

2D Structure	Local AU	Position	Conservation	Predicted By
<p>675 7mer-m8 696</p> <p>5'-tccccAAGTCCACTTCCTTC-3' UTR</p> <p>3'-auuuacUUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC 7mer-m8</p>		<input type="checkbox"/>	
<p>1630 Offset 6mer 1651</p> <p>5'-catttcctTTCAGTTTCCTTT-3' UTR</p> <p>3'-auuuacuuAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Offset 6mer</p>		<input type="checkbox"/>	
<p>4113 Imperfect match 4133</p> <p>5'-cccAAGAATT-ACCTTCCTTC-3' UTR</p> <p>3'-auUACUUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	
<p>4536 Imperfect match 4559</p> <p>5'-gacATGATTCATCCATTCCTTC-3' UTR</p> <p>3'-auUACUUAAGU--UAAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	
<p>4993 Imperfect match 5015</p> <p>5'-ttttAAATCTTATTTTCCTTC-3' UTR</p> <p>3'-auuuACUUA-AGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	
<p>5467 Offset 6mer 5487</p> <p>5'-acATTTAATAC-ATTCCTTTA-3' UTR</p> <p>3'-auUUACUUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Offset 6mer</p>		<input type="checkbox"/>	
<p>5599 Offset 6mer 5623</p> <p>5'-taATGTCAAAATGTTTCCTTTA-3' UTR</p> <p>3'-auUUAC--UUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Offset 6mer</p>		<input type="checkbox"/>	
<p>6190 Offset 6mer 6210</p> <p>5'-caAAT-ACTTTAATTCCTTT-3' UTR</p> <p>3'-auUUACUUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Offset 6mer</p>		<input type="checkbox"/>	
<p>6268 Offset 6mer 6290</p> <p>5'-taAATAATTCGGTTTCCTTC-3' UTR</p> <p>3'-auUUACUUAAG-UUAAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Offset 6mer</p>		<input type="checkbox"/>	
<p>6446 7mer-m8 6469</p> <p>5'-acAATGAATATTAATTCCTTC-3' UTR</p> <p>3'-auUUAC-UUA-AGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC 7mer-m8</p>		<input type="checkbox"/>	
<p>7483 Offset 6mer 7503</p> <p>5'-tgAGTGAG--CGATTTTCCTTTA-3' UTR</p> <p>3'-auUUACUUAAGUU-AAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Offset 6mer</p>		<input type="checkbox"/>	
<p>8445 Imperfect match 8464</p> <p>5'-aaATGCCTTT--TTTCCTTC-3' UTR</p> <p>3'-auUUACUUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	
<p>8598 Imperfect match 8620</p> <p>5'-taAAAGAA-ACAATTTTCCTTCa-3' UTR</p> <p>3'-auUUACUUAAGUU--AAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	
<p>9295 Imperfect match 9317</p> <p>5'-tctcTGACTTCAGCTTCCTTC-3' UTR</p> <p>3'-auuuAC-UUAAGUUAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	
<p>10658 Imperfect match 10680</p> <p>5'-tgAAGGTGTTAGTTTCCTTCa-3' UTR</p> <p>3'-auUUACUUAAGUU-AAAGGAAGA-5' miRNA</p> <p>3'pairing Seed</p>	<p>TTCCTTC Imperfect</p>		<input type="checkbox"/>	

Figure 1: The binding sites of hsa_circRNA_001481 with hsa-miR-1252-5p, are shown in 2D structure interactions

2D Structure	Local AU	Position	Conservation	Predicted By
779 Offset 6mer 802 5'-tgaaTTTCTTTATTTATCTCTCTa-3' UTR 3'-gaagACAAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
1496 8mer 1519 5'-taTTTATATATCTTGGTCTCTCCa-3' UTR 3'-gaAGACAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M) (T)
1564 Imperfect match 1589 5'-atTCTTTCTTAACTTTTTCCCTCCa-3' UTR 3'-gaAGACAGAGA--GAAAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
1698 Offset 6mer 1720 5'-ctcCTCTTTCCTTAATCTCTCT-3' UTR 3'-gaaGACAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
1733 Imperfect match 1754 5'-ttTCTGTC-CTTTCTCCCTCCc-3' UTR 3'-gaAGACAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
2314 Imperfect match 2336 5'-acatttaCTTTTTTTCTTTTct-3' UTR 3'-gaagacaGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
5011 Imperfect match 5033 5'-ttTCTTACGCTGTTCTCTTCTg-3' UTR 3'-gaAGACAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
6275 Imperfect match 6299 5'-ttTCTGTTTCCTTTCTTCTCCCa-3' UTR 3'-gaAGA-CAGAGA-AAAG-AGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
8445 Imperfect match 8469 5'-aaaaTGCCTTTTTTCTTTCTCTTc-3' UTR 3'-gaagACAGAGAAAAG--AGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
8763 Imperfect match 8784 5'-cttacGTC-CTGTATTCTTTCCt-3' UTR 3'-gaagaCAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)
10230 7mer-m8 10252 5'-tggagggaTTGTATCTCTCCc-3' UTR 3'-gaagacagagAAAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M) (T)
10301 Imperfect match 10323 5'-gaTTTGAACCTTTTAACTTTTCCt-3' UTR 3'-gaAGACAGAGA-AAAGAGAGAGGu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	(M)

Figure 2: The binding sites of hsa_circRNA_001481 with hsa-miR-4644 along with predicted tool and Local AU

2D Structure	Local AU	Position	Conservation	Predicted By
<p>Imperfect match</p> <p>397 5'-taATAACTTGAATTATCTTTa-3' UTR</p> <p>3'-guUUUUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>2672 5'-taAGAAGAATAATTATCTTTt-3' UTR</p> <p>3'-guUUUUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>5266 5'-caAAAAGGAACAATACTTTTg-3' UTR</p> <p>3'-guUUUUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>5747 5'-ctaAGATGATTATACTTTTg-3' UTR</p> <p>3'-guUUUUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>6182 5'-agAGAAGC-CAATACTTTTa-3' UTR</p> <p>3'-guUUUUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>6935 5'-acttGAGCACAAAGTGCCTTTt-3' UTR</p> <p>3'-guuuUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>7799 5'-cacAAACTTTAATATGCCTTTc-3' UTR</p> <p>3'-guuuUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>7863 5'-gaAAAACATGTCATGATCTTTt-3' UTR</p> <p>3'-guUUUUGGU---GUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	
<p>Imperfect match</p> <p>8436 5'-ttAGTATTAATAATGCCTTTt-3' UTR</p> <p>3'-guUUUUGGUUUUAUGGAAAc-5' miRNA</p> <p>3' pairing Seed</p>			<input type="checkbox"/>	

Figure 3: The binding sites of hsa_circRNA_001481 with hsa-miR-548m are presented.

2D Structure	Local AU	Position	Conservation	Predicted By
780 7mer-A1 802 5'-gaATTTCTTTATTTATCTCTCTa-3' UTR 3'-ugUAGUGUAGGAAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M <input checked="" type="checkbox"/> T
1683 Imperfect match 1707 5'-ccATC-TGCCCTTCCCTCTCTTc-3' UTR 3'-ugUAGUGUAGGAAGG--GGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
1698 6mer 1720 5'-ctcctcttTCCTTAATCTCTCT-3' UTR 3'-uguaguguAGGAAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
1714 Imperfect match 1736 5'-ctcTCTTTTCCTTCCCTTTTc-3' UTR 3'-uguAGUGUAGGAAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
1795 Imperfect match 1819 5'-tccTTCCTTTTTCTCTCCCTTTTc-3' UTR 3'-uguAGUGUAGGAAG--GGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
2315 Imperfect match 2337 5'-catTTACTTTTTTTCTTTTCTa-3' UTR 3'-uguAGUGUAGGAAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
6269 Imperfect match 6292 5'-aaATAATTTCTGGTTTCCTTTCTt-3' UTR 3'-ugUAGUGUAGG-AAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
8468 Imperfect match 8488 5'-ccccCACCACC--CCCCTCTTTt-3' UTR 3'-guaGUGUAGGAAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M
9278 Imperfect match 9300 5'-cacTTACTACCTGCACTTCTCTg-3' UTR 3'-uguAGUGUAGGAAGGGGAGAGAu-5' miRNA 3'pairing Seed			<input type="checkbox"/>	<input checked="" type="checkbox"/> M

Figure 4: The binding sites of hsa_circRNA_001481 with miRNA (hsa-miR-6758-5p) response elements (MRE)

2D Structure	Local AU	Position	Conservation	Predicted By
<p>668 5'-ttTGTATCC¹⁰CCCAAGTCCACTT¹⁵CCTTCC²⁰-3' UTR 3'-agGACA-AGA¹⁰G--UCGGG-GAAGGGAGG¹⁵a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing Imperfect match Seed</p>			<input type="checkbox"/>	M
<p>1565 5'-ttCT-TTCTTAAC¹⁰TTTTT¹⁵CCCTCC²⁰a-3' UTR 3'-agGACAAGA¹⁰GUCG-GGGAAGGGAGG¹⁵a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 8mer Seed</p>			<input type="checkbox"/>	M T
<p>1655 5'-tatgcaTTTCA--TTTT¹⁰CCCTCC¹⁵c-3' UTR 3'-aggacaAGA¹⁰GUCGCGGAA¹⁵GGGAGG²⁰a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 7mer-m8 Seed</p>			<input type="checkbox"/>	M T
<p>1676 5'-ccCTGCCCATCTGC¹⁰CCTTCC¹⁵CTCt-3' UTR 3'-agGACAAG--AGUCG¹⁰GGGAAGGGAGG¹⁵a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 6mer Seed</p>			<input type="checkbox"/>	M
<p>1728 5'-ccCT-TTTTCTGT¹⁰CTTCTT¹⁵CCCTCC²⁰c-3' UTR 3'-agGACAAGA¹⁰GUCGGG--GAAAGGGAGG¹⁵a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 7mer-m8 Seed</p>			<input type="checkbox"/>	M T
<p>1758 5'-ttTTGAGTTCA¹⁰TTTCCTT¹⁵CCTTCC²⁰-3' UTR 3'-agGACAAGA¹⁰GUCGGGAA¹⁵GGGAGG²⁰a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing Imperfect match Seed</p>			<input type="checkbox"/>	M
<p>1778 5'-ttcccTTCC¹⁰TGCCCTCCTT¹⁵CCTTCC²⁰t-3' UTR 3'-aggacAAGA¹⁰GUCGGGAA¹⁵GGGAGG²⁰a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing Imperfect match Seed</p>			<input type="checkbox"/>	M
<p>4537 5'-acaTGATTCA-TCCATT¹⁰CTTTCC¹⁵c-3' UTR 3'-aggACAAGA¹⁰GUCGGGAA¹⁵GGGAGG²⁰a-5' miRNA 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing 3'pairing Imperfect match Seed</p>			<input type="checkbox"/>	M

Figure 5: The binding sites of hsa_circRNA_001481 with hsa-miR-6797-5p response elements

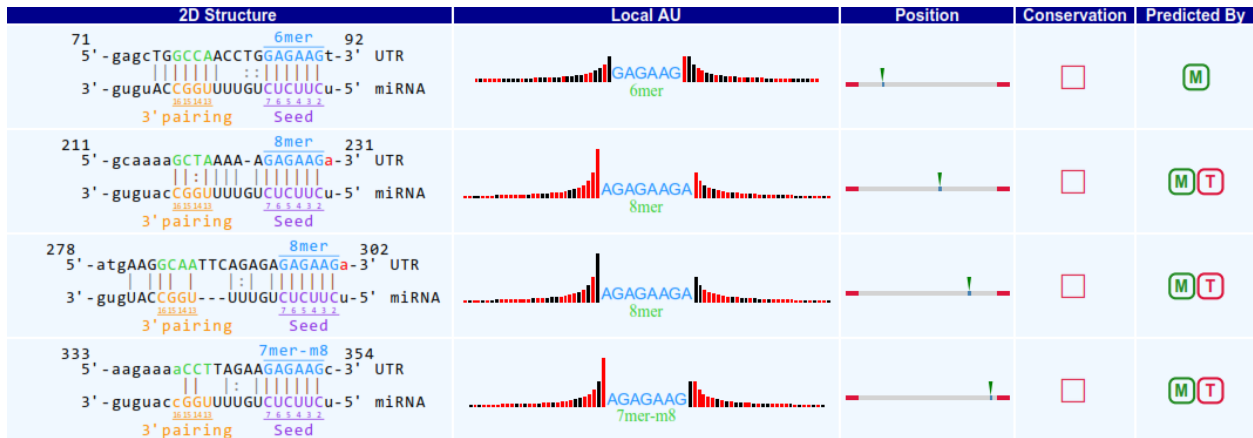


Figure 6: The binding interactions of hsa_circRNA_000479 with hsa-miR-942-5p response elements

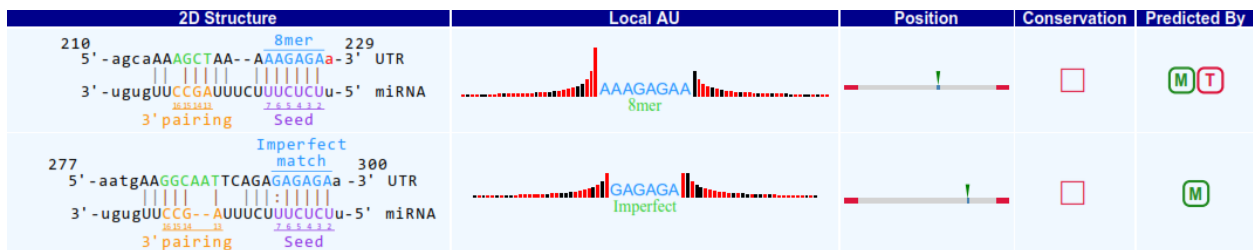


Figure 7: The binding interactions of hsa_circRNA_000479 with hsa-miR-4753-3p response elements

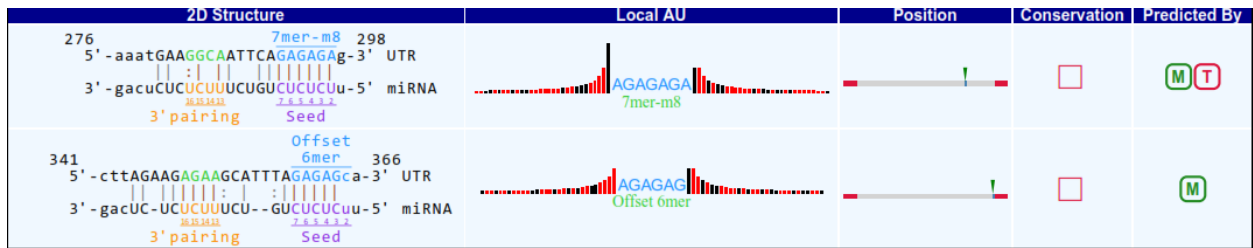


Figure 8: The binding interactions of hsa_circRNA_000479 with hsa-miR-6873-3p response element

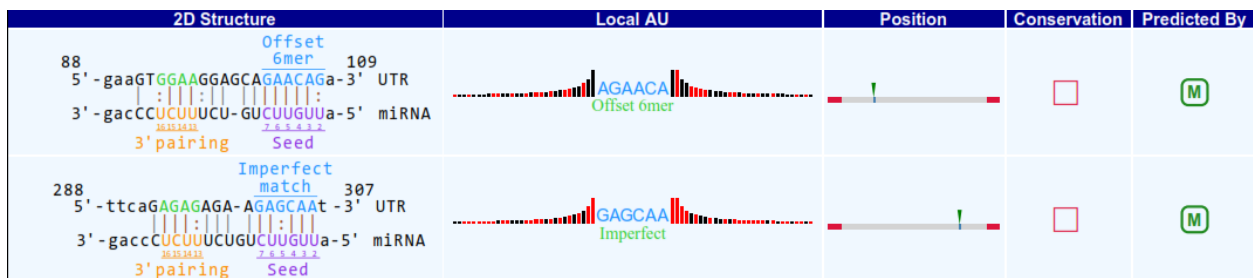


Figure 9: The binding interactions of hsa_circRNA_000479 with hsa-miR-6739-3p response element

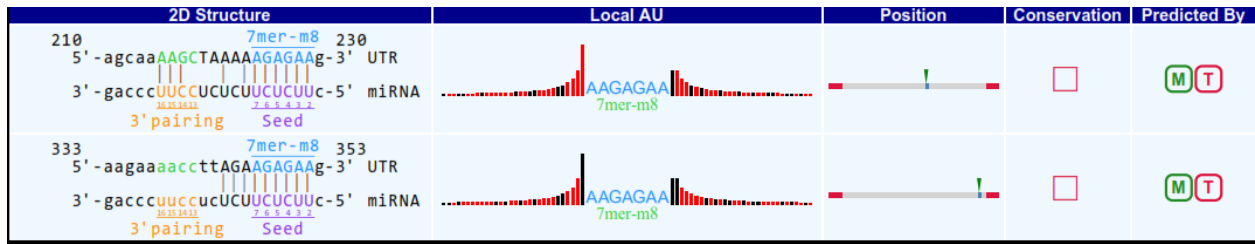


Figure 10: The binding interactions of hsa_circRNA_000479 with hsa-miR-6809-3p response element