Table 1. miR-874 putative target genes involved in tumor progression. (source: Targetscan (www.targetscan.org), miRBase (www.mirbase.org), miRanda (www.microrna.org) and miRDB (www.mirdb.org))

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Seed Location at 3'UTR</th>
<th>Target score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Matrixmetalloproteinase-2 (MMP-2)</td>
<td>412,425,889</td>
<td>53/67</td>
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<tr>
<td>Uokinase Plasminogen Activator (uPA)</td>
<td>291,470</td>
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<td>Protein Tyrosine Phosphatase, Non-receptor type-12 (PTPN12)</td>
<td>339</td>
<td>82</td>
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<td>Nuclear Factor of Activated T-cell-5, Tonicity-responsive (NFAT5)</td>
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<td>Activating Transcription Factor-7 (ATF-7)</td>
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<td>p21 protein (Cdc42/Rac)-Activated Kinase-3 (PAK3)</td>
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<td>p21 protein (Cdc42/Rac)-Activated Kinase-7 (PAK7)</td>
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<td>LIM Domain Containing-2 (LIMD2)</td>
<td>131,537,1600,1750</td>
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<td>Platelet/Endothelial Cell Adhesion Molecule (PECAM1)</td>
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<td>Mitogen-Activated Protein Kinase Kinase-1 (MAP3K1)</td>
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<td>RAB27A, MemberRAS Oncogene Family (RAB27A)</td>
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<td>Vascular Endothelial Growth Factor-A (VEGF A)</td>
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<td>Signal Transducers and Activators of Transcription-3 (Stat3)</td>
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<td>AT Rich Interactive Domain-3B (BRIGHT-Like) (ARID3B)</td>
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<td>Cut-like Homeobox-1 (CUX1)</td>
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<td>Sortilin-1 (SORT1)</td>
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<td>R-Spondin-1 (RSPO1)</td>
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<td>Protein Kinase-C eta (PRKCH)</td>
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<td>Fibroblast Growth Factor-1 (FGF1)</td>
<td>2535</td>
<td>73</td>
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</tbody>
</table>