

Supporting Information

Dynamic Origins of Differential RNA Binding Function in Two dsRBDs from the miRNA “Microprocessor” Complex

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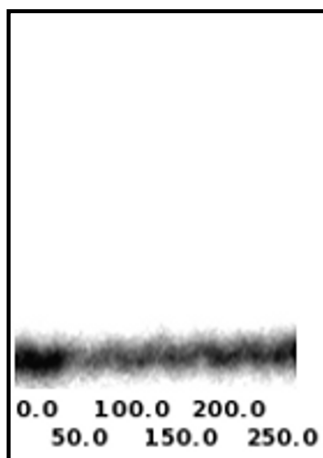


Figure S1: EMSA gel of Droscha-dsRBD that demonstrates Droscha-dsRBD does not bind pri-miR-16-1. Protein concentration (μM) is shown below the lanes.

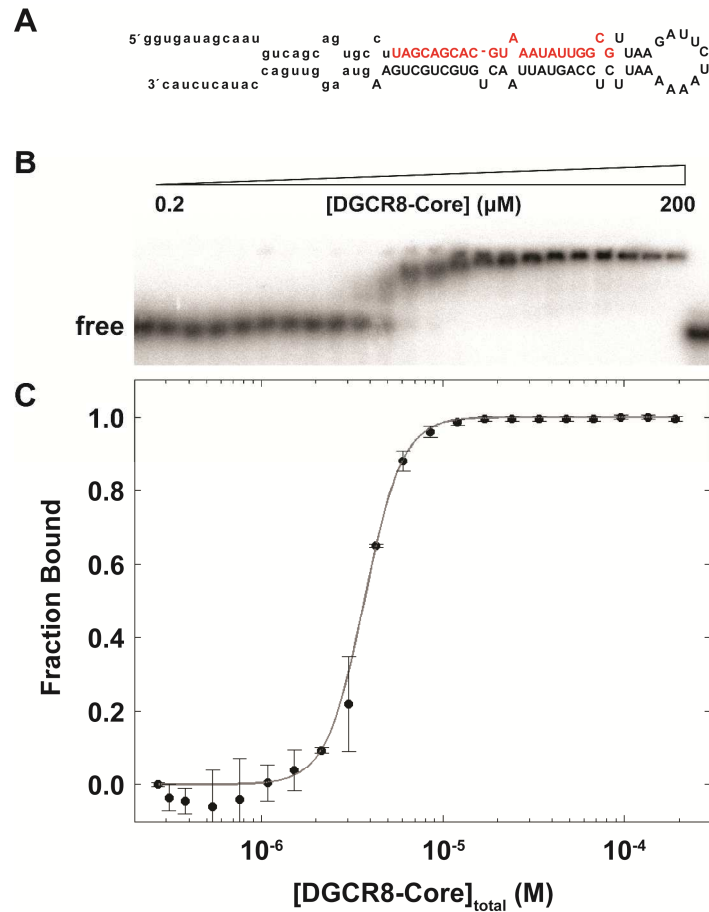


Figure S2: EMSA assay of pri-miR-16-1 binding to DGCR8-Core. (A) Predicted secondary structure of pri-miR-16-1 with the sequence of the mature miRNA shown in red and the region removed by Drosha cleavage indicated through lower-case letters. (B) Representative gel showing addition of 2-200 μ M DGCR8-Core to 0.25 nM pri-miR-16-1. (C) Fitted EMSA fraction bound as a function of DGCR8-Core concentration with data points and uncertainties represented by filled circles and the best fit to the data shown in grey.

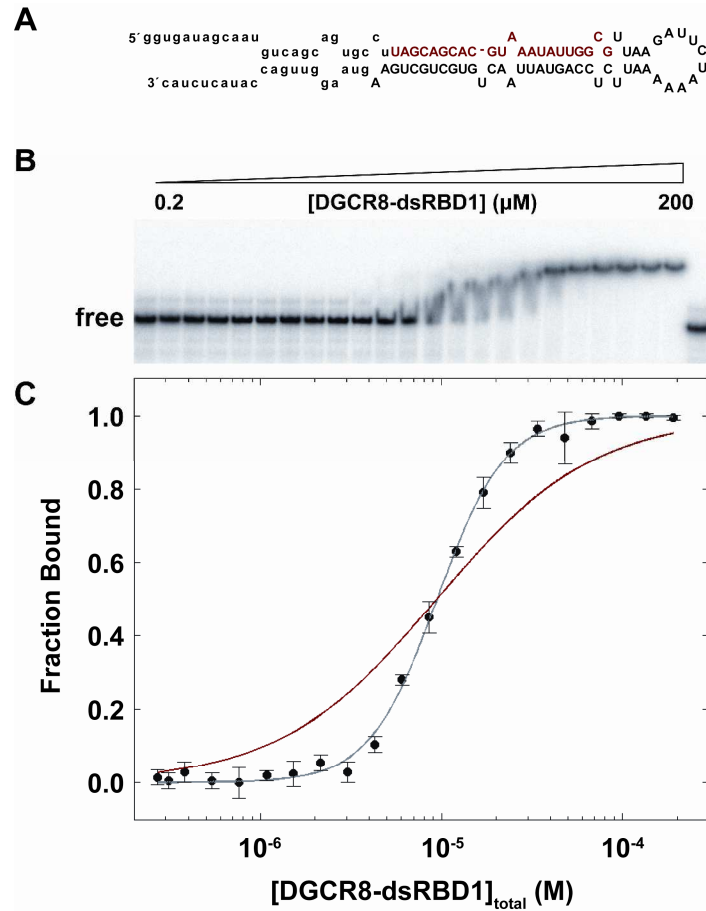


Figure S3: EMSA assay of pri-miR-16-1 binding to DGCR8-dsRBD1. (A) Predicted secondary structure of pri-miR-16-1 with the sequence of the mature miRNA shown in red and the region removed by Drosha cleavage indicated through lower-case letters. (B) Representative gel showing addition of 2-200 μM DGCR8-dsRBD1 to 0.25 nM pri-miR-16-1. (C) Fitted EMSA fraction bound as a function of DGCR8-dsRBD1 concentration with data points and uncertainties represented by filled circles. The N-independent and identical sites best fit to the data is shown in red and the fully cooperative best fit to the data is shown in grey.

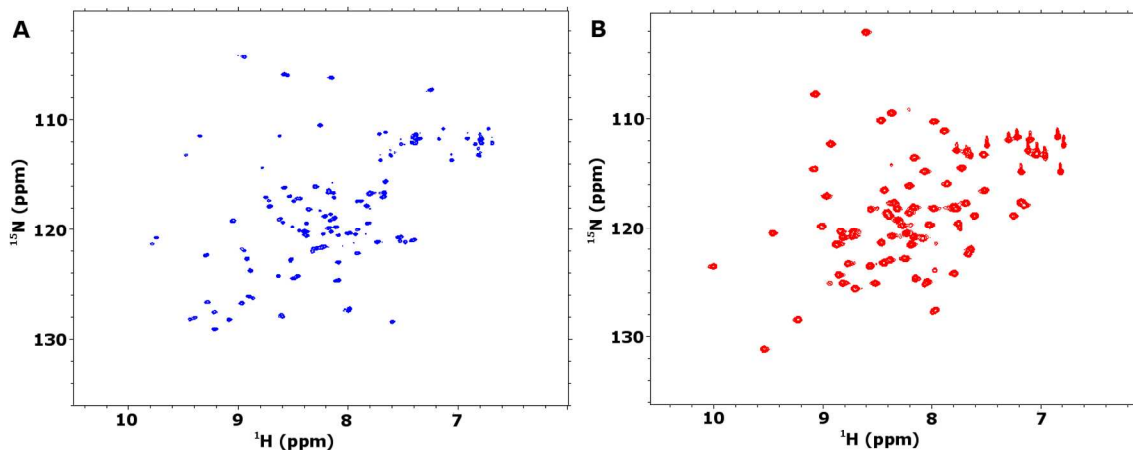


Figure S4: The representative $^1\text{H},^{15}\text{N}$ -HSQC spectra of (A) Drosha-dsRBD and (B) DGCR8-dsRBD1.

Table S1: Chemical shifts (ppm) from the backbone assignment of Drosha-dsRBD.

Residue	N	H	CO	CA	CB
G1258	-	-	173.7	45.27	-
N1259	119.4	7.82	176.2	54.98	34.04
D1260	122.8	8.51	174.8	54.61	29.14
P1261	-	-	178.0	65.41	32.80
K1262	117.0	7.68	180.6	60.41	31.86
S1263	119.0	8.12	176.8	61.38	62.25
Q1264	121.9	8.32	178.5	58.76	28.87
L1265	120.3	8.44	176.9	58.27	41.06
Q1266	116.7	7.67	177.8	58.42	28.19
Q1267	116.8	8.13	179.0	58.72	27.97
C1268	199.3	8.16	177.5	58.37	39.24
C1269	119.9	8.50	177.6	62.02	33.332
L1270	120.2	7.92	179.0	57.56	41.62
T1271	111.4	7.71	175.4	64.23	69.66
L1272	121.1	7.40	176.9	54.82	41.61
R1273	120.8	7.52	176.0	56.38	30.65
T1274	119.1	8.61	174.2	61.44	70.29
E1275	124.3	8.63	177.1	57.60	29.52
G1276	111.5	8.62	173.7	45.17	-
K1277	118.3	8.26	174.4	52.77	39.02
E1278	119.9	8.17	174.1	52.05	40.88
P1279	-	-	176.2	62.90	32.04
D1280	121.7	8.28	174.6	54.79	43.25
I1281	116.5	8.17	174.0	58.06	40.14
P1282	-	-	174.8	63.17	32.05
L1283	124.6	8.49	174.8	53.70	45.13
Y1284	123.8	8.88	176.2	57.78	39.77
K1285	122.4	9.29	175.0	55.08	36.87
T1286	122.7	8.91	174.8	63.21	68.08
L1287	129.1	9.22	177.2	55.44	43.28
Q1288	115.7	7.66	173.9	55.49	32.05
T1289	119.5	8.38	173.3	61.87	70.65
V1290	121.6	8.22	174.8	60.29	35.49
G1291	110.6	8.25	172.1	43.76	-
P1292	-	-	177.7	62.12	32.37

S1293	114.4	8.78	177.7	62.06	62.84
H1294	-	-	174.8	56.04	30.36
A1295	128.5	7.59	174.3	51.61	18.03
R1296	123.0	8.08	177.0	55.34	32.15
T1297	116.2	8.57	173.5	62.39	70.65
Y1298	127.6	9.22	174.9	57.32	40.67
T1299	117.1	8.75	173.9	61.78	70.15
V1300	128.2	9.40	172.7	59.98	35.94
A1301	126.3	8.87	174.5	49.56	23.77
V1302	118.7	8.16	173.0	57.62	34.53
Y1303	126.7	9.28	175.2	56.32	42.90
F1304	119.3	9.04	175.1	56.66	42.83
K1305	128.3	9.08	176.3	57.58	29.49
G1306	104.3	8.94	173.6	45.16	-
E1307	121.2	7.73	175.2	54.28	31.76
R1308	126.7	8.96	176.7	56.95	30.06
I1309	121.9	8.95	174.8	61.37	39.81
G1310	107.4	7.24	172.2	45.43	-
C1311	120.8	9.75	172.3	57.04	36.41
G1312	111.5	9.35	170.5	44.58	-
K1313	117.1	8.52	176.7	53.96	37.15
G1314	106.0	8.58	171.0	45.99	-
P1315	-	-	174.7	63.70	31.81
S1316	111.5	7.38	173.7	56.11	66.6
I1317	124.4	8.45	177.4	65.23	37.08
Q1318	118.1	8.36	178.8	59.57	27.88
Q1319	116.8	7.81	178.8	58.92	29.18
A1320	124.7	8.09	179.0	55.86	18.44
E1321	117.9	8.72	178.7	59.66	29.83
M1322	116.8	7.80	178.6	58.94	32.01
G1323	106.2	8.15	176.3	47.27	-
A1324	127.9	8.60	178.5	55.08	17.64
A1325	120.3	8.39	179.5	55.45	17.45
M1326	116.1	8.30	178.3	59.09	32.96
D1327	120.4	7.99	177.7	57.78	43.24
A1328	119.8	8.10	180.0	54.81	19.07
L1329	117.1	8.46	179.3	58.15	42.25
E1330	117.7	7.83	178.7	58.72	30.10
K1331	117.5	7.88	177.6	57.74	33.88
Y1332	120.5	8.22	174.8	59.57	38.38
N1333	121.1	7.56	173.7	52.48	38.09
F1334	122.2	7.92	173.8	56.92	38.70
P1335	-	-	176.4	63.10	29.12
Q1336	120.6	8.39	175.2	55.80	29.39
M1337	127.3	7.99	-	56.94	33.76

Table S2: Chemical shifts (ppm) from the backbone assignment of DGCR8-dsRBD1.

Residue	N	H	CO	CA	CB
G504	-	-	173.7	45.12	-
I505	119.5	7.95	175.7	60.83	38.84
P507	-	-	175.7	63.5	31.83
N508	123.7	7.89	177.8	54.76	40.74
G509	114.0	8.29	174.2	45.55	-
K510	120.8	8.01	176.1	56.08	34.02
S511	118.0	8.47	174.8	57.54	65.01
E512	123.3	9.993	178.4	62.03	28.31
V513	118.0	7.70	178.7	66.23	32.58
C514	122.1	7.59	177.4	63.01	27.05
I515	121.2	8.39	179.1	65.15	38.15
L516	120.2	8.64	177.6	58.45	40.80
H517	119.6	8.19	177.8	60.92	31.10
E518	117.9	8.25	178.8	59.70	29.30
Y519	120.5	8.29	177.6	62.10	38.86

M520	116.8	8.89	178.7	59.57	31.21
Q521	117.9	8.09	177.3	58.76	28.79
R522	117.5	7.61	177.3	58.67	31.03
V523	115.9	8.13	176.7	64.74	32.69
L524	117.7	7.07	176.1	55.58	43.50
K525	114.6	7.99	175.4	56.62	28.91
V526	113.0	6.96	173.8	59.72	35.62
R527	121.3	8.11	174.3	52.83	30.88
P528	-	-	175.3	62.41	32.41
V529	122.7	8.17	174.9	61.87	33.56
Y530	125.4	8.63	174.9	57.59	39.97
N531	121.3	8.80	173.4	51.68	41.04
F532	120.2	8.76	175.4	57.48	41.51
F533	118.7	8.31	173.3	55.73	40.90
E534	120.7	8.74	175.7	55.62	31.21
C535	123.0	8.36	174.1	56.69	29.56
E536	124.8	8.86	175.6	57.01	29.17
N537	121.8	7.56	174.6	51.01	39.07
P538	-	-	178.3	64.44	31.86
S539	110.9	7.80	174.7	59.81	63.63
E540	118.6	7.17	171.1	53.48	30.56
P541	-	-	177.4	64.07	32.34
F542	117.8	7.72	173.5	57.95	40.19
G543	109.2	8.29	173.0	42.48	-
A544	123.1	8.69	174.7	50.56	22.73
S545	114.3	9.00	174.3	56.84	66.69
V546	122.7	8.31	175.5	61.12	33.27
T547	119.6	8.93	173.7	59.55	71.52
I548	121.3	8.79	176.7	61.05	39.37
D549	130.9	9.46	175.6	55.31	40.03
G550	101.8	8.53	173.7	45.23	-
V551	124.0	7.71	175.6	61.80	33.68
T552	124.8	8.74	174.5	64.39	69.01
Y553	128.2	9.15	174.6	57.60	39.19
G554	110.1	7.90	171.2	45.07	-
S555	113.3	8.08	172.8	56.84	66.84
G556	107.5	8.99	170.6	45.59	-
T557	110.0	8.38	173.7	58.84	71.55
A558	120.3	9.38	175.9	51.55	23.98
S559	112.0	8.85	173.4	59.79	63.61
S560	113.0	7.45	-	56.15	66.72
K561	-	-	177.8	60.53	32.24
K562	118.4	8.13	179.2	59.70	32.38
L563	118.6	7.53	179.4	57.33	42.14
A564	124.4	8.08	178.9	56.12	17.15
K565	117.5	8.27	178.0	60.47	32.62
N566	116.3	7.44	177.6	57.04	38.80
K567	120.3	8.16	179.1	60.14	33.15
A568	123.3	8.49	180.9	55.29	18.12
A569	124.1	8.78	179.2	55.69	17.88
R570	120.5	8.65	177.5	59.89	29.62
A571	119.0	8.24	180.4	54.56	18.64
T572	115.7	7.78	175.7	68.16	67.98
L573	124.8	8.44	177.1	58.72	41.17
E574	114.2	7.65	177.9	58.74	29.66
I575	117.4	7.10	177.7	63.93	39.63
L576	118.0	7.91	177.5	57.22	44.06
I577	118.4	8.33	173.1	58.50	38.51
P578	-	-	177.7	64.46	31.70
D579	116.3	8.36	176.2	54.43	39.89
F580	120.6	8.09	176.0	60.16	39.54
V581	119.4	7.67	175.2	62.13	32.52
K582	124.8	7.97	175.7	56.30	32.81
Q583	127.3	7.89	180.5	57.29	30.10