Supplementary Table S1. MicroRNAs predicted to target RUNX1 3' UTR (NM_001001890 - 4334 nt) by TargetScan analysis

MicroRNA	Position in RUNX1 3'UTR	predicted pairing of target region (top) and miRNA (bottom)	seed match	context + score	context + score percentile	PCT
hsa-miR-27a	321-328	5' ...GAUUCCCGGAGGGAAACUGUGAA... ||||||| 3' CGCCUUGAAUCGGUGACACUU	8mer	-0.24	91	0.9
	348-354	5' ...UCUGAUUUAGCAAUGCUGUGAAU... ||||| |||||| 3' CGCCUUGAAUCGGU--GACACUU	7mer-1A	-0.13	73	0.7
hsa-miR-27b	321-328	5' ...GAUUCCCGGAGGGAAACUGUGAA... ||||||| 3' CGUCUUGAAUCGGUGACACUU	8mer	-0.23	90	0.9
	348-354	5' ...UCUGAUUUAGCAAUGCUGUGAAU... ||||| |||||| 3' CGUCUUGAAUCGGU--GACACUU	7mer-1A	-0.13	73	0.7
hsa-miR-128	321-327	5' ...GAUUCCCGGAGGGAAACUGUGAA... |||||| 3' UUUCUCUGGCCAAGUGACACU	7mer-1A	-0.07	50	0.79
hsa-miR-9	408-414	5' ...ACCAAGUUGUUUAUUCCAAAGAG... |||||| 3' AGUAUGUCGAUCUAUUGGUUUCU	7mer-1A	-0.06	54	0.61
hsa-miR-4735-3p	498-505	5' ...AUUUUUAAUUUUUCCGCACCUUA... |||||| ||||||| 3' UACAGAUUAAACU--CGUGGAAA	8mer	-0.39	97	0.78
hsa-miR-18a	498-505	5' ...AUUUUUAAUUUUUCCGCACCUUA... ||||||| 3' GAUAGACGUGAUCUACGUGGAAU	8mer	-0.31	93	0.78
hsa-miR-18b	498-505	5' ...AUUUUUAAUUUUUCCGCACCUUA... ||||||| 3' GAUUGACGUGAUCUACGUGGAAU	8mer	-0.3	92	0.78
hsa-miR-144	734-740	5' ...UGGGUCAUUUUUAACUACUGUAU... ||| |||||| 3' UCAUGUAGUAGAU-AUGACAU	7mer-1A	-0.04	37	0.3
	3619-3626	5' ...UCUUAGGUUUGCUAAAUACUGUA... ||||||| 3' UCAUGUAGUAGAUAUGACAU	8mer	-0.1	65	0.43
hsa-miR-101	734-740	5' ...UGGGUCAUUUUUAACUACUGUAU... |||||| 3' AAGUCAAUAGUGUCAUGACAU	7mer-1A	-0.04	30	0.3
	3620-3626	5' ...CUUAGGUUUGCUAAAUACUGUAG... |||||| 3' AAGUCAAUAGUGUCAUGACAU	7mer-1A	-0.04	28	0.3
hsa-miR-23a	926-932	5' ...AAAAAAAGAAUGAGUAAUGUGAU... ||||||| 3' CCUUUAGGGACCGUUACACUA	7mer-m8	> -0.02	29	0.2
hsa-miR-23b	926-932	5' ...AAAAAAAGAAUGAGUAAUGUGAU... ||||||| 3' CCAUUAGGGACCGUUACACUA	7mer-m8	> -0.02	29	0.2
hsa-miR-23c	926-932	5' ...AAAAAAAGAAUGAGUAAUGUGAU... ||||||| 3' CCCAUUAGUGACCGUUACACUA	7mer-m8	> -0.02	28	0.2
hsa-miR-30a	955-962	5' ...GUUAUCCAGAAGUAU-UGUUUACA... ||||| ||||||| 3' GAAGGUCAGCUCCUACAAAUGU	8mer	-0.1	67	0.92
	3365-3371	5' ...AACAAAAUGCCUUUUUGUUUACC... ||||||| 3' GAAGGUCAGCUCCUACAAAUGU	7mer-m8	> -0.02	28	0.46
hsa-miR-30b	955-962	5' ...GUUAUCCAGAAGUAUUGUUUACA... ||||||| 3' UCGACUCACAUCCUACAAAUGU	8mer	-0.09	63	0.92
	3365-3371	5' ...AACAAAAUGCCUUUUUGUUUACC... ||||||| 3' UCGACUCACAUCCUACAAAUGU	7mer-m8	-0.02	35	0.46
hsa-miR-30c	955-962	5' ...GUUAUCCAGAAGUAUUGUUUACA... ||||||| 3' CGACUCUCACAUCCUACAAAUGU	8mer	-0.09	63	0.92
	3365-3371	5' ...AACAAAAUGCCUUUUUGUUUACC... ||||||| 3' CGACUCUCACAUCCUACAAAUGU	7mer-m8	-0.02	35	0.46
hsa-miR-30d	955-962	5' ...GUUAUCCAGAAGUAU-UGUUUACA... ||||| ||||||| 3' GAAGGUCAGCCCCUACAAAUGU	8mer	-0.1	67	0.92
	3365-3371	5' ...AACAAAAUGCCUUUUUGUUUACC... ||||||| 3' GAAGGUCAGCCCCUACAAAUGU	7mer-m8	> -0.02	28	0.46
hsa-miR-30e	955-962	5' ...GUUAUCCAGAAGUAU-UGUUUACA... ||||| ||||||| 3' GAAGGUCAGUUCCUACAAAUGU	8mer	-0.1	66	0.92
	3365-3371	5' ...AACAAAAUGCCUUUUUGUUUACC... ||||||| 3' GAAGGUCAGUUCCUACAAAUGU	7mer-m8	> -0.02	27	0.46
hsa-miR-761	1667-1673	5' ...ACUCAUAAAUACUAACUGCUGAU... |||||| 3' ACACAGUCAAAGUGGGACGACG	7mer-1A	-0.01	17	0.49
hsa-miR-214	1667-1673	5' ...ACUCAUAAAUACUAACUGCUGAU... |||||| 3' UGACGGACAGACACGGACGACA	7mer-1A	> -0.01	16	0.49
hsa-miR-3619-5p	1667-1673	5' ...ACUCAUAAAUACUAACUGCUGAU... |||||| 3' CGACGUGGUCGGACGGACGACU	7mer-1A	> -0.01	15	0.49
hsa-miR-215	1747-1753	5' ...CGUUGAAACGAUUUCAGGUCAAC... |||||| 3' CAGACAGUUAAGUAUCCAGUA	7mer-1A	-0.02	16	< 0.1

<table>
<tr><td>hsa-miR-192</td><td>1747-1753</td><td>5' ...CGUUGAAACGAUUUCAGGUCAAC...
||||||
3' CCGACAGUUAAGUAUCCAGUC</td><td>7mer-1A</td><td>-0.02</td><td>16</td><td>< 0.1</td></tr>
<tr><td>hsa-miR-200a</td><td>1787-1793</td><td>5' ...AGCAGGACUUCAGAACAGUGUUU...
|||||||
3' UGUAGCAAUGGUCUGUCACAAU</td><td>7mer-m8</td><td>-0.02</td><td>34</td><td>0.66</td></tr>
<tr><td>hsa-miR-141</td><td>1787-1793</td><td>5' ...AGCAGGACUUCAGAACAGUGUUU...
|||||||
3' GGUAGAAAUGGUCUGUCACAAU</td><td>7mer-m8</td><td>-0.02</td><td>33</td><td>0.66</td></tr>
<tr><td>hsa-miR-217</td><td>1929-1936</td><td>5' ...AUUUGUUUUACACACAUGCAGUA...
|||||||
3' AGGUUAGUCAAGGACUACGUCAU</td><td>8mer</td><td>> -0.03</td><td>6</td><td>0.41</td></tr>
<tr><td>hsa-miR-302a</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
||||| |||||||
3' AGUGGUUUUGUACCU--UCGUGAAU</td><td>7mer-m8</td><td>-0.02</td><td>39</td><td>0.84</td></tr>
<tr><td>hsa-miR-302b</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
||||| |||||||
3' GAUGAUUUUGUACCU--UCGUGAAU</td><td>7mer-m8</td><td>-0.02</td><td>39</td><td>0.84</td></tr>
<tr><td>hsa-miR-302c</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
||||| |||||||
3' GGUGACUUUGUACCU--UCGUGAAU</td><td>7mer-m8</td><td>-0.02</td><td>39</td><td>0.84</td></tr>
<tr><td>hsa-miR-302d</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
||||| |||||||
3' UGUGAGUUUGUACCU--UCGUGAAU</td><td>7mer-m8</td><td>-0.02</td><td>39</td><td>0.84</td></tr>
<tr><td>hsa-miR-302e</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||| |||||||
3' UUCGUACCU--UCGUGAAU</td><td>7mer-m8</td><td>> -0.02</td><td>34</td><td>0.84</td></tr>
<tr><td>hsa-miR-372</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
||| |||||||
3' UGCGAGUUUACAGCGUCGUGAAA</td><td>7mer-m8</td><td>> -0.02</td><td>30</td><td>0.84</td></tr>
<tr><td>hsa-miR-520a-3p</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||||||
3' UGUCAGGUUUCCCUUCGUGAAA</td><td>7mer-m8</td><td>> -0.02</td><td>27</td><td>0.84</td></tr>
<tr><td>hsa-miR-520e</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||||||
3' GGGAGUUUUUCCUUCGUGAAA</td><td>7mer-m8</td><td>> -0.02</td><td>25</td><td>0.84</td></tr>
<tr><td>hsa-miR-373</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||||||
3' UGUGGGGUUUUAGCUUCGUGAAG</td><td>7mer-m8</td><td>> -0.02</td><td>25</td><td>0.84</td></tr>
<tr><td>hsa-miR-520b</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||||||
3' GGGAGAUUUUCCUUCGUGAAA</td><td>7mer-m8</td><td>> -0.02</td><td>20</td><td>0.84</td></tr>
<tr><td>hsa-miR-520c-3p</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||||||
3' UGGGAGAUUUUCCUUCGUGAAA</td><td>7mer-m8</td><td>> -0.02</td><td>20</td><td>0.84</td></tr>
<tr><td>hsa-miR-20a</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' GAUGGACGUGAUAUUCGUGAAAU</td><td>7mer-m8</td><td>> -0.02</td><td>28</td><td>0.9</td></tr>
<tr><td>hsa-miR-520d-3p</td><td>1936-1942</td><td>5' ...UUACACACAUGCAGUAGCACUUU...
|||||||
3' UGGGUGGUUUCUCUUCGUGAAA</td><td>7mer-m8</td><td>> -0.02</td><td>26</td><td>0.84</td></tr>
<tr><td>hsa-miR-106b</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' UAGACGUGACAGUCGUGAAAU</td><td>7mer-m8</td><td>> -0.02</td><td>28</td><td>0.9</td></tr>
<tr><td>hsa-miR-93</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' GAUGGACGUGCUUGUCGUGAAAC</td><td>7mer-m8</td><td>> -0.02</td><td>28</td><td>0.9</td></tr>
<tr><td>hsa-miR-20b</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' GAUGGACGUGAUACUCGUGAAAC</td><td>7mer-m8</td><td>> -0.02</td><td>28</td><td>0.9</td></tr>
<tr><td>hsa-miR-17</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' GAUGGACGUGACAUUCGUGAAAC</td><td>7mer-m8</td><td>> -0.02</td><td>27</td><td>0.9</td></tr>
<tr><td>hsa-miR-106a</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' GAUGGACGUGACAUUCGUGAAAA</td><td>7mer-m8</td><td>> -0.02</td><td>27</td><td>0.9</td></tr>
<tr><td>hsa-miR-519d</td><td>1937-1943</td><td>5' ...UACACACAUGCAGUAGCACUUUG...
|||||||
3' GUGAGAUUUCCCUCCGUGAAAC</td><td>7mer-m8</td><td>> -0.02</td><td>24</td><td>0.9</td></tr>
<tr><td>hsa-miR-135a</td><td>2688-2694</td><td>5' ...GGAGAAGUAUUGAAU---AAGCCAUU...
|||| |||||||
3' AGUGUAUCCUUAUUUUUCGGUAU</td><td>7mer-m8</td><td>-0.06</td><td>31</td><td>0.52</td></tr>
<tr><td>hsa-miR-135b</td><td>2688-2694</td><td>5' ...GGAGAAGUAUUGAAU---AAGCCAUU...
|||| |||||||
3' AGUGUAUCCUUACUUUUCGGUAU</td><td>7mer-m8</td><td>-0.06</td><td>31</td><td>0.52</td></tr>
<tr><td>hsa-miR-1</td><td>3228-3234</td><td>5' ...ACCUGUUUCUUUGGGACAUUCCG...
|||||| |||||||
3' UAUGUAUGAAGAAA---UGUAAGGU</td><td>7mer-m8</td><td>> -0.02</td><td>23</td><td>0.42</td></tr>
<tr><td>hsa-miR-206</td><td>3228-3234</td><td>5' ...ACCUGUUUCUUUGGGACAUUCCG...
||| |||||||
3' GGUGUGUGAAGGAAUGUAAGGU</td><td>7mer-m8</td><td>> -0.02</td><td>20</td><td>0.42</td></tr>
<tr><td>hsa-miR-613</td><td>3228-3234</td><td>5' ...ACCUGUUUCUUUGGGACAUUCCG...
|||||||
3' CCGUUUCUUCCUUGUAAGGA</td><td>7mer-m8</td><td>> -0.02</td><td>11</td><td>0.42</td></tr>
<tr><td>hsa-miR-184</td><td>3232-3238</td><td>5' ...GUUUCUUUGGGACAUUCCGUCCU...
|||||||
3' UGGGAAUAGUCAAGAGGCAGGU</td><td>7mer-m8</td><td>-0.22</td><td>58</td><td>0.33</td></tr>
<tr><td>hsa-miR-429</td><td>3436-3442</td><td>5' ...UGUUUUUAGCCAGGUCAGUAUUG...
||||| |||||||
3' UGCCAAAAUGGUCU--GUCAUAAU</td><td>7mer-m8</td><td>-0.02</td><td>45</td><td>0.47</td></tr>
<tr><td>hsa-miR-200c</td><td>3436-3442</td><td>5' ...UGUUUUUAGCCAGGUCAGUAUUG...
||| |||||||
3' AGGUAGUAAUGGGCC--GUCAUAAU</td><td>7mer-m8</td><td>> -0.02</td><td>38</td><td>0.47</td></tr>
<tr><td>hsa-miR-200b</td><td>3436-3442</td><td>5' ...UGUUUUUAGCCAGGUCAGUAUUG...</td><td>7mer-m8</td><td>> -0.02</td><td>38</td><td>0.47</td></tr>
</table>

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<tr><th></th><th></th><th></th><th></th><th></th><th></th><th></th></tr>
<tr><td></td><td></td><td>||||| |||||||
3' AGUAGUAAUGGUCC-GUCAUAAU</td><td></td><td></td><td></td><td></td></tr>
<tr><td>hsa-miR-383</td><td>3450-3456</td><td>5' ...UCAGUAUUGAUGAGGCUGAUCAU...
||||||
3' UCGGUGUUAGUGGAAGACUAGA</td><td>7mer-1A</td><td>-0.05</td><td>30</td><td>< 0.1</td></tr>
<tr><td>hsa-miR-139-5p</td><td>3621-3627</td><td>5' ...UUAGGUUUGCUAAAUACUGUAGG...
|||||||
3' GACCUCUGUGCACGUGACAUCU</td><td>7mer-m8</td><td>-0.12</td><td>68</td><td>0.17</td></tr>
<tr><td>hsa-miR-129-5p</td><td>3765-3772</td><td>5' ...AGGGGAAAUGAAUGUGCAAAAAA...
|||||||
3' CGUUCGGGUCUGGCGUUUUUC</td><td>8mer</td><td>-0.06</td><td>88</td><td>< 0.1</td></tr>
<tr><td>hsa-miR-4262</td><td>3758-3764</td><td>5' ...UUGUUCUAGGGGAAAUGAAUGUG...
||| |||||||
3' GUCCAUCAGACUUACAG</td><td>7mer-m8</td><td>-0.1</td><td>72</td><td>0.77</td></tr>
<tr><td>hsa-miR-181a</td><td>3758-3764</td><td>5' ...UUGUUCUAGGGGAAAUGAAUGUG...
|||||||
3' UGAGUGGCUGUCGCAACUUACAA</td><td>7mer-m8</td><td>-0.06</td><td>57</td><td>0.77</td></tr>
<tr><td>hsa-miR-181b</td><td>3758-3764</td><td>5' ...UUGUUCUAGGGGAAAUGAAUGUG...
|||||||||
3' UGGGUGGCUGUCGUUACUUACAA</td><td>7mer-m8</td><td>-0.06</td><td>57</td><td>0.77</td></tr>
<tr><td>hsa-miR-181c</td><td>3758-3764</td><td>5' ...UUGUUCUAGGGGAAAUGAAUGUG...
|||||||
3' UGAGUGGCUGUCCAACUUACAA</td><td>7mer-m8</td><td>-0.07</td><td>61</td><td>0.77</td></tr>
<tr><td>hsa-miR-181d</td><td>3758-3764</td><td>5' ...UUGUUCUAGGGGAAAUGAAUGUG...
|||||||
3' UGGGUGGCUGUUGUUACUUACAA</td><td>7mer-m8</td><td>-0.07</td><td>61</td><td>0.77</td></tr>
</table>

Targetscan analysis - release 6.2 (June 2012) - showing only sites conserved among vertebrates

TOT miRNA = 60