

Supplementary Information

Supplementary Table S1.

Sequences of target genes of ribozymes

Positive Clones

1. FADD: 5'- CACTCGGTGTCGTCCAGCCTG-3'
2. 5'- CTGCTCGCCTCCCTGCGGCGC-3'
3. 5'- GCTCTCAGGTCCTGCCAGATG-3'
4. Caspase3: 5'- TCAATGGACTCTGGAATATCC-3'
5. 5'- TCGGTCTGGTACAGATGTCGA-3'
6. 5'- ACATCTCGGTCTGGTACA-3'
7. Caspase 8: 5'- TGGCCTCCCTCAAGTTCCTGA-3'
8. 5'- GAATTGAGGTCTTTTAAGTT-3'
9. 5'- TCCAGAGACTCCAGGAAA-3'
10. Caspase 9: 5'- CGAGGGAGTCAGGCTCTTC-3'
11. 5'- GAAGACGAGTCCCCTGG-3'
12. Ets-1: 5'- CTTTTCCCCTCCCCGGATATG-3'
13. 5'- TTAATGGAGTCAACCCAGCCT-3'
14. PTEN: 5'- ATGGGGAAGTAAGGACCAGAG-3'
15. 5'- ACTTTTGGGTAAATACATTC-3'
16. BIN1: 5'- ATGGACACGTACCTGGGCCAG-3'
17. Apaf1: 5'- ATTCCTACGTATCATTCTACA-3'
18. 5'- GAAGTCTGTATTAGCTGCAG-3'
19. 5'- CCAAGGTCTCTCTTGATCT-3'
20. FKHRL1: 5'- CGATCCTGTACGTGGCCCCT-3'
21. 5'- CGGGCTGCTCCTTGAGGAC-3'
22. 5'- GGAAACCTGTCCTACGCGGA-3'
23. MSX2: 5'- GCGCCGCGTCAAGGTCTCCA-3'
24. 5'- ACCGCGCTCGGGAAGCGC-3'
25. 5'- CAGCTTCAGTCTCCCCTTCC-3'

26. DAXX: 5'- CTGAGGTGGTCCCATTCTC-3'
27. 5'- GCTGGCGCTCTATGTGGCAG-3'
28. Bid: 5'- GTTCCAGCCTCAGGGATGAG-3'
29. 5'- CCAGCCGGTCGGAGGAGGA-3'
30. gadd34: 5'- TGGGCCTCCTCAGCCGCGCC-3'
31. 5'- ACCAGTGTCCCTAGAGGGC-3'
32. 5'- TCTGCCTTGTCTCCAGGATC-3'
33. HtrA2: 5'- ACCCCTGACCTCCGGGGCCCTG-3'
34. 5'-ACCCCGGGTCCCCGGGCAC-3'
35. 5'- CTCCGGCCGTCCTCGCCGC-3'
36. Bcl-10: 5'- TTTACGTGTATACCTGTGTG-3'
37. 5'- CCAAAGGTCTGGACACCCT-3'
38. Agl-2: 5'- TCCAGAGGGTCGATAAAGAC-3'
39. 5'- CAGTGA CTGTCAGGTCGATC-3'
40. 5'- CGGGACA ACTCCGGGATGA-3'
41. BAK: 5'- AGGAGCAGGTAGCCCAGGAC-3'
42. 5'- AGAGATGGTCACCTTACCTC-3'
43. 5'- GTGGTGGCTCTTCTGGGCTT-3'
44. ASK: 5'- GGGAAAAGTATTTTACCTTG -3'
45. 5'- TCGAATTTCTCCTGTACCAA -3'
46. 5'- TCAAATAGTATATTATCAAA -3'
47. RIP-PK: 5'- GAAGGTGTCTCTGTGTTTCC-3'
48. ASC: 5'- ACAAGCTGGTCAGCTTCTAC-3'
49. 5'- CGCGAGGGTCACAAACGTTG-3'
50. c-fos: 5'- TACTACCACTCACCCGCAG-3'
51. 5'- ATGAGAAGTCTGCTTTGCA-3'
52. Max: 5'- CAACCGAGGTTTCAATCTGCG-3'
53. 5'- ATATCCAGTATATGCGAAG-3'
54. 5'- AGCACCATCTCTGCCTTCGAT-3'
55. SMAC: 5'- GGTGTTTCTCAGAATTGATA-3'
56. 5'- TCCCTTAGTAGTGAAGCATT-3'
57. 5'- CACCAAGAGTACTTGAAGCT-3'

58. AIF: 5'- ATCAACAGTAGGAGCTGGT-3'
59. 5'- TCCGGGCTCGGGATCCTGG-3'
60. 5'- GGAAGAAGGTAGTACAGCTGG-3'
61. CIDE-a: 5'- GGAGCCCTCATCAGGCCCC-3'
62. 5'- GCCAGCACGTCCCCACTTGC-3'
63. 5'- CCACCATGTATGAGATGTAC-3'
64. RICK: 5'- CGCGGGCGCCTCTGGCACTGT-3'
65. 5'- GCATGATGTCCCTCTCACA-3'
66. p300: 5'- AGTGCTAGTCCTATGGGAGT-3'
67. 5'- TGCATATGCTCGGAAAGTTGA -3'
68. 5'- ACCTAGTCGTACCCCCACCCC-3'
69. UG1: 5'- GCCTGCACTCTACTTGGATA-3'
70. UG2: 5'- GGAAAATGCTCGTGACTTTC-3'
71. UG3: 5'- GGGAGCAGGTCCTGGTGGAT-3'
72. UG4: 5'- CAGGGTCTGTATAGAAAACAT-3'
73. UG5: 5'- CATTCTTTGTA ACTTCATGG-3'
74. UG6: 5'- ATCTTCATGTAAACAGTTCT-3'
75. UG7: 5'- TAATATGCGTATGGTGTGCGAT -3'
76. UG8: 5'- GAGTTTTGGTAATAGACACA-3'
77. UG9: 5'- AGGGACAAGTAATAATAAA-3'
78. UG10: 5'- CGCGGACGTGCGCATGGGAC-3'
79. UG11: 5'- AACAGCAGTAACTTGGTAAT-3'
80. UG12: 5'- GAATCCAAGTAAAACAATAA -3'
81. UG13: 5'- TTGTTAAAGTCTGATGTTAAC -3'
82. UG14: 5'- CCAAACCCCTAAAACAGAG-3'
83. UG15: 5'- CTGTGCTGTCCCCGTGAAC-3'
84. UG16: 5'- TCCCCTTCCTCACCAGAGCC -3'
85. UG17: 5'- GGGGTTGCTCCCCCTAAATC -3'
86. UG18: 5'- AACCGCCCGTCATGTCTCTC -3'
86. UG19: 5'- GCCAGCTACTCAACACCCTA -3'
87. UG20: 5'- GAGGGGGGCTCTTGCTTTAT -3'
88. UG21: 5'- GTTGTGGAGTACGCTTTGGA -3'

89. UG22: 5'- GGCAGCCTGTATTTTACCC-3'
90. UG23: 5'- GAGAGCAGTCAAGAGACCA -3'
91. UG24: 5'- TGGGGAGGTAATAATTTGA -3'
92. UG25: 5'- CCTGAAGGTAGCCACCTCG -3'
93. UG26: 5'- TTCCTACTGTCACATAGCC -3'
94. UG27: 5'- TCTGATACCTCTTAAAATGG -3'
95. UG28: 5'- AGCCAAAGTACTGGGTAA -3'
96. UG29: 5'- TGTGAAATCTCCCAATTTTT -3'
97. UG30: 5'- AGACCCTCCTCTCCACAT -3'
98. UG31: 5'- TATTCTAGTTTCTAACCA-3'
99. UG32: 5'- TGCCCCGAGTCAAGTGGGGCT-3'
100. UG33: 5'- GGCCACCTCGTTACGACATG -3'
101. UG34: 5'- AGGGAGCCTCGCTAACCAC -3'
102. UG35: 5'- AGCCGATGTATAGGAAATG -3'
103. UG36: 5'- GAATTTTACTCAGAATAAA -3'
104. UG37: 5'- TCTGCTGGTAAAGCTGTTAT -3'
105. UG38: 5'- GATTGGGAGTACCAGTGAAG -3'
106. UG39: 5'- TCATAGGGCTCAAATGCATC -3'
107. UG40: 5'- AAAGGTTAGTACTCCAGTAG-3'
108. UG41: 5'- CTTGAATGGTCACTTAAAGT -3'
109. UG42: 5'- GCAGAGTTGTAATCTCCTCT -3'
110. UG43: 5'- GCTGCAATGTACCCAAATGG -3'
111. UG44: 5'- CTGATTCTCTCAAATAGAG-3'
112. UG45: 5'- TTGATAGTGTATAGAACATTT -3'
113. UG46: 5'- TGAGAGCGTCATATATACC-3'
114. UG47: 5'- AGATTTTTGTATACATTAAT -3'
115. UG48: 5'- GATGGAGGCTCAGATCACA-3'
116. UG49: 5'- GGAGAACGGTCACTATCCGG-3'
117. UG50: 5'- TGCTGGCACTCCTCATTTCG -3'
118. UG51: 5'- TGAATACTGTCAGTGCCACA -3'
119. UG52: 5'- TTTTGAGGTACCTATTTGG -3'
120. UG53: 5'- CTCCAAGTCACAATGCTG-3'

121. UG54: 5'- AAGCTGATGTCCTAATTCAA -3'
122. UG55: 5'- CACTCTGTTCTATCAATAT-3'
123. UG56: 5'- GAAGCAGTACTTAACTCG -3'
124. UG57: 5'- ATCTTGAGGTCACAGGGAA-3'
125. UG58: 5'- AAGACTGTCCAAACTGT-3'
126. UG59: 5'- ACTCTAAGTCACTGATGC-3'
127. UG60: 5'- GGAAGTAAGTATTCAGGGGGT-3'

False positive clones

1. Gastrin: 5'- ACCCTTAGGTACAGGGGCCAA-3'
2. Heregulin: 5'- TTGTGCAAGTAAGAAAAGAAA-3'
3. LEF1: 5'- CCCATACATGTCAAATGGATCT-3'
4. Gu BP: 5'- TTCACCCAGTCCATCCGGATA-3'
5. AF-6: 5'-GGATTTGCCTCTCCCACCACCCC-3'
6. myotilin: 5'- ACCAAGAACTCCTGATCATGA-3'
7. UG61: 5'- TCCCAGGTATCGAACAAT -3'
8. UG62: 5'- TGATAAAGGTAGAAAACACTG -3'