177015139G>A	C	C	C	C	rs200015643	T=4/C=10296	unknown	A946	-21	het	Hungary	VUR, Rt duplex, dysplasia
MIR320A	chr8:22102546G>A	G				rs372063644	A=6/G=10292	A=1/G=5007	A1931	-22	het	Germany	VUR
MIR320A	chr8:22102519G>A	G				rs200301891	A=22/G=10278	A=5/G=5003	A1259	-21	het	Macedonia	VUR, Lt duplex
									A2901	-21	het	Macedonia	Lt single cortical cyst
									A3044	-21	het	Albania	VUR
									A5058	-21	het	Albania	Hypoplastic Kidney Rt
									A5139	-21	het	Russian	NS, B VUR
									A960	-21	het	Albania	UPJO
									VURF0139	-772	het	unknown	Healthy
										-774	het	unknown	VUR
										-775	het	unknown	VUR
										-776	het	unknown	VUR
Benign variants (non-segregation)													

MIR93	chr7:99691447C>T	C	NA	C	C	n/a	unknown	unknown	A1089	-21	het	Macedonia	UPJO
									A1905	-21	het	Serbia	VUR
										-22	WT	Serbia	VUR
										-11	WT	Serbia	Healthy
										-12	het	Serbia	Healthy
MIR126	chr9:139565134C>T	C	C	C	C	rs199992070	T=1/C=10283	A=2/G=5006	A1243	-21	het	Germany	ESRD
										-32	het	Germany	Lt VUR, small LK
										-31	WT	Germany	Lt VUR, small LK
									P1422	-1	het	unknown	UPJO

Abbreviations used: *Mm*, *Mus musculus*; *Gg*, *Gallus gallus*; *Xt*, *Xenopus tropicalis*; *Dr*, *Danio rerio*; EVS, Exome variant Server; 1000G, 1000 Genomes Project; het, heterozygous; rt, right; VUR, vesicoureteral reflux