

RIMap-RISC: A transcriptome-wide database of structurally modeled human microRNA interactions

(Additional file 1)

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CURL command and results

A curl query to RMap-RISC (Gencode v46) retrieves SIRT1-201-miR-34a-5p

interactions in the 3'UTR. Only human data are supported; omit the “hsa” prefix in the miRNA name.

```
curl "https://rimap-risc.api.major.iric.ca/api/data" -H "Content-Type: application/json" -d '{"gencode": "v46", "transcriptName": "SIRT1-201", "miRName": "miR-34a-5p", "UTR3": "true"}'
```

The results are returned in Json format:

[illegible]

Python program and results

```
import requests
import json

# URL of the RIMap-RISC API datapoint
url = 'https://rimap-risc.api.major.irc.ca/api/data'

# JSON payload for the request
payload = {
    "gencode": "v46",
    "transcriptName": "SIRT1-201",
    "miRName": "miR-34a-5p",
    "minSeed": "6mer",
    "UTR5": False,
    "CDS": True,
    "UTR3": True,
    "supplementaryPaired": False,
    "seedAccessible": 0.0,
    "supplementaryAccessible": 0.0,
    "conserved": 0
}

try:
    # Send the POST request
    response = requests.post( url, json=payload )

    # Check if the request was successful
    if response.status_code == 200:
        print( "Request was successful!" )
        response_data = response.json()

        # Print the entire response as a formatted JSON string
        print( json.dumps( response_data, indent=4 ) )

        # Extract specific parts of the response
        miRNA_target_pair = response_data.get( 'miRNATargetPair', 'N/A' )
        binding_landscape = response_data.get( 'bindingLandscape', 'No interactions found' )
        transcript_regions = response_data.get( 'transcriptRegions', [] )
        binding_positions = response_data.get( 'bindingPositions', [] )
        transcript_accessibility = response_data.get( 'transcriptAccessibility', [] )

        print( "\n--- Interaction Results ---" )
        print( f"miRNA-Target Pair: {miRNA_target_pair}" )
        print( f"Binding Landscape:\n{binding_landscape}" )
        print( f"Transcript Regions: {transcript_regions}" )
        print( f"Binding Positions: {binding_positions}" )
        print( f"Accessibility Scores: {transcript_accessibility}" )

    else:
        print( f"Request failed with status code: {response.status_code}" )
        print( response.text )

except Exception as e:
    print( f"An error occurred: {e}" )
```

```

Interaction Results ---
miRNA-Target Pair: SIRT1-201:miR-34a-5p
Binding Landscape:
5'-auaaaaacaccgcagcguaggaccauuacugccA-3' SIRT1-201 [3719..3749] (3UTR) target site: 8mer-w8 in: TarBase-v9.0
      |||:|||||!||| | :||||| Al-7mer-w8(0.39) 5mer(0.04) bridge: 8 phastcons: 27.00 dG: -56.92 Kd: 19
3'-----uguugGUCAUucc----GUGACGGU-5' hsa-miR-34a-5p

5'-auugaucuuuuuccacaaguauua---aacugcca-3' SIRT1-201 [3176..3206] (3UTR) target site: 7mer-Al in: TarBase-v9.0
      |:|:|:|!| | :||||| Al-6mer(0.14) suppress(0.40) bridge: 1 phastcons: 22.00 dG: -39.84 Kd: 125
3'-----uguugGUCC--A-uucuGUGACGGU-5' hsa-miR-34a-5p

5'-auuuauucuuuuuuuuaaagcuuag-c-cugccc-3' SIRT1-201 [3494..3524] (3UTR) target site: 6mer
      | ! | :||:||||:| | |||| 7mer-b7(0.28) 4mer(0.24) bridge: 3 phastcons: 24.00 dG: -45.84 Kd: 322
3'-u-g-----u---ugGUCAUuccUGUCAGGU-5' hsa-miR-34a-5p

5'-ucag-uugcuuuagaacaauagugc-cugccu-3' SIRT1-201 [3079..3109] (3UTR) target site: 6mer
      :||| !:|!! | || !| |||| 7mer-b7(0.46) suppress(0.13) bridge: 15 phastcons: 24.00 dG: -43.03 Kd: 322
3'-uguugGUCA-----u-uc-uGUGACGGU-5' hsa-miR-34a-5p

5'-ucuuuaaacacaaaauuuuuuaaacacuggcA-3' SIRT1-201 [2794..2824] (3UTR) target site: 8mer-xG3 in: TarBase-v9.0
      :||| |!:|| | :|||||:| Al-7mer-x3(0.22) suppress(0.46) bridge: 9 phastcons: 30.00 dG: -44.40 Kd: 1281
3'----uguug-GUCAu-----ucuGUGACGGU-5' hsa-miR-34a-5p


Transcript Regions: [65, 2309, 4106]
Binding Positions: [3719, 3176, 3494, 3079, 2794]
Accessibility Scores: [0.1185, 0.1276, 0.1368, 0.1447, 0.1495, 0.1502, 0.1481, 0.1463, 0.1468, 0.1488, 0.1496, 0.1469,
0.1409, 0.1333, 0.1265, 0.1222, 0.1209, 0.1225, 0.1263, 0.1311, 0.1352, 0.1375, 0.1382, 0.138, 0.1382, 0.1396, 0.1437,
0.15, 0.1556, 0.1582, 0.1577, 0.1563, 0.1555, 0.1558, 0.1566, 0.1569, 0.1547, 0.1491, 0.1407, 0.1322, 0.1266, 0.1256,
0.1297, 0.1381, 0.1477, 0.1544, 0.1556, 0.1519, 0.1474, 0.1458, 0.1476, 0.1501, 0.1506, 0.149, 0.147, 0.146, 0.1453,
0.1435, 0.1406, 0.1383, 0.1388, 0.1426, 0.1473, 0.1494, 0.1471, 0.1419, 0.1373, 0.1373, 0.1431, 0.1526, 0.1617, 0.1658,
0.1626, 0.1547, 0.1467, 0.1413, 0.1385, 0.1376, 0.1396, 0.1462, 0.1563, 0.1665, 0.1735, 0.176, 0.1742, 0.1688, 0.1602,
0.1497, 0.1402, 0.1341, 0.1317, 0.1313, 0.1312, 0.1318, 0.1347, 0.1397, 0.1446, 0.1473, 0.1478, 0.1475, 0.1475, 0.1469,
0.145, 0.1426, 0.142, 0.1441, 0.1465, 0.1452, 0.1385, 0.1293, 0.1222, 0.1202, 0.1232, 0.1291, 0.1355, 0.141, 0.1448,
0.1468, 0.1466, 0.1441, 0.1402, 0.1375, 0.138, 0.1406, 0.1419, 0.1397, 0.1347, 0.1294, 0.125, 0.1218, 0.1201, 0.1207,
0.1235, 0.1269, 0.1292, 0.1305, 0.1328, 0.138, 0.145, 0.1507, 0.1519, 0.1488, 0.1437, 0.1395, 0.1372, 0.1365, 0.1369,
0.1385, 0.1406, 0.1416, 0.1407, 0.1401, 0.1428, 0.1503, 0.1598, 0.1665, 0.1672, 0.1629, 0.1568, 0.1518, 0.1485, 0.146,
0.143, 0.1402, 0.1388, 0.1397, 0.1435, 0.149, 0.1528, 0.1509, 0.1417, 0.1292, 0.1202, 0.1195, 0.1258, 0.1349, 0.1428,
0.1486, 0.1527, 0.1547, 0.1538, 0.15, 0.1452, 0.1418, 0.1415, 0.1443, 0.149, 0.1541, 0.1564, 0.1536, 0.1463, 0.1374,
0.1297, 0.1239, 0.1199, 0.1181, 0.1184, 0.1194, 0.1196, 0.1183]
```

Fig. S1 How to use RIMap-RISC's information page.

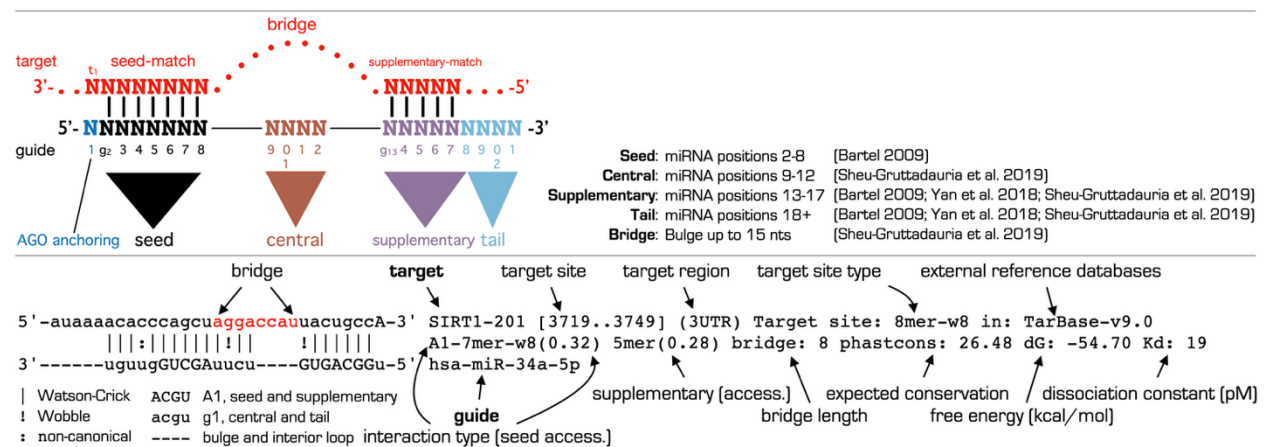
Clicking the “How to use RIMap-RISC” button gives the general directions to use the web site and shows the guide-target regions and a plausible interaction between miR-34a-5p and Sirt1. The lower part gives details about the bipartite duplex folding algorithm, transcript accessibility computation, evolutionary conservation computation, and dissociation constants interpolation.

How to use RIMap-RISC :

1. Select a pair: a Gencode v46 protein-coding transcript and a MiRBase microRNA.
2. Start your query by either:
 - a. setting a detection mode, or
 - b. filling the parameters and clicking **MAP/RUN**.
3. If the selected pair has been computed previously, results will appear instantly. For new pairs, computation typically completes in under one minute and rarely exceeds three minutes.
4. View the results displayed below the Query panel.
5. Use **DOWNLOAD INTERACTIONS** to save your results.
6. Follow the **TarBase-v9.0** link to access experimental evidence for your selected pair.

Note: RIMap-RISC is incrementally populated as users submit new requests.

Definitions and methods used in RIMap-RISC :



Bipartite duplex folding mimicking RISC:

The seed duplex, seed::MRE[seed-match] and the supplementary duplex, supplementary::MRE[supplementary-match] are folded separately to mimic the independent folding in the two chambers. The final duplex is constrained by the seed and supplementary duplexes. MREs are 31 nucleotides (nts); folding is with MC-Flashfold [Dallaire & Major 2016].

Transcript accessibility: Accessibility is calculated from the results of overlapping tiling windows' 2D structure predictions using MC-Flashfold. The values indicate the highest accessibility of the nucleotide (nt) in the seed (g2-g5) and supplementary region (g13-g16). A value > 0.15 indicates an accessible region.

Conservation: PhastCons scores are derived from multiple alignments across 100 vertebrates [Siepel et al. 2005]. These scores approximatively reflect the number of nts conserved throughout the entire transcript sequence. A region with a score ≥ 21 is considered conserved. A score of -1 indicates that no conservation data could be retrieved from PhastCons (usually a 31mer that does not match the genome of reference); those with scores of -1 are shown regardless of the "Minimum conservation" score selected.

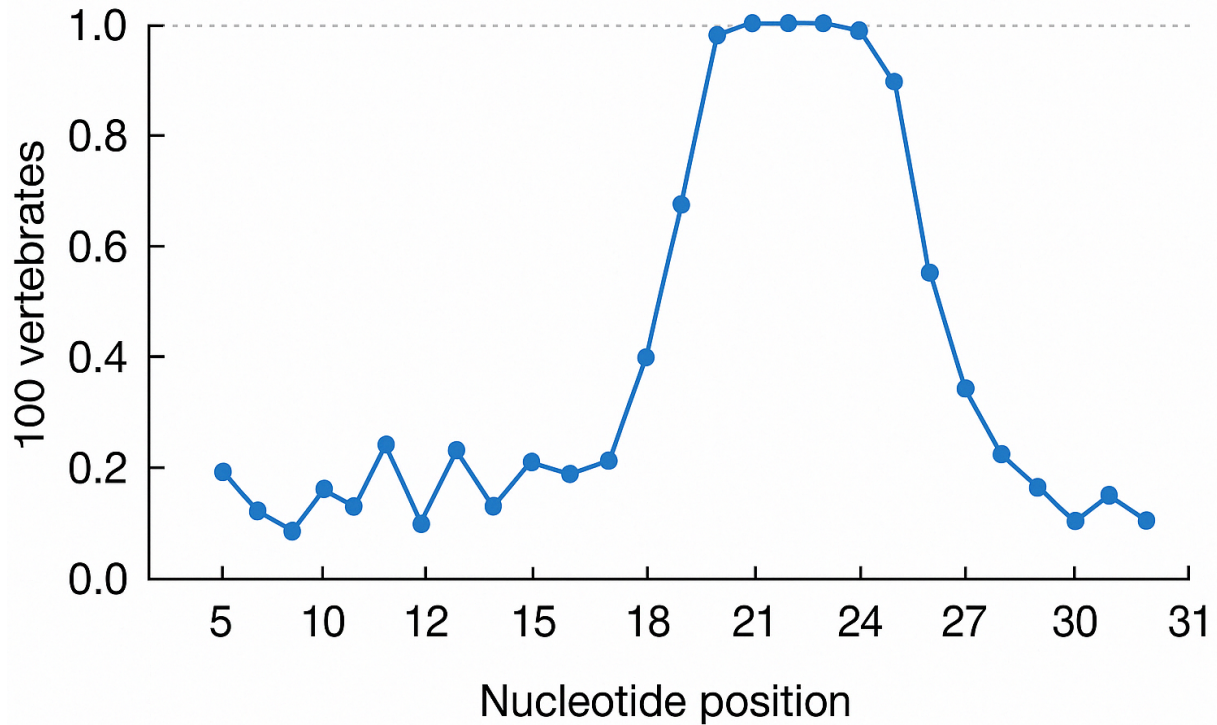
Dissociation constants: Absolute K_D values derived and interpolated from RNA Bind-n-Seq data [Jouravleva et al. 2022].

The upper/Query part shows the parameters. Below it the MAP/RUN button and resulting interactions. The “DOWNLOAD INTERACTIONS” button allows to save the interactions. A link to TarBase-v9.0 can be followed to find experimental support for the selected pair. The lower part shows the locations of the interactions in the transcript and the transcript’s accessibility.

[illegible]

Fig. S3 Evolutionary conservation of the 31-nucleotide binding sites.

Each bar represents the PhastCons conservation score at a specific nucleotide position within the 31-mer target region. Scores range from 0 (no conservation) to 1.0 (high conservation), reflecting the evolutionary constraint at each position across multiple species. The total conservation score summarizes the degree of evolutionary conservation of the entire 31-mer.



Sensitivity Benchmark

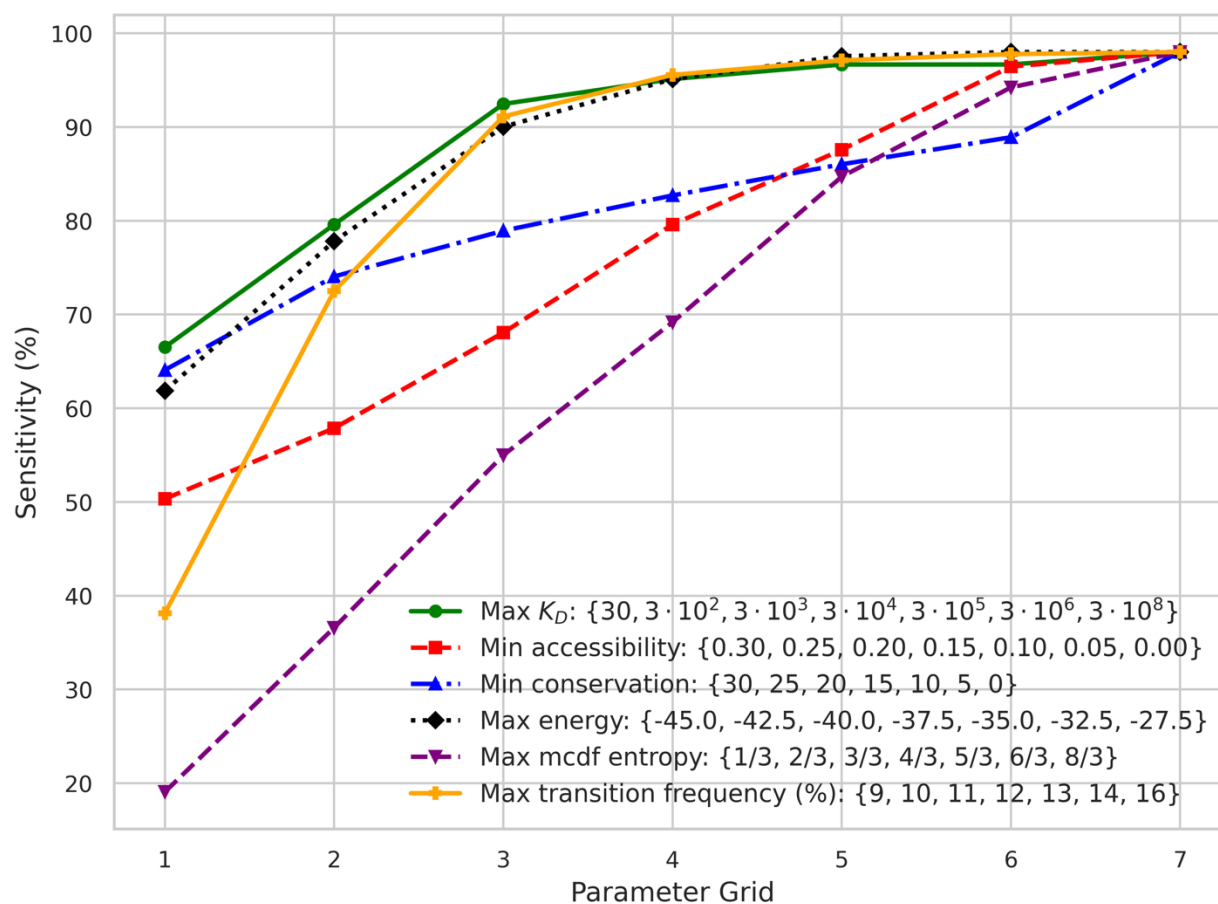
Results over miRecords. On the miRecords dataset, when predictions were restricted to strong canonical 7-mer interactions with a K_D of at most 30 pM, the measured sensitivity reached 66.5%. Relaxing the K_D threshold progressively increased sensitivity, ultimately reaching 98.0% when no restriction was applied ($K_D \leq 3 \times 10^8$). Overall, RIMap-RISC recovered nearly all interaction sites (442 out of 451 sites). The few remaining cases correspond to putative sites with limited experimental evidence, such as sites #2 and #3 of the RHOA-202:miR-155-5p pair.

The same benchmarking procedure was repeated to isolate the influence of the other parameters on RIMap-RISC sensitivity. These results, summarized in **Fig. S4**, illustrate how sensitivity progressively increases as constraints are relaxed, converging toward nearly complete recovery of experimentally validated sites. When varying the minimum accessibility, minimum conservation and maximum entropy thresholds, sensitivities increased practically linearly (**Fig. S4**). On the contrary, when varying the maximum free energy and transition frequency thresholds, sensitivities experienced rapid growth like that of K_D (**Fig. S4**).

Among the six interaction features, the dissociation constant, free energy change and transition frequency emerged as the most discriminative filters, with sensitivity increasing sharply within the first parameter increments. Notably, 92.5% of benchmark interactions exhibited predicted K_D values below 3 nM, 90.0% showed ΔG values lower than -40 kcal/mol, and 91.1% had a transition frequency below 11% as computed by mcdF. In contrast, entropy, conservation and accessibility scores influenced sensitivity in a near-linear manner, reflecting their uniform distribution across the dataset. This behavior limits their utility as selective filters for identifying biologically relevant miRNA-transcript interactions.

Fig. S4 Influence of interaction features on RIMap-RISC sensitivity over miRecords' interactions.

Interaction features include dissociation constants, accessibility scores, conservation scores, free-energy changes, entropy estimates, and transition frequencies. Each parameter spans seven threshold values, as specified in the figure legend. Sensitivities are reported as percentages of miRecords' interactions present in RIMap-RISC.



K_D correlation tables

Table S1 t₁ nucleotide.

		RISCulate (nM)	miR-1 (95%CI)	miR-155 (95%CI)	miR-124 (95%CI)	miR-7 (95%CI)	let-7a (95%CI)	lys-6 (95%CI)	miR-34b (95%CI)	miR-449a (95%CI)	AVG
	t2t8_t1A	2.000	1.341	2.958	1.513	2.441	1.183	3.254	3.261	2.061	2.252
	t2t8_t1C	3.585	3.835	4.411	3.921	4.770	2.995	5.652	5.297	3.642	4.315
	t2t8_t1U	3.585	3.252	4.548	3.502	3.277	2.588	5.425	4.981	3.100	3.834
	t2t8_t1G	3.585	3.535	5.888	3.793	3.886	3.133	6.380	5.034	3.177	4.353
	t2t7_t1A	6.966	4.130	5.179	6.648	6.089	4.819	6.600	5.892	4.260	5.452
	t2t7_t1C	8.422	6.364	6.762	8.744	8.395	6.195	8.616	7.683	5.836	7.324
	t2t7_t1U	8.422	5.803	6.754	8.324	6.707	6.049	8.349	7.317	5.114	6.802
	t2t7_t1G	8.422	6.243	7.924	8.626	7.133	6.533	9.366	7.313	5.225	7.295
	t2t6_t1A	8.937	7.936	9.602	8.208	7.682	7.907	8.618	8.271	7.167	8.174
	t2t6_t1C	10.555	9.930	10.235	10.109	9.176	9.225	9.648	9.675	8.285	9.535
	t2t6_t1U	10.555	9.429	10.260	9.648	8.025	9.036	9.618	9.338	7.746	9.138
	t2t6_t1G	10.555	9.710	10.843	10.333	8.374	9.691	10.479	9.455	7.882	9.596
		correlation:	0.947	0.918	0.992	0.965	0.979	0.956	0.972	0.953	0.980
		mean correlation:	0.960								

Table S2 Bulges.

RISCulate (nM)	miR-1 (95%CI)	miR-155 (95%CI)	miR-124 (95%CI)	miR-7 (95%CI)	let-7a (95%CI)	lys-6 (95%CI)	miR-34b (95%CI)	miR-449a (95%CI)	AVG
7.995	8.109	9.482	7.759	9.575	9.426	3.424	10.301	9.976	8.507
7.995	7.662	7.965	3.869	8.225	8.030	8.636	9.778	9.643	7.976
7.995	4.335	9.571	7.822	4.575	9.250	8.844	4.221	3.969	6.573
7.995	9.301	9.890	9.188	10.552	10.949	8.988	10.604	9.994	9.933
8.998	9.196	9.408	7.405	10.300	8.989	3.424	7.798	8.421	8.118
8.998	7.662	7.965	8.521	8.225	9.329	9.108	9.767	9.654	8.779
8.998	10.057	9.769	7.822	10.842	9.250	8.832	9.966	8.756	9.412
8.998	10.743	10.389	9.678	12.431	11.101	10.605	10.604	9.994	10.693
8.875	7.190	9.408	7.811	11.096	6.607	5.812	11.104	11.185	8.777
8.875	7.662	9.835	7.295	8.225	8.935	8.922	9.767	9.654	8.787
8.875	9.943	9.165	7.822	8.719	9.250	8.832	7.914	7.614	8.657
8.875	10.193	10.707	6.010	12.070	10.344	9.741	11.576	11.656	10.287
6.814	7.190	9.173	7.906	6.908	6.607	5.812	5.181	4.676	6.682
6.814	7.815	9.349	6.128	4.895	4.594	5.733	8.004	8.349	6.859
6.814	4.385	9.165	9.075	8.719	8.002	9.169	7.914	7.614	8.005
6.814	8.735	5.847	6.010	4.810	7.468	6.817	7.316	6.735	6.717
correlation:	0.528	0.405	0.211	0.673	0.540	0.243	0.523	0.530	0.692
mean correlation:	0.457								

Table S3 Mismatches/non-canonical base pairs.

	RISCulate (nM)	miR-1 (95%CI)	miR-155 (95%CI)	miR-124 (95%CI)	miR-7 (95%CI)	let-7a (95%CI)	lys-6 (95%CI)	miR-34b (95%CI)	miR-449a (95%CI)	AVG
8mer-x2A	8.266	9.080	8.420	5.928	9.790	8.578	8.783	9.182	8.781	8.568
8mer-x2U	8.266		8.463	7.003			9.010			8.159
8mer-x2G	8.266	9.149		7.098	9.591	7.753		9.051	8.404	8.508
8mer-x3A	10.323	10.249	10.093	8.869	11.626	10.349	8.800	11.290	11.462	10.342
8mer-x3U	10.323		10.255	9.375		10.354	9.533			9.880
8mer-x3G	10.323	11.119	10.701	9.791	12.170	10.778		11.770	11.237	11.081
8mer-x4A	9.644	9.293	8.796	9.061	10.028	9.711	9.320	8.668	8.937	9.227
8mer-x4C	9.644	9.221	9.160		10.116		9.144	10.176	10.465	9.714
8mer-x4G	9.644	10.834	9.698	10.565	11.789	11.471		10.612	11.550	10.931
8mer-x5A	9.486	10.071	7.380	10.158	10.183	9.891	9.503	9.128	9.182	9.437
8mer-x5C	9.486	8.558	8.944		8.776			9.114	9.112	8.901
8mer-x5G	9.486	11.224		10.351	11.414	9.065	10.016	11.368	11.427	10.695
8mer-x6U	10.050	9.145	10.426	9.778	11.048	8.984	9.408	10.456	11.164	10.051
8mer-x6C	10.050	10.626		9.853		9.878	9.739			10.024
8mer-x6G	10.050		11.113	10.860	10.936			10.294	10.685	10.777
8mer-x7A	7.660	6.064	8.358	8.691	7.633	7.151	7.665	7.897	7.653	7.639
8mer-x7U	7.660		9.930	7.971	7.568	7.509	8.678	7.310	7.007	7.996
8mer-x7G	7.660	8.371	9.603	8.265	6.131	7.584	9.210			8.194
8mer-x8U	4.998	2.032	4.645	6.480	5.117	3.522	6.406	4.556	3.170	4.491
8mer-x8C	4.998	2.731	4.952	6.329	5.388		6.780			5.236
8mer-x8G	4.998			8.129	7.220	5.744		7.083	3.665	6.369
	correlation:	0.669	0.317	0.805	0.867	0.764	0.679	0.765	0.813	0.834
	mean correlation:	0.710								

Table S4 Wobbles.

	RISCulate (nM)	miR-1 (95%CI)	miR-155 (95%CI)	miR-124 (95%CI)	miR-7 (95%CI)	let-7a (95%CI)	lys-6 (95%CI)	miR-34b (95%CI)	miR-449a (95%CI)	AVG
8mer-w2	8.407	8.290	9.757		8.414	7.815	9.744	8.906	8.423	8.764
8mer-w3	9.040	10.125			10.809		9.406	9.170	8.053	9.512
8mer-w4	9.432			8.963		8.732	10.553			9.416
8mer-w5	8.451		8.487	8.091		8.626	9.512			8.679
8mer-w6	8.200	8.170	7.386		8.816	9.740	9.158	8.293	8.340	8.557
8mer-w7	6.094	6.694						6.546	7.007	6.749
8mer-w8	4.234	3.416	6.109			3.830	6.482	4.139	3.495	4.578
	correlation:	0.974	0.806	1.000	0.923	0.916	0.974	0.994	0.932	0.995
	mean correlation:	0.940								

Table S5 Deletions.

	RISCulate (nM)	miR-1 (95%CI)	miR-155 (95%CI)	miR-124 (95%CI)	miR-7 (95%CI)	let-7a (95%CI)	lys-6 (95%CI)	miR-34b (95%CI)	miR-449a (95%CI)	AVG
8mer-b2	7.004	8.812	4.360	6.405	9.795	8.638	4.756	8.775	6.503	7.256
8mer-b3	8.038	8.812	10.290	6.405	9.795	10.980	4.756	8.775	6.503	8.290
8mer-b4	9.737	10.367	10.290	11.085	10.833	10.764	4.756	11.193	10.622	9.989
8mer-b5	10.202	10.367	10.413	11.085	10.833	10.764	9.990	10.259	9.921	10.454
8mer-b6	10.067	10.085	10.768	10.192	11.125	9.439	10.193	10.921	9.826	10.319
8mer-b7	6.748	6.367	8.984	7.952	6.404	7.805	8.140	6.107	4.245	7.000
	correlation:	0.879	0.679	0.865	0.804	0.678	0.461	0.884	0.948	1.000
	mean correlation:	0.775								

Table S6 Correlations between luciferase assay fold-change and estimated K_D values or free energy across alternative structure candidates for *Mink1*:miR-124 interaction.

Seed refers to the perfect reverse complement. G, U, A, C represent the nucleotide at t_6 in each variant.

K_{Db} is the K_D of the b(5.6) structure. K_{DM} is the K_D of the MFE structure. Energies in kcal/mol.

	Control (Luc)	+miR-124 (Luc)	Fold change	Seed type selected by K_D	Best K_D (pMol)	K_{Db} (pMol)	K_{DM} (pMol)	ΔG (MFE)	ΔG (best K_D)	ΔG b(5.6)
Seed	11	7	0.636	7mer	12		12	-23.245	-23.245	
G	14	11	0.786	7mer-b7	322	337	4090	-21.882	-19.657	-21.197
U	9	9.5	1.056	7mer-b(5.6)	1408	1408	1408	-21.204	-21.204	-21.204
A	9	9.5	1.056	7mer-b(5.6)	1408	1408	1408	-21.523	-21.523	-21.523
C	10	9	0.900	7mer-b(3.4)	765	1408	1533	-21.067	-21.041	-21.031
r					0.991	0.830	0.075	0.835	0.327	-0.538
r²					0.982	0.688	0.006	0.698	0.107	0.289

Table S7 RABS-SHAPE reactivity for 11 mRNA targets when bound to miR-34a-5p-AGO in TRANS.

SHAPE reactivity levels color-coded: blue low flexibility (highly probably involved in base pairing); red high reactivity (highly probably not involved in base pairing); white cutoff point for base pairing. Gray regions in the mRNA tails indicate low probability for base pairing. The structures are predicted by the bipartite RMap-RISC folding algorithm. True positives (TP) black bars; sensitivity (sty); false positives gray bars.

Transcript (variant) position	Target Site Shape Reactivity	TP Sty FP
	seed 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31	
BCL2 (201) 1780	5'-ggcaaaacgucgaauacagcua-uuuacugccA-3' BCL2-201 [1780..1810] (3UTR) target site: 8mer-w8 :: A1-7mer-w8(0.69) 5mer(0.22) bridge: 3 phastcons: -1.00 dG: -49.29 Kd: 19 3'-----u---g-----uugGUCGAuucUGACGGu-5' hsa-miR-34a-5p Accgucauuuaucgacuaagcugcaaaacgg uGGCAGUGuc<u>uu</u>AGCUGguugu	11 1.0 1
NOTCH1 (204) 8086	5'-uguacuuuuuuuuuacacagaaa---cacugccu-3' NOTCH1-204 [8086..8116] (3UTR) target site: 7mer-m8 in: TarBase-v9.0 : :: 7mer(0.08) suppress(0.24) bridge: 1 phastcons: -1.00 dG: -41.50 Kd: 12 3'-----u---guug-GUCGAuucUGACGGu-5' hsa-miR-34a-5p uccgucacaaagacacauuuuuauuuucaugu uGGCAGUG<u>u</u>AGCUGguugu	7 1.0 4
CDK6 (201) 2457	5'-auuacacuguaucuuucugcc-acacacugccu-3' CDK6-201 [2457..2487] (3UTR) target site: 7mer-m8 in: TarBase-v9.0 :: :: :: 7mer(0.10) suppress(0.20) bridge: 3 phastcons: -1.00 dG: -46.74 Kd: 12 3'-----uguugGUCGAuucUGACGGu-5' hsa-miR-34a-5p uccgucacacaccgucuuucaugucacauua uGGCAGUGuc<u>uu</u>AGCUGguugu	12 1.0 2

CCND1 (201) 3097	5'-guuuuuuuuuuacaaugucauuacugccA-3' CCND1-201 [3097..3127] (3UTR) target site: 8mer-w8 in: TarBase-v9.0 !!!:!!!:!! A1-7mer-w8(0.20) suppress(0.03) bridge: 13 phastcons: 31.00 dG: -43.75 Kd: 19 3'-uguugGUCGAu-----u-c-----uGUGACGGu-5' hsa-miR-34a-5p Accgucauauacuguaacauuuuguuuuuuug uGGCAGUGu-----c-u-----uAGCUGguugu	7 1.0 4
SIRT1 (201) 3719	5'-auaaaacaccagcuaggaccauuacugccA-3' SIRT1-201 [3719..3749] (3UTR) target site: 8mer-w8 in: TarBase-v9.0 : : : : : ! A1-7mer-w8(0.39) 5mer(0.04) bridge: 8 phastcons: 27.00 dG: -56.92 Kd: 19 3'-----uguugGUCGAuuc-----GUGACGGu-5' hsa-miR-34a-5p Accgucauuaccaggaucgacccacaaaaua uGGCAGUG---GucuuAGCUGguugu	21 1.0 1
HNF4a (201) 1699	5'---aacauggccuaagggccacauccacugccA-3' HNF4A-201 [1699..1729] (3UTR) target site: 8mer in: TarBase-v9.0 A1-7mer(0.14) offset-4mer-w16w17(0.02) bridge: 14 phastcons: 1.00 dG: -44.81 Kd: 4 3'-uguug-GUCGA--uuc-----GUGACGGu-5' hsa-miR-34a-5p Accgucaccuacaccgggaauccgguacaa uGGCAGUG-----ucuuAGCUGguu	9 0.8 0
CD44 (201) 3089	5'-gacauuaguccacuauguguuuuacugccA-3' CD44-201 [3089..3119] (3UTR) target site: 8mer-w8 A1-7mer-w8(0.32) suppress(0.64) bridge: 9 phastcons: 0.00 dG: -44.64 Kd: 19 3'-uguug---GUCGAuuc-u-----GUGACGGu-5' hsa-miR-34a-5p Accgucauuguuguguaucaccggauuacag uGGCAGUG----u-cuuAGCUGguugu	7 0.9 5
NOTCH2 (201) 10114	5'-gguuucagugagaggaggacaacacugccu-3' NOTCH2-201 [10114..10144] (3UTR) target site: 7mer-m8 in: TarBase-v9.0 !::: 7mer(0.33) offset-4mer-w14(0.26) bridge: 13 phastcons: -1.00 dG: -48.29 Kd: 12 3'-uguugGUCGAuuc-----GUGACGGu-5' hsa-miR-34a-5p uccgucacaacaggaggaguagugacuuugg uGGCAGUG-----ucuuAGCUGguugu	13 1.0 3

PNUTS PPP1R10 (201) 4173	5'-gggccgaaagucacacacacug---cacugccu-3' PPP1R10-201 [4173..4203] (3UTR) target site: 7mer-m8 in: TarBase-v9.0 :: :: 7mer(0.21) suppress(0.18) bridge: 1 phastcons: -1.00 dG: -39.59 Kd: 12 3'-----u--guugGUCG-A-uucuGUGACGGu-5' hsa-miR-34a-5p uccgucacguacacacugaaaguccggg uGGCAGUG_uA-GCUGguugu	8 1.0 0
WNT1 (201) 1681	5'-ucuccgaggagacccuuguu--g-cacugccc-3' WNT1-201 [1681..1711] (3UTR) target site: 7mer-m8 in: TarBase-v9.0 :: :: 7mer(0.31) suppress(0.31) bridge: 1 phastcons: 14.00 dG: -39.93 Kd: 12 3'-----uguugG--UCGAuucuGUGACGGu-5' hsa-miR-34a-5p cccgucacguuguuccccagagggcgccucu uGGCAGUG_ucAGCU--Gguugu	12 0.9 0
DLL1 (201) 3284	5'-ugucgcggccggccgucgucgacugccu-3' DLL1-201 [3284..3314] (3UTR) target site: 7mer-m8 ! ! ! : !: ! 7mer(0.23) offset-4mer-w16(0.16) bridge: 8 phastcons: -1.00 dG: -49.97 Kd: 12 3'-----uguug-GUCGA----uucuGUGACGGu-5' hsa-miR-34a-5p uccgucacggcguccgcccggcccggcgcugu / uGGCAGUGucuu---AGCUGguugu	16 0.9 0