Table S1: Primers used to generate mouse, human and chicken HMGA2 3'UTR fragments. Forward primers (F) are SpeI tailed and reverse primers (R) are NotI tailed. Coordinates indicate position downstream of stop codon.

Description	Sequence	Coordinates
0-F-mouse	atatactagtGCCGACATTCAATTTCTACCTC	6-27
100-R-mouse	atatagcggccgCGCAGGAAGTAGAAAGACCGTG	88-109
100-F-mouse	atatactagtGGGTGGGGCGGG	110-121
200-R-mouse	atatagcggccgcCCTGGGACTGTGAAGGGATTACAAAG	193-218
200-F-mouse	atatactagTTTAGTGAAAAACTGCTGTAAACACGGG	219-246
300-R-mouse	atatagcggccgcATCAGATCCACAAACTATTAGTAAGTTAAGG	291-321
300-F-mouse	atatactagtAAGCAAGGGTGTGTGGTTGAAG	322-343
400-R-mouse	atatagcggccgcTGCTTTTCTTATACGAATGCCCCC	408-431
400-F-mouse	atatactagTTGTGTGTGACTCTGTGTCCAC	432-453
500-R-mouse	atatagcggccgcGGAGAGTAGTGTCTAGTTCTCATCTTTG	500-527
500-F-mouse	atatactagTTTCTTTGTGTATAATCTTGTAGACACTTACTTG	528-562
600-R-mouse	atatagcggccgcTAGCTGTATGAAAAGATACACCAGCATTTTGTCTC	597-631
600-F-mouse	atatactagtGCAAACCAGAATAGGTTATGCTCG	632-656
700-R-mouse	atatagcggccgcTGCTGCTGTGTATGAGTCCATAAATG	713-738
700-F-mouse	atatactagtGGAGTGATAAGCCCACAAGCTC	739-760
800-R-mouse	atatagcggccgcGTTATCTCCGATGCTTCAAGGCTG	821-844
800-F-mouse	atatactagTAGCTGAGTAAAATGATCCTGTTTTGGAATTTAATG	845-881
900-R-mouse	atatagcggccgcTTTCGCTCCTCCCATGTCATCAC	914-936
900-F-mouse	atatactagtCCGAAATCTCTTTTGCTATATAAAGGACAC	937-967
1000-R-mouse	atatagcggccgcAGAGAGGCGAGGGAGAGAAG	1023-1042
1000-F-mouse	atatactagtCTCCTCTCTATATTCCCTGTTCTTCATTGTG	1043-1073
1100-R-mouse	atatagcggccgcGGATGTAACACGCAGGCTTCATC	1113-1135
1100-F-mouse	atatactagTGTAACACCTTTCATTTTGACATAAGATGGC	1136-1166
1200-R-mouse	atatagcggccgcTGCATCTCTGGCTAAAAGTGCAG	1193-1215
1200-F-mouse	atatactagtATAATCCCCACTCCTCAATACTACCTC	1216-1243
1300-R-mouse	atatagcggccgcTTTTTCCTTTCTCTTGCAGGGCTTG	1316-1340
1300-F-mouse	atatactagtAAAAAGCCCACCAAAACCAAACC	1341-1363
1400-R-mouse	atatagcggccgcACATGCATAGCCTGCTGAGAC	1430-1451
1400-F-mouse	atatactagTTCTATGACTTTTTTTTTTTTTAATTAAAATGTTACAAATGC	1452-1494
1500-R-mouse	atatagcggccgcTCAAAACTGTTTCAAATTAATGTAACAATCTAGC	1510-1543
1500-F-mouse	atatactagtGTCAAGTTGCTCCTAGGTTCTTAAGG	1544-1569
1600-R-mouse	atatagcggccgcAAACTTGGAGACTTATATTTGAACACTACAGATG	1612-1645
1600-F-mouse	atatactagtGTACCTCAAATGAATTATTGAAACAAATGGACTTC	1646-1680
1700-R-mouse	atatagcggccgcGGAAATCAATGAGTGATATAGGCTGCAAG	1723-1751
1700-F-mouse	atatactagTTCCCCCATGTTTGAAGGAGC	1752-1773
1800-R-mouse	atatagcggccgcGCAAAAGTATGTAAAAAAATTGTGTTTCTATCAAGTG	1819-1855
1800-F-mouse	atatactagtAAAAATAAATGAATTAAAATCAAGCCAACCTTCAAAGAAAC	1856-1896
1900-R-mouse	atatagcggccgCTTAGAAATCTATTTTTTTCCTTTTTCATTGCATTAGGC	1928-1967
1900-F-mouse	atatactagtATTTGTTGCCTAGAAGAATATGCTTGACC	1968-1996
2000-R-mouse	atatagcggccgcGCGTCCAAAACAAATCTGCTTGAG	2045-2068
2000-F-mouse	atatactagTTCTTGTGTAGAGTTTCTATGCCTTTCTCTC	2069-2099

2100-R-mouse	atatagcggccgcACACAAGCCACTATGAGAAACTACC	2133-2170
2100-F-mouse	atatactagtCAGTATAAGTTAATACTGAAGCCAAATGAAACAAAC	2171-2207
2200-R-mouse	atatagcggccGCACGTGGCCTTTGAAGTAACCTC	2239-2262
2200-F-mouse	atatactagtCGCTCTGAGACTGGCAGATG	2263-2282
2300-R-mouse	atatagcggccgcATTTGATTATTTAATGCATTGTTAACAGTCATGTTG	2329-2364
2300-F-mouse	atatactagtAAACAGTGGCTTATAAATATCAGATTCTCATTCC	2365-2398
2400-R-mouse	atatagcggccgcCGAGTCTGGCCAACACGAG	2462-2480
2400-F-mouse	atatactagtGCACACCGAGCAATTTCCATC	2481-2502
2500-R-mouse	atatagcggccgcTATACTGGGACTTAAGAGGTAGTAGTGTG	2547-2575
2500-F-mouse	atatactagtCCTCATTTTTCATACTGAAAAAAAAGAAAAAAAAGAG	2576-2612
2600-R-mouse	atatagcggccgcAACAGTCTTATAAAATTTATCTCCCACAAAAATAAAC	2673-2709
2600-F-mouse	atatactagTTTTACTGTTGTTGGTCACAGCTAAGTAAG	2710-2739
2700-R-mouse	atatagcggccgcTAATCGTCTTGATAAGTTTCTCCTGCAAAC	2782-2811
2700-F-mouse	atatactagtACTGCATCCAACTTTCTCCCC	2812-2832
2800-R-mouse	atatgcggccgCACAGACAGCGACTCTACAC	2872-2891
2800-F-mouse	atatactagtATTGTACTTGGACGGCTTGC	2892-2911
2900-R-mouse	atatagcggccGCCCACAGAGGCTGTTATGTTTATTG	2952-2977
0-F-chicken	atatactagtCGCACCATGCAATTTCTACCTC	6-27
100-R-chicken	atatgcggccgcAAAAGTGGAAAGACCATGGCAATAG	81-105
100-F-chicken	atatactagtGCCTGGGGGGAAAAAAATTGC	106-126
200-R-chicken	atatgcggccgCCTGGGACTGTGAAGGGATTATAAAGAAG	156-184
200-F-chicken	atatactagTTTAGTGAAAAACTGCTGTAACACAATGG	185-213
300-R-chicken	atatgcggccgcAGCAGCTCAAACAAACTATTAGTAGGTTAAG	259-289
300-F-chicken	atatactagtAAGTAAGGGTGACTGGGTCAAG	290-311
400-R-chicken	atatgcggccgcAGCCTTTCCTATTTCAATGCCC	387-408
400-F-chicken	atatactagtGGGTGTGTAACACCTAGCCTTG	409-430
500-R-chicken	atatgcggccgcAAAAAGTAGTATCTATCCCTTATCTTTGGTGTTC	478-511
500-F-chicken	atatactagTTTTTTTTTTTTTTTTTTGTAACCTTCCTGTAG	512-544
600-R-chicken	atatgcggccgCAGCTGAATGAAGTGAGAGTTCAGC	612-636
600-F-chicken	atatactaGTAATCGGAAGAAAGAGCAACATGAAAAAG	637-666
700-R-chicken	atatgcggccgcTGCTGATATGTTTGTATGTAAAACTATACAACG	705-737
700-F-chicken	atatactagtGAAGTAGTAGTAAACAAAATGAGCAGCC	738-765
800-R-chicken	atatgcggccgcATCATTTCTGTTTCCACAGAAAACAC	819-844
800-F-chicken	atatactagTGACACCAAACACTAACGCCATTAATG	845-871
900-R-chicken	atatgcggccgcGGTACCTTTCTACACGATTTAAAACACTTATC	888-919
900-F-chicken	atatactagTCAAAATTAATCGTGAGTTTATCTGAACAAAAC	920-952
1000-R-chicken	atatgcggccgcTCTGGTGCAGGGTGAGTGGAATTAG	979-1003
1000-F-chicken	atatactagTTTCAAACAGGATGGATCTCTCCTTATTAC	1004-1033
1100-R-chicken	atatgcggccgcTTAAAGTAATACACAAGCTTAACTGAGGTACATG	1062-1095
1100-F-chicken	atatactagtGCAATGTATTTTGACATAGGATGGTTGAC	1096-1124
1200-R-chicken	atatgcggccgcTGCATCTGTTGCTAAAAGTGCTG	1171-1193
1200-F-chicken	atatactagtATATTACCCCACTACTCAAAGCTACC	1194-1219
1300-R-chicken	atatgcggccgcATTTCCTGCATTGAATGTGTATAGCAGC	1260-1287
1300-F-chicken	atatactagtATTTACTGGGTAGATAATCATGAGAATCTTC	1288-1318

1400-R-chicken	atatgcggccgcAAATACATAGTCATGCTGAAACACAATAAAG	1371-1401
1400-F-chicken	atatactagtCTCTCTCTCCTTTTGTTTTTTGTTTTTTTTAATG	1402-1435
1500-R-chicken	atatgcggccgcACAAAAATATATTCAAGTTAACAGTACATTACACAG	1462-1497
1500-F-chicken	atatactagtACTGAATTGCTGATAGGTTTGTAAGG	1498-1523
1600-R-chicken	atatgcggccgcAAACTTGGACAGTAATATTTAAACATTACAGC	1569-1600
1600-F-chicken	atatactaGTACCTCAAATGAATTGTTTAAAGAAATGGAC	1601-1632
1700-R-chicken	atatgcggccgCAAAACTAATGCTGAAAGTAAGAAGTTCATTC	1671-1702
1700-F-chicken	atatactagtAGACGTTTGAAACAGTTAGGACTGC	1702-1727
1800-R-chicken	atatgcggccgcACGAAAGTAATTTAAAATGTATTCATTTTCCACAAG	1765-1800
1800-F-chicken	atatactagtATTTAAAAAAAAAAAAATGAACAAAAAAAGACCTTC	1801-1836
1900-R-chicken	atatgcggccgcTTTTAAACACATATTTGTGATTGCATTATGC	1884-1914
1900-F-chicken	atatactAGTAATTAGTAGATTGTAAGAAAATACTTGACAAG	1916-1950
2000-R-chicken	atatgcggccGCATTTAAAATAAATCTGGCTGAAACATATTAC	1983-2015
2000-F-chicken	atatactagTTCTTCTGTAGAGTTTTTTTATTCTCCTCCTC	2016-2047
2100-R-chicken	atatgcggccgcACAGACACCTTCCTGAGAAAC	2170-2190
2100-F-chicken	atatactagTGGCACGGCTTTCGTAGC	2191-2208
2200-R-chicken	atatgcggccgcGTCCGCAGTTCTTGACTCTGC	2256-2276
2200-F-chicken	atatactagtCTCCTCAAAAGACTGCAGAGGG	2277-2298
2300-R-chicken	atatgcggccgcAGCTCGGGTTATTTTTTGTTCACTTC	2362-2387
2300-F-chicken	atatactagtATGCAGTAGCCCTAGCAGG	2388-2406
2400-R-chicken	atatgcggccgcGAAGTGTGACACACACCCAG	2551-2570
2400-F-chicken	atatactagtAACCTCCGAGAGACTGACC	2571-2589
2500-R-chicken	atatgcggccgcTATAGTAGGCCCTAAGAGGTAGTAATGTG	2641-2669
2500-F-chicken	atatactagtCCTCATTTTTTCAGACTGAAAAATTGCATG	2670-2699
2600-R-chicken	atatgcggccgcAACAGTCGTATAAAATTTATCTCCCAC	2756-2782
2600-F-chicken	atatactagtCTTTGCTGTCATTGGTCACTGC	2783-2804
2700-R-chicken	atatgcggccgcTAAACATCTTGAAGCGTTTTTTTTTTTCCTG	2858-2889
2700-F-chicken	atatactagtACTGCAGTTTACTTTTTCTTTTGAGTGTC	2890-2918
2800-R-chicken	atatgcggccgCGTAGACAGCAGCTCTACATGAAG	2939-2962
2800-F-chicken	atatactagtATTGTACTTCGAATCGCTTGCTTGTTG	2963-2989
2900-R-chicken	atatgcggccgcGATCACAGAGGCTATGATGTTTATTGTG	3027-3054
0-F-human	atatactagtGCCAACGTTCGATTTCTACCTCAG	6-29
100-R-human	atatgcggccgCAGATGAAAGTGGAAAGACCATGG	87-110
100-F-human	atatactagtGGGTGGGGTGGGGTGGGGTGGGGGAGGGGGGGGTGGGGTGGGGAGAAATC	111-160
200-R-human	atatgcggccgCCTGGGACTGTGAAGGGATTACAAAG	195-220
200-F-human	atatactagTTTAGTGAAAAACTGCTGTAAACACAGG	221-248
300-R-human	atatgcggccgcATCAGATCAACAAACTATTAGTAGGTTAAGAAAAAAG	287-323
300-F-human	atatactagtAAGCAAGAGTGGGCGGGTG	324-342
400-R-human	atatgcggccgCGTTCTTCCTATATGAATGCCCGAC	412-436
400-F-human	atatactagtCGGTGTGTAACACTGTGTACACC	437-459
500-R-human	atatgcggccgcGAAAGTAGTATCTAGTCCTTATCTTTGGTGTTC	505-537
500-F-human	atatactagTCTTTTTCGTATAATCTTGTAGACACTTACTTGATG	538-573
600-R-human	atatgcggccgcTAGCTGAATGAAAGGATACATCAGCATTTC	603-632
600-F-human	atatactagtACAAACTAGAAAAGGTTATGTTCATTTTTCAAAAAGG	633-669

700-R-human	atatgcggccgCTGCTGATATGTGTGATATCCATAAATAGAAGAG	695-728
700-F-human	atatactagtGAGTAATAAATTTACTCACAGCACTTGTTTTC	729-760
800-R-human	atatgcggccgcGTTTCCTTAAATGCTCTGAGGCTGAC	833-858
800-F-human	atatactagTAGACAAGTAAAATTATCCTCTTTGTAATTTAATGAAAAGG	859-899
900-R-human	atatgcggccgcTTTCGCTCCTCCCACCTCATAATTAG	929-954
900-F-human	atatactagTCTAAATTTCTTTTGCTATAGTTATACATCAATTTAAAAAGC	955-996
1000-R-human	atatgcggccgcAGGAAGAGAGAGAGAGAAAGACAC	1029-1052
1000-F-human	atatactagtCTCCCTCTCTCTTTTCATTGTGTATCAG	1053-1080
1100-R-human	atatgcggccgcTTGAAGTAACACATATGCTTAATTTGAGGTAAG	1103-1137
1100-F-human	atatactaGTAATACGTTTTGACATAAGATGGTTGACC	1138-1167
1200-R-human	atatgcggccgcTGCATCTCTGGCTAAAAGTGCAG	1212-1234
1200-F-human	atatactagtATATATCCCCACTACTCAATACTACCTCTG	1235-1264
1300-R-human	atatgcggccgcTTTTCTTGCATTGCTTGTGTATAGCAG	1303-1330
1300-F-human	atatactagtAAACTTACTGGGTAGGTGATTCTAATCATC	1331-1360
1400-R-human	atatgcggccgcAAATACATAGTCATGCTGAAACACAGTAAGG	1405-1435
1400-F-human	atatactagTTCTATGTTTTTTTAATTAAAAATTTTTAAAATACTTGTTTCAGC	1436-1480
1500-R-human	atatgcggccgcTAAAAAATTTTCAAGTTAATGTAGAAATCTAGCAGAG	1483-1519
1500-F-human	atatactagtACCAAGTCGCTCCTAGGTTCTTAAG	1520-1544
1600-R-human	atatgcggccgcAGACTTGGAGGGTAATATTTAAATATTACAGTCAAATC	1580-1617
1600-F-human	atatactaGTACCTCAAATGAATTCTTTAAGGAGATGGAC	1618-1649
1700-R-human	atatgcggccgcAAAAACAAATGAATGCTGCAAGTAACAAGTTC	1692-1723
1700-F-human	atatactagTCAATGTTTGAAATAGTTCAAACTGCAGC	1724-1752
1800-R-human	atatgcggccGCAAAAGTATGTAAAAACGTGTTCCTTTCTATCAAATG	1784-1821
1800-F-human	atatactagtAAAATAAGTAAATAATAAATAAAATAAAAGCCAACCTTCAAAGAAAC	1822-1868
1900-R-human	atatgcggccgCTTAAAAACACATATTTTTGATTGCATTATGCAAAAGC	1902-1939
1900-F-human	atatactagtATTAGTTGAATATAAGAAAATGCTTGACAAATATTTTCATG	1940-1980
2000-R-human	atatgcggccGCGTTTAAAATAAATCTGGTTGAGACATATTAC	2004-2036
2000-F-human	atatactagTTCTTATGTAGAGTTTTTATGCCTTTCTCTCC	2037-2068
2100-R-human	atatgcggccgcACAAAAGCCGTCATGAGAAACTACC	2117-2141
2100-F-human	atatactagtCAGTATGGCTTTTAGTACTGAAGCCAAATGAAACTC	2142-2177
2200-R-human	atatgcggccgcGTATGTGGCCTTTGAAACTACCTCC	2206-2230
2200-F-human	atatactagtCTCTCTGAGACTGGCAGATCG	2231-2251
2300-R-human	atatgcggccgcATTTGCTTATTTAACGCACAGTTAACAGTAATG	2301-2333
2300-F-human	atatactagtAAACAGTGGCTCATAAAAATAAAAGTCGC	2334-2362
2400-R-human	atatgcggccgCATGTTTGGCCAACATGAGCAATTG	2422-2446
2400-F-human	atatactaGTGCACCGAGTGATTTCCATC	2447-2467
2500-R-human	atatgcggccgcTATACTGGGACTTAAGAGGTAGTAGTGTG	2514-2542
2500-F-human	atatactagtCCTCATTTTTCATACTGAAAAAAAAAGCTTGTG	2543-2575
2600-R-human	atatgcggccgcAACAGTCCTATAAAATTTATCTCCCACAAAAATAAAC	2619-2655
2600-F-human	atatactagtCTTTGCTGTTGTTGGTCGCAG	2656-2676
2700-R-human	atatgcggccgcTAAACGTCTTGATACTTTTCTCCTGCAAAC	2728-2757
2700-F-human	atatactagtACTGCAGTTGACTTTCTCCCTG	2758-2779
2800-R-human	atatgcggccgCATAGACAGCAATTCTACATAAAGAACAAAG	2807-2837
2800-F-human	atatactagtATTGTACTTTGAATCGCTTGCTTGTTG	2838-2864

2900-R-human	atatgcggccgcGATCACAGAGGCTGTTATGTTTATTG	2904-2929

Table S2: Primers used to generate human *Pim1* 3'UTR fragments. Forward primers (F) are NheI tailed and reverse primers (R) are NotI tailed. Coordinates indicate position downstream of stop codon.

Description	Sequence	Coordinates
0-F	atatgctagcCAGCCTTTCTGGCAGGTCCTC	1-21
100-F	atatgctagcGACAGTGCTTGATACAGGAACAAC	103-126
200-F	atatgctagcGGCCTCAACTCCTCCCATAG	206-225
300-F	atatgctagcCTGCCATGGAACTGTTTCCTTC	308-329
400-F	atatgctagcTCCCTGTCACCTCTTCCGACTC	412-433
500-F	atatgctagcAAAATCTGCCTGGGTTTTGTTCCC	514-537
600-F	atatgctagcCCACCTGCCCTTTTTTCTGCC	618-638
700-F	atatgctagcCAAAAAATGCACAAACAATGCAATCAAC	719-746
800-F	atatgctagcTTTTGCCTTTAAGTTATTTTACCTGTTTTTGTTTC	822-856
900-F	atatgctagcCCCTTCCTATTCCAAGCTTCC	926-946
1000-F	atatgctagcTTTGTGGGGTGACGGGACTC	1029-1048
1100-F	atatgctagcGGGAGGGGCATTGCTGACTG	1132-1151
1200-F	atatgctagcAGCCTGCTGGTTTTATCTGAGTG	1234-1256
100-R	atatgcggccgcCTGCTTGGCGAGACGTGTCAC	82-102
200-R	atatgcggccgcTAGGACCCCTGGAGAGTCAC	186-205
300-R	atatgcggccgcGGTTCTGACCCACCCCCAC	289-307
400-R	atatgcggccgcCTTAAAATGGTGCTAGTCCTATCCC	387-411
500-R	atatgcggccgcTGGAGAAGCAGCAGGTAAAAGAG	491-513
600-R	atatgcggccgcCTCAGCGTTTGGCCCTG	601-617
700-R	atatgcggccgcTGTGTGTGAGGTCTTGGCTTTG	697-718
800-R	atatgcggccgcTTTCTTAAAAATTAGATCCACTACAATC	794-821
900-R	atatgcggccgcAACCAAATAAATAAATAAATAAATACATAAC	895-925
1000-R	atatgcggccgcCAGAGCAAGCGTCGCAGC	1011-1028
1100-R	atatgcggccgcCATCACCCACAGAGCCGG	1114-1131
1200-R	atatgcggccgcACCTGCTGCTCAAAACACAG	1214-1233
1300-R	atatgcggccgcTTAAGACAAAAGGTTTTTATTCAAAAAACG	1308-1337

Table S3: Primers used to generate mouse 50mer HMGA2 3'UTR fragments. Forward primers (F) are SpeI tailed and reverse primers (R) are NotI tailed. Coordinates indicate position downstream of stop codon.

Description	Sequence	Coordinates
50-R-mouse	atatgcggccgCTTCTCCCTTCAAAAGATCCAACTGATGCTGAGGTAGAAATTGAATGTCG	9-57
50-F-mouse	atatactagtACACTGCAGTGACCAGTTATTCTTAACTGCCACGGTCTTTCTACTTCCTG	58-107
150-R-mouse	atatgcggccgCGATTTCGCCCACCCCGGCCCCGCCCCTCGCCCAGCCCCGCCCCCGCCCCACCCactagt	99-163
150-F-mouse	atatactagtCATAACCTTGAGAAGGACTATATTAATCACTTTGTAATCCCTTCACAGTC	164-213
250-R-mouse	atatgcggccgcAGTTGCATTGTTAAACTGTGTCCCCCGTGTTTACAGCAGTTTTTCACT	222-269
250-F-mouse	atatactagTTTAATGACTGTTTTCTTTTTCCTTAACTTACTAATAGTTTGTGGATCTG	270-318
350-R-mouse	atatgcggccgcGTAGTGACTGATTAAGCCCACCACAGAGGTTTTCTTCAACCACACACCCTTG	325-376
350-F-mouse	atatactagtATGCAAACCCTAAACCGGCACCCTGGTGACCGGGGGCATTCGTATAAGAA	377-426
450-R-mouse	atatgcggccgcATGATCATGGTGGGGGTGGCATCTGAGTGGACACAGAGTCACACACAA	432-479
450-F-mouse	atatactagtAGAAAATCTGCTTAGGACACCAAAGATGAGAACTAGACACTACTCTCC	480-527

550-R-mouse	atatgcggccgcAAAAAAAGAAAAAAAAATCAAGTAAGTGTCTACAAGATTATACACAAA	532-579
550-F-mouse	atatactagtACTTTTCAATTCTGAATGAGACAAAATGCTGGTGTATCTTTTCATACAGC	580-629
650-R-mouse	atatgcggccgCTTTTTGAAAAACAAAACAAAGCAAAAAACGAGCATAACCTATTCTGG	638-684
650-F-mouse	atatactagtGGAAGTAAACGAGAACCGTTGACTCCTCCATTTATGGACTCATACACAGCAGC	685-737
750-R-mouse	atatgcggccgcTGGCTGTGTAGATTTCCCGAGGCGGGAAAGAGAGCTTGTGGGCTTATCACTCCac	735-791
750-F-mouse	atatactagtAAAGCCACTTAGCCATAAATGACACTTGTCAGCCTTGAAGCATCGGAGAT	792-841
850-R-mouse	atatgcggccgcTTAACCTTTTCATTAAATTCCAAAACAGGATCATTTTACTCAGCTA	845-890
850-F-mouse	atatactagtCAGTACCCAATGAACCCACCCAAGTGATGACATGGGAGGAGCGAAA	891-936
950-R-mouse	atatgcggccgcTTATTATTTTTTTTTAAAAAATAGTGTCCTTTATATAGCAAAAGAGAT	942-989
950-F-mouse	atatactagtAAACAGCTCCCGCTCTCTGTCCTCTCTCCCTCCCTTCTCTCCCTCGCCTC	990-1039
1050-R-mouse	atatgcggccgcTCACGGACACTGGTACACAATGAAGAACAGGGAATATAGAGAGGAG	1043-1088
1050-F-mouse	atatactagtAAGACCGCAGTACCACTTACCTCAGATGAAGCCTGCGTGTTACATCC	1089-1135
1150-R-mouse	atatgcggccgcAAGATAATGCACCTCGGCTAGCCATCTTATGTCAAAATGAAAGGTGTT	1139-1186
1150-F-mouse	atatactagtGGTTCGGACTGCCATCTCTGCATTCACGCTGCACTTTTAGCCAGAGATGC	1187-1236
1250-R-mouse	atatgcggccgcGCTGTAAATTCACTGTAGCATTCAGAGGTAGTATTGAGGAGTGGGGAT	1241-1288
1250-F-mouse	atatactagtCCTGCACTTGTTACACGCTGCTAGACACAAGCCCTGCAAGAGAAAGGAAA	1289-1338
1350-R-mouse	atatgcggccgcGGGATGGCTGAGATGCCGACCCAGTAAGGTTTGGTTTGGTTTTGGTGGGC	1346-1395
1350-F-mouse	atatactagtCAGTTCTCGACCATTCTTCTCTGTACTCTTACTCCGTCTCAGCAGGCTAT	1396-1445
1450-R-mouse	atatgcggccgcACAAGCATTTGTAACATTTTAATTAAAAAAAAAAAAAGTCATAGAA	1452-1497
1450-F-mouse	atatactagtGGCAGCTTTCCTGCTAGATTGTTACATTAATTTGAAACAGTTTTGA	1498-1543
1550-R-mouse	atatgcggccgcGTAGTGTCACTGAAAAAAAAATTCTCCTTAAGAACCTAGGAGCAACTT	1547-1594
1550-F-mouse	atatactagTTGTATCACACACACACATCTGTAGTGTTCAAATATAAGTCTCCAAGTTT	1596-1644
1650-R-mouse	atatgcggccgcTTCCTTGCAAATCAGGAAGTCCATTTGTTTCAATAATTCATTTGAGGT	1648-1695
1650-F-mouse	atatactagtCTACCTCCACACTTCCAAAGGAACGAACTTGCAGCCTATATCACTCATTG	1696-1745
1750-R-mouse	atatgcggccgcAATGTTTCAATGAGGGAGAGGTGAGGTTTGAGCTCCTTCAAACATGGGGG	1754-1803
1750-F-mouse	atatactagTTTTTTGGTAAAAGACACTTGATAGAAACACAATTTTTTTACATACTTTT	1804-1852
1850-R-mouse	atatgcggccgcGTAGCAAAATTTCAAGTTTCTTTGAAGGTTGGCTTGATTTTAATTCAT	1864-1911
1850-F-mouse	atatactagtAACCAGCTCAGCCTTTTGCCTAATGCAATGAAAAAGGAAAAAAATAGATT	1912-1961
1950-R-mouse	atatgcggccgcTAAAATACATGAAAAAATATCGGTCAAGCATATTCTTCTAGGCAACAA	1970-2017
1950-F-mouse	atatactagtCACAATGTGATTTTTGTAAAAAAATGTCTCAAGCAGATTTGTTTTGGACG	2018-2067
2050-R-mouse	atatgcggccgcAAAGTCAGCACACTTAATAGGAGAGAAAGGCATAGAAACTCTACACAA	2072-2119
2050-F-mouse	atatactagtCCAGAGTGTTACCCACTGGGCCAGGAGGTAGTTTCTCATAGTGGCTTGTG	2120-2169
2150-R-mouse	atatgcggccgcATGGTTGTTTGTTTGTTTCATTTGGCTTCAGTATTAACTTATACTG	2171-2216
2150-F-mouse	atatactagtGTCTCTTCCAGCTGTTTTCAGGGAGGTTACTTCAAAGGCCACGTGC	2217-2262
2250-R-mouse	atatgcggccgcATAGCTCCTTTGGCGACTCACAACAGTGAGCCATCTGCCAGTCTCAGAGCG	2263-2313
2250-F-mouse	atatactagtGGAGAGATTAAAATTCAACATGACTGTTAACAATGCATTAAATAATCAAA	2314-2363
2350-R-mouse	atatgcggccgcTCTGTAAGGCCCATCCGAAGACCCGGAATGAGAATCTGATATTTATAAGCC	2372-2422
2350-F-mouse	atatactagtAACCTCATTTTGGCCAGCTCATAAAAACTGAAGCAGCTTCTCGTGTTGGCCAGAC	2423-2477
2450-R-mouse	atatgcggccgcAGGAAATAAGGAATAACTTCATCAGAGATGGAAATTGCTCGGTGTGC	2481-2527
2450-F-mouse	atatactagtGTATGTTGTACAATCAAAACACACTACTACCTCTTAAGTCCCAGTATA	2528-2575
2550-R-mouse	atatgcggccgCTGTTCCATTGGACACAAGCCTTTTTTTTTCTCTTTTTTTTCTTTTTTTTCAGTATG	2587-2642
2550-F-mouse	atatactagTGAGAACATCATAAAATTTTTATATATATAGTTTATTTTTGTGGGAGATA	2643-2691
2650-R-mouse	atatgcggccgcTAGAGAAGTTAGATGTCCAGTCTTACTTAGCTGTGACCAACAACAG	2715-2760
2650-F-mouse	atatactagtCCATTTCTGCAAGCTAAGTATGTTTGCAGGAGAAACTTATCAAGACGATT	2761-2810

2750-R-mouse	atatgcggccgcAGAGGGCACACAAAGGAACGGGGAGAAAGTTGGATGCAGT	2812-2851
2750-F-mouse	atatactagtGACTTCGTTCTCTGTTCCTTGTGTAGAGTCGCTGTCTGTG	2852-2891
2850-R-mouse	atatgcggccgCACTAGAGAAGGTATTGCCACAAGCAAGCCGTCCAAGTACAAT	2893-2934
2850-F-mouse	atatactagtGATTATCACTGTCTGCACAATAAACATAACAGCCTCTGTGGGC	2935-2977

Table S4: Random-sequence controls. Table shows full sequence of random-sequence controls, including restriction sites for cloning (SpeI at 5', NotI at 3')

Random 50mer1	atatactagtACATTAGCAGATCAAAATAACTGAGATCGATTACCTAAAGTAACAGCACTgcggccgcatat
Random 50mer2	atatactagtATTAGTCACTGTCTACAAAGAGGCGAGACACCCATCCTCTTTGGGTGATCgcggccgcatat
Random 50mer3	atatactagtCTACATTGAATTTCAATTCTCAAACTGAGGACAGCGTAGTATCTGTCGGTgcggccgcatat
Random 100mer1	atatactagtACATTAGCAGATCAAAATAACTGAGATCGATTACCTAAAGTAACAGCACTATTAGTCAC TGTCTACAAAGAGGCGAGACACCCATCCTCTTTGGGTGATCgcggccgcatat
Random 100mer2	atatactagtCTACATTGAATTTCAATTCTCAAACTGAGGACAGCGTAGTATCTGTCGGTCGTATTCGTG TATAAGTCAAGAATGGAACATACTTTGAAATAAGCGGCATgcggccgcatat
Random 100mer3	atatactagtTGTAACACGTCTCCTATCGTCTTCCATTCTCTGGATTTACCTTGGTGTTGAAGCTTCCGTA TCGTCAATCATAGCAATGGATATCAATAGTCTTGTATGTgcggccgcatat
Random 200mer1	atatactagtACATTAGCAGATCAAAATAACTGAGATCGATTACCTAAAGTAACAGCACTATTAGTCAC TGTCTACAAAGAGGCGAGACACCCATCCTCTTTGGGTGATCCTACATTGAATTTCAATTCTCAAA CTGAGGACAGCGTAGTATCTGTCGGTCGTATTCGTGTATAAGTCAAGAATGGAACATACTTTGAA ATAAGCGGCATgcggccgcatat
Random 200mer2	atatactagtCATCAGGCAATGAGTGTTATTACCACCACGACGTACATTTTCTGTTCTCTCATCAATCCA TTTTCACCTTTTATTAAGGTTATAGCACTTGGTTAATACTCTACATTGAATTTCAATTCTCAAACT GAGGACAGCGTAGTATCTGTCGGTCGTATTCGTGTATAAGTCAAGAATGGAACATACTTTGAAAT AAGCGGCATgcggccgcatat
Random 200mer3	atatactagtACATTAGCAGATCAAAATAACTGAGATCGATTACCTAAAGTAACAGCACTATTAGTCAC TGTCTACAAAGAGGCGAGACACCCATCCTCTTTGGGTGATCCATCAGGCAATGAGTGTTATTACC ACCACGACGTACATTTTCTGTTCTCTCATCAATCCATTTTCACCTTTTATTAAGGTTATAGCACTTG GTTAATACTgcggccgcatat
Random 400mer1	atatactagtAAATCACACTTGTAAACGTTAAACATGCATGTATCTTAATATGGAGCATTTTACAATGGT GTAGGCTAGTAATCTAGCTATTTAAACGGGTTGTACTTTAATTCTGTCTAGACTATCGGTGTCAAT ATCGCCACTTGTTCAATTAACCTCTAAAAGCCATAACTTATATCGTTTAAATCATCACGTATTGTA ATCCCGCCAGAAATACTGTAACTTTAGAAGGCATTAGAGTATATTGGCTGCCACAATCCCAACGA AGCACTATTTGACTCCAATTCGCCTCTATATTTCTTGATTGGAGGCATTATTGATTCACGTCCAGC TGCGGGGAGTCAACGGATTGGTGTCATCAGCTATCCCCTGACTAAGGCTTATTCGGGGTTAGACA GCCCATTCACCCgcggccgcatat
Random 400mer2	atatactagtAAACATCTACCCGTAGAGCTTTAACAGATGTGGTCCTTATATACTCAAGAACCCTCCCC AGACGCGGGTTGCAATGTAATTCTCTATTTCGTCTGCTTTATTAAGTACACGCATCCCCCTCACGC ATGATCTAACAGGCACGCTCGCTCTTATACGTGGACTGCATCCGGTCATTTAATTATCCCACGTA GCGTGAAGTAGAAACATATTTCCATATAAGTCCCTGTCGTATTTCAAAGATAATAAGATACATCT AAGCGAATTCTACCCCCCTTTATACCTGTACTCACTCTTATCACAGATTTAGCCATTTCCAAACTC TCAGACCTGTATGAATACTCTTTCGATCCTTGGGATACTTGTGTAATGTAATAACAGCACATTCA AGAGGGCTACACAAgcggccgcatat
Random 400mer3	atatactagtACATTAGCAGATCAAAATAACTGAGATCGATTACCTAAAGTAACAGCACTATTAGTCAC TGTCTACAAAGAGGCGAGACACCCATCCTCTTTGGGTGATCCTACATTGAATTTCAATTCTCAAA CTGAGGACAGCGTAGTATCTGTCGGTCGTATTCGTGTATAAGTCAAGAATGGAACATACTTTGAA ATAAGCGGCATCATCAGGCAATGAGTGTTATTACCACCACGACGTACATTTTCTGTTCTCTCATC AATCCATTTTCACCTTTTATTAAGGTTATAGCACTTGGTTAATACTTGTAACACGTCTCCTATCGT CTTCCATTCTCTGGATTTACCTTGGTGTTGAAGCTTCCGTATCGTCAATCATAGCAATGGATATCA ATAGTCTTGTATGTgcggccgcatat

Table S5: Primers used to amplify 100mer HMGA2 3'UTR fragments containing disrupted let-7 target sites. These primers overlap with the mutated let-7 site. Remaining primers used in this experiment did not overlap with let-7 target sites and were therefore identical to primers in Table S1. Forward primers (F) are SpeI tailed and reverse primers (R) are NotI tailed. Coordinates indicate position downstream of stop codon.

Description	Sequence	coordinates
0-F-mouse-let-7m	atatactagtGCCGACATTCAATTTCTAACGC	6-27
1200-F-mouse-let-7m	atatactagtATAATCCCCACTCCTCAATACTAACGC	1136-1166
1600-F-mouse-let-7m	atatactagtGTAACGCAAATGAATTATTGAAACAAATGGACTTC	1646-1680
2500-R-mouse-let-7m	atatagcggccgcTATACTGGGACTTAAGCGTTAGTAGTGTG	2547-2575

Table S6: Primers used to generate mutations in 200mers where the two corresponding 100mers would meet. These are the mutagenic inside primers; outside primers were from table S1.

Description	Sequence
Junct. mut. primer 432-631 F	GACACTAGATCATAGAAAATGTGTATAATCTTGTAGACACTTACTTGATTTTTTTTTC
Junct. mut. primer 432-631 R	GATTATACACATTTTCTATGATCTAGTGTCTAGTTCTCATCTTTGGTGTC
Junct. mut. primer 2365-2575 F	GTGTTGGCCAGATCATAGAAAACGAGCAATTTCCATCTCTGATGAAG
Junct. mut. primer 2365-2575 R	GAAATTGCTCGTTTTCTATGATCTGGCCAACACGAGAAGCTG
Junct. mut. primer 2481-2709 F	CACACTCTACCTCTTAAGTCCCAGTACTACTCATTTTTCATACTGAAAAAAAAG
Junct. mut. primer 2481-2709 R	CTTTTTTTTCAGTATGAAAAATGAGTAGTACTGGGACTTAAGAGGTAGAGTGTG

Table S7: Primers used to generate HMGA2 3'UTR 50mer fragments with a substitution mutation at tiling intervals across the 50mer. Forward primers (F) are SpeI tailed and reverse primers (R) are NotI tailed. If a forward or reverse primer is not indicated, this indicates that a wild type primer was used from Table S3.

Description	Sequence
Scan_mut1_528-579_F	atatactagtATTAGTCACTGTTAATCTTGTAGACACTTACTTG
Scan_mut1_528-579_R	atatgcggccgcAAAAAAAGAAAAAAAAATCAAGTAAGTGTCTACAAGATTAACAGTGAC
Scan_mut2_528-579_F	atatactagtTTCTTTGATTAGTCACTGTTAGACACTTACTTG
Scan_mut2_528-579_R	atatgcggccgcAAAAAAAGAAAAAAAAATCAAGTAAGTGTCTAACAGTGACTAATCAAA
Scan_mut3_528-579_F	atatactagtTTCTTTGTGTATAATATTAGTCACTGTTACTTG
Scan_mut3_528-579_R	atatgcggccgcAAAAAAAGAAAAAAAAATCAAGTAACAGTGACTAATATTATACACAAA
Scan_mut4_528-579_F	atatactagtTTCTTTGTGTATAATCTTGTAGAATTAGTCACTG
Scan_mut4_528-579_R	atatgcggccgcAAAAAAAGAAAAAAAAACAGTGACTAATTCTACAAGATTATACACAAA
Scan_mut5_528-579_F	atatactagtTTCTTTGTGTATAATCTTGTAGACACTTACTATTAG
Scan_mut5_528-579_R	atatgcggccgcAAAAAAAGACAGTGACTAATAGTAAGTGTCTACAAGATTATACACAAA
Scan_mut6_528-579_R	atatgcggccgcACAGTGACTAATAAAAATCAAGTAAGTGTCTACAAGATTATACACAAA
Scan_mut1_631-684_F	atatactagtATTAGTCACTGTAGGTTATGCTCGTTTTTTG
Scan_mut1_631-684_R	atatgcggccgcTTTTTGAAAAACAAAACAAAGCAAAAAACGAGCATAACCTACAGTGAC
Scan_mut2_631-684_F	atatactagtGCAAACCAATTAGTCACTGTCTCGTTTTTTG
Scan_mut2_631-684_R	atatgcggccgcTTTTTGAAAAACAAAACAAAGCAAAAAACGAGACAGTGACTAATTGG
Scan_mut3_631-684_F	atatactagtGCAAACCAGAATAGGTATTAGTCACTGTTTG
Scan_mut3_631-684_R	atatgcggccgcTTTTTGAAAAACAAAACAAAGCAAACAGTGACTAATACCTATTCTGG
Scan_mut4_631-684_R	atatgcggccgcTTTTTGAAAAACAAAAACAGTGACTAATCGAGCATAACCTATTCTGG
Scan_mut5_631-684_R	atatgcggccgcTTTTTGAAACAGTGACTAATGCAAAAAACGAGCATAACCTATTCTGG
Scan_mut6_631-684_R	atatgcggccgcACAGTGACTAATAAAACAAAGCAAAAAACGAGCATAACCTATTCTGG
Scan_mut1_990-1042_F	atatactagtATTAGTCACTGTCTCTCTGTCCTCTCTCCCTCCCTTCTCTCCCTCGCCTC
Scan_mut2_990-1042_F	atatactagtAAACAGCTATTAGTCACTGTCCTCTCTCCCTCCCTTCTCTCCCTCGCCTC
Scan_mut3_990-1042_F	atatactagtAAACAGCTCCCGCTCTATTAGTCACTGTCCTCCCTTCTCTCCCTCGCCTC
Scan_mut4_990-1042_F	atatactagtAAACAGCTCCCGCTCTCTGTCCTCATTAGTCACTGTCTCTCCCTCGCCTC
Scan_mut4_990-1042_R	atatgcggccgcAGAGAGGCGAGGGAGAGACAGTGACTAATG
Scan_mut5_990-1042_F	atatactagtAAACAGCTCCCGCTCTCTGTCCTCTCTCCCTCATTAGTCACTGTCGCCTC
Scan_mut5_990-1042_R	atatgcggccgcAGAGAGGCGACAGTGACTAATGAG
Scan_mut6_990-1042_F	atatactagtAAACAGCTCCCGCTCTCTGTCCTCTCTCCCTCCCTTCTCTATTAGTCAC
Scan_mut6_990-1042_R	atatgcggccgcAACAGTGACTAATAGAGAAGGGAGGGAG

Table S8: Primers used to delete candidate AREs from full length HMGA2 (intact or let-7 disrupted) reporter constructs. These are the mutagenic inside primers; outside primers were from table S1.

Description	Sequence
Mut-ARE-I-del-F	CTTTGTGTATAATCTTGTAGACACTTACTTGAACTTTTCAATTCTGAATGAGACAAAATG
Mut-ARE-I-del-R	CAGAATTGAAAAGTTCAAGTAAGTGTCTACAAGATTATACACAAAGAAAGGAGAGTAG
Mut-ARE-II-del-F	CTAGCAAACCAGAATAGGTTATGCTCGAAAAAGGGAAGTAAACGAGAACC
Mut-ARE-II-del-R	CAACGGTTCTCGTTTACTTCCCTTTTTCGAGCATAACCTATTCTGGTTTG
Mut-ARE-III-del-F	AAAAAATAATAAAAACAGCTCCCGCTCTCTGTCCCTCGCCTCTCTCTCC
Mut-ARE-III-del-R	CAGGGAATATAGAGAGGAGAGAGAGGCGAGGGACAGAGAGCGGGAGCTG

Table S9: Hairpins used in knockdown experiments.

Target transcript	TRC shRNA hairpin reference
GFP	TRCN0000072181
GFP	TRCN0000072182
GFP	TRCN0000072197
GFP	TRCN0000072201
LacZ	TRCN0000072223
LacZ	TRCN0000072224
HuR	TRCN0000276129
HuR	TRCN0000285493

Table S10: Primers used in qRT-PCR assays, forward primers (F), reverse primers (R).

Description	Sequence
HuR-F	CTCGGTTTGGGCGGATCATC
HuR-R	TTCTGCCTCCGACCGTTTG
GAPDH-F	CCTGTTCGACAGTCAGCCG
GAPDH-R	CGACCAAATCCGTTGACTCC