### Suppl. Table S1: TargetScanHuman Prediction of microRNA hsa-miR-19b-3p targets.

<table>
<thead>
<tr>
<th>Gene Symbol (Ensemble)</th>
<th>Predicted consequential pairing of target region (top) and miRNA (bottom)</th>
<th>Site type</th>
<th>Context++ score</th>
<th>Context++ score percentile</th>
<th>Weighted context++ score</th>
<th>Conserved branch length</th>
<th>PCT</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>PPP2R5E (ENST00000337537.7)</strong></td>
<td>Position 505-512 of PPP2R5E 3'UTR has-miR-19b-3p</td>
<td>5' ...UUAAACUUCUUUCUUUUGCACA...</td>
<td>8mer</td>
<td>-0.34</td>
<td>96</td>
<td>-0.34</td>
<td>4.765</td>
</tr>
<tr>
<td></td>
<td>3' AGUCAAAAACGUAAUCUAACGUUGU</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Position 3584-3591 of PPP2R5E 3'UTR has-miR-19b-3p</td>
<td>5' ...AUCACUGAUUUCUUUUGCACA...</td>
<td>8mer</td>
<td>-0.21</td>
<td>86</td>
<td>-0.04</td>
<td>3.108</td>
</tr>
<tr>
<td></td>
<td>3' AGUCAAAAACGUAAUCUAACGUUGU</td>
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**Luciferase target construct**

<table>
<thead>
<tr>
<th>Construct</th>
<th>Predicted target site (top) and mutated target site cloned into luciferase reporter construct (bottom)</th>
</tr>
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<tbody>
<tr>
<td>Luc PPP2R5E TS</td>
<td>5’-TCGAGTTTAACATCTTTTCTTTTCGCACATCTTCCCTGAGTTGATGCTCCT-3’</td>
</tr>
<tr>
<td>Luc PPP2R5E mTS</td>
<td>5’-TCGAGTTTAACATCTTTTCTTTTCGCACATCTTCCCTGAGTTGATGCTCCT-3’</td>
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<tr>
<td><strong>BCL2L11 (ENTST00000393256.7)</strong></td>
<td>Position 4092-4098 of BCL2L11 3'UTR has-miR-19b-3p</td>
<td>5’ ...CUUGGUACUUGUGUUGUUGCACA...</td>
<td>7mer m8</td>
<td>-0.23</td>
<td>88</td>
<td>-0.06</td>
<td>7.317</td>
</tr>
<tr>
<td>3’ AGUCAAAAACGUAAUCUAACGUUGU</td>
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<tr>
<td>Luc BCL2L11 TS</td>
<td>5’-TCGAGTTTTCCTGGCTTACCTGTGTTTGCACGTGATGATTGGACT-3’</td>
</tr>
<tr>
<td>Luc BCL2L11 mTS</td>
<td>5’-TCGAGTTTTCCTGGCTTACCTGTGTTTGCACGTGATGATTGGACT-3’</td>
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</tbody>
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Context++ score and features that contribute to the context++ score are evaluated as in (Agarwal et al., 2015). Conserved branch lengths and PTC are evaluated as in (Friedman et al., 2009), with an expanded 84-species alignment as described in (Agarwal et al., 2015). Table was adapted from targetscan.org (May 22nd, 2017).