Figure S1

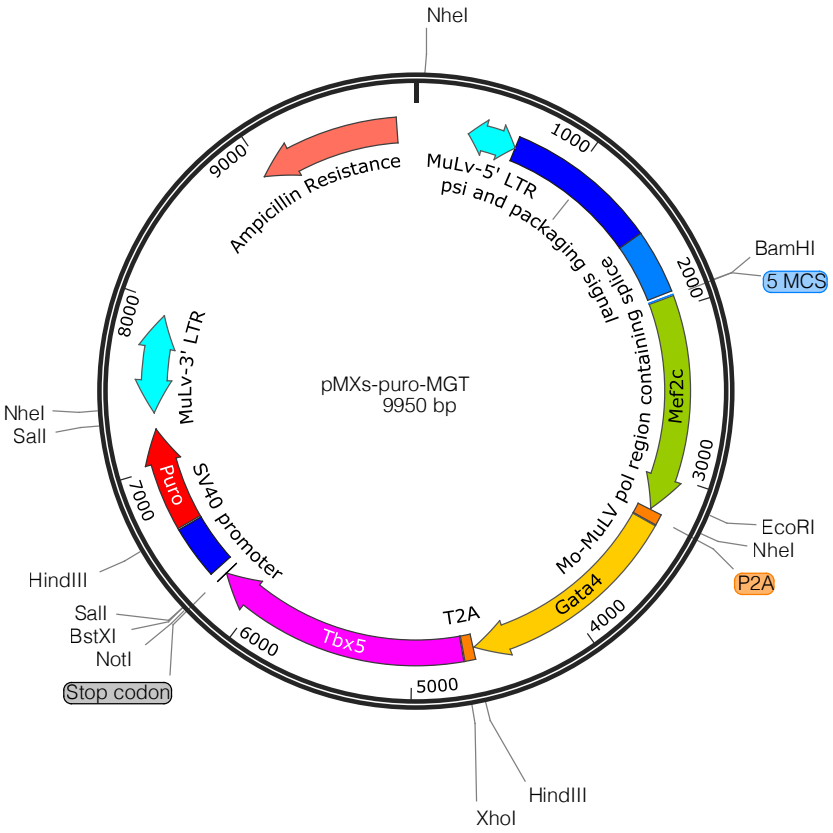
NheI
1000
MuLv-5' LTR
psi and packaging signal
splice
2000
BamHI
5 MCS
Mef2c
3000
EcoRI
NheI
P2A
Gata4
4000
T2A
Tbx5
5000
HindIII
XhoI
6000
SalI
BstXI
NotI
Stop codon
HindIII
7000
Puro
SV40 promoter
NheI
SalI
8000
MuLv-3' LTR
9000
Ampicillin Resistance
pMXs-puro-MGT
9950 bp
Mo-MuLV pol region containing

Table S1. Sequences of shRNA oligoes used for RNAi screen.

Names and sequences of shRNAs cloned in pLKO.1 vetor		
shRNA library for screen		
Target Gene Symbol	**TRC Id**	**Target Sequence (Sense)**
shKdm5c_1	TRCN0000295415	CCGGAGCAAGCTACCCGGGAATATACTCGAGTATATTCCCGGGTAGCTTGCTTTTTTG
shKdm5c_2	TRCN0000295348	CCGGATATTCTGACTCCAAGGTATTCTCGAGAATACCTTGGAGTCAGAATATTTTTTG
shKdm5c_3	TRCN0000287995	CCGGCGCATTGTTTATCCCTATGAACTCGAGTTCATAGGGATAAACAATGCGTTTTTG
shKdm5c_4	TRCN0000287921	CCGGCGCTCTCACTATGAACGCATTCTCGAGAATGCGTTCATAGTGAGAGCGTTTTTG
shKdm5c_5	TRCN0000287994	CCGGGCCCAATATCCAGTCTCTCAACTCGAGTTGAGAGACTGGATATTGGGCTTTTTG
shKdm5c_6	TRCN0000097857	CCGGCGCATTGTTTATCCCTATGAACTCGAGTTCATAGGGATAAACAATGCGTTTTTG
shKdm5c_7	TRCN0000097858	CCGGCGCTCTCACTATGAACGCATTCTCGAGAATGCGTTCATAGTGAGAGCGTTTTTG
shKdm5c_8	TRCN0000097859	CCGGGCCCAATATCCAGTCTCTCAACTCGAGTTGAGAGACTGGATATTGGGCTTTTTG
shKdm5c_9	TRCN0000097856	CCGGGCATTGTTTATCCCTATGAAACTCGAGTTTCATAGGGATAAACAATGCTTTTTG
shKdm5d_1	TRCN0000098105	CCGGCCTAAGAAGTATTCCCTGTATCTCGAGATACAGGGAATACTTCTTAGGTTTTTG
shKdm5d_2	TRCN0000098106	CCGGCCTTTACTACACCTATCTTATCTCGAGATAAGATAGGTGTAGTAAAGGTTTTTG
shKdm5d_3	TRCN0000098107	CCGGGCAGAACACTTAGAGGATGTACTCGAGTACATCCTCTAAGTGTTCTGCTTTTTG
shKdm5d_4	TRCN0000098108	CCGGGCAATGTAACACAGATCCATTCTCGAGAATGGATCTGTGTTACATTGCTTTTTG
shKdm5d_5	TRCN0000098109	CCGGGCCTGTTATGACTGTCCAGATCTCGAGATCTGGACAGTCATAACAGGCTTTTTG
shMll1_1	TRCN0000304329	CCGGACGAAGATGACTTATACTATTCTCGAGAATAGTATAAGTCATCTTCGTTTTTTG
shMll1_2	TRCN0000310900	CCGGCTGATTCGCAAACCAATATTTCTCGAGAAATATTGGTTTGCGAATCAGTTTTTG
shMll1_3	TRCN0000301690	CCGGCGCCTTCACTTGACCATAATTCTCGAGAATTATGGTCAAGTGAAGGCGTTTTTG
shMll2_1	TRCN0000239234	CCGGGTTCATCGAGTTGCGACATAACTCGAGTTATGTCGCAACTCGATGAACTTTTTG
shMll2_2	TRCN0000239233	CCGGGACTGGTCTAGCCGATGTAAACTCGAGTTTACATCGGCTAGACCAGTCTTTTTG
shMll2_3	TRCN0000239232	CCGGCACCCACACCTACCTCATTTACTCGAGTAAATGAGGTAGGTGTGGGTGTTTTTG
shMll5_1	TRCN0000241161	CCGGACTCCAACTTCAATCACTTTACTCGAGTAAAGTGATTGAAGTTGGAGTTTTTTG
shMll5_2	TRCN0000241164	CCGGGCAACTTCTGGAGCGTTATTTCTCGAGAAATAACGCTCCAGAAGTTGCTTTTTG
shMll5_3	TRCN0000241165	CCGGATGCAGTGTTTGGCAACATATCTCGAGATATGTTGCCAAACACTGCATTTTTTG
shPhf23_1	TRCN0000238013	CCGGTGGGATCTGATCACGTGTTACCTCGAGGTAACACGTGATCAGATCCCATTTTTG
shPhf23_2	TRCN0000238016	CCGGGCGGAGAACCATTGAGGATTTCTCGAGAAATCCTCAATGGTTCTCCGCTTTTTG
shPhf23_3	TRCN0000238017	CCGGCCACTCTCTCCCACATCATTGCTCGAGCAATGATGTGGGAGAGAGTGGTTTTTG
shCtcf_1	TRCN0000039019	CCGGGCAGAGAAAGTAGTTGGTAATCTCGAGATTACCAACTACTTTCTCTGCTTTTTG
shCtcf_2	TRCN0000039020	CCGGCGGAACACAATGGCAAGACATCTCGAGATGTCTTGCCATTGTGTTCCGTTTTTG
shCtcf_3	TRCN0000039021	CCGGCCCATTAACATAGGAGAGCTTCTCGAGAAGCTCTCCTATGTTAATGGGTTTTTG
shCtcf_4	TRCN0000039022	CCGGCCGATGATATGTCACACCTTACTCGAGTAAGGTGTGACATATCATCGGTTTTTG
shCtcf_5	TRCN0000039023	CCGGGCCATCATTCAGGTCGAAGATCTCGAGATCTTCGACCTGAATGATGGCTTTTTG
shBcorl1_1	TRCN0000085728	CCGGGCCTTATCAATGCCAGCATTACTCGAGTAATGCTGGCATTGATAAGGCTTTTTG
shBcorl1_2	TRCN0000085730	CCGGGCACAGTGAAATCCCGTTATACTCGAGTATAACGGGATTTCACTGTGCTTTTTG
shBcorl1_3	TRCN0000085731	CCGGGCCACTCTAAGGAACTCATTTCTCGAGAAATGAGTTCCTTAGAGTGGCTTTTTG
shBcorl1_4	TRCN0000085732	CCGGGTGGTCAATGACAACCTAGAACTCGAGTTCTAGGTTGTCATTGACCACTTTTTG
shBcor_1	TRCN0000081963	CCGGCCCACTGTGTACAGTGTGTTACTCGAGTAACACACTGTACACAGTGGGTTTTTG
shBcor_2	TRCN0000081965	CCGGCCCGGATATTCCGTAGCAATTCTCGAGAATTGCTACGGAATATCCGGGTTTTTG
shBcor_3	TRCN0000081966	CCGGCCACTTAGAAATTGTACGATTCTCGAGAATCGTACAATTTCTAAGTGGTTTTTG
shBcor_4	TRCN0000081967	CCGGCCAGAATTTGTGACCTACCAACTCGAGTTGGTAGGTCACAAATTCTGGTTTTTG
shRad21_1	TRCN0000175873	CCGGGCACCAGAAATTATGTGACTACTCGAGTAGTCACATAATTTCTGGTGCTTTTTTG
shRad21_2	TRCN0000175503	CCGGCCATGTATTTGAGTGCAACTTCTCGAGAAGTTGCACTCAAATACATGGTTTTTTG
shRad21_3	TRCN0000174832	CCGGGCTTAGCGATTATTCTGATATCTCGAGATATCAGAATAATCGCTAAGCTTTTTTG
shRad21_4	TRCN0000176084	CCGGGATGAGTTCCTCAAAGAGTTTCTCGAGAAACTCTTTGAGGAACTCATCTTTTTTG
shRad21_5	TRCN0000216543	CCGGGCTTATAATGCCATTACTTTACTCGAGTAAAGTAATGGCATTATAAGCTTTTTTG
shStag2_1	TRCN0000108975	CCGGCGACCCTGAAATTGTAGGATACTCGAGTATCCTACAATTTCAGGGTCGTTTTTG
shStag2_2	TRCN0000108976	CCGGGCGCTTCTTGACCTTATCAATCTCGAGATTGATAAGGTCAAGAAGCGCTTTTTG
shStag2_3	TRCN0000108977	CCGGCCTCAACATTTAGTGGCATAACTCGAGTTATGCCACTAAATGTTGAGGTTTTTG
shStag2_4	TRCN0000108978	CCGGCCGATTTCTTTGATCCAGCTTCTCGAGAAGCTGGATCAAAGAAATCGGTTTTTG
shStag2_5	TRCN0000108979	CCGGCCTGATGAAGATGACGCATATCTCGAGATATGCGTCATCTTCATCAGGTTTTTG
shPhf12_1	TRCN0000084419	CCGGCCAACTCACTTCGAGCATTTACTCGAGTAAATGCTCGAAGTGAGTTGGTTTTTG
shPhf12_2	TRCN0000084420	CCGGCGGAGAAATCGAGATAAATATCTCGAGATATTTATCTCGATTTCTCCGTTTTTG
shPhf12_3	TRCN0000084422	CCGGCCTGAACCGAATCCACAAGAACTCGAGTTCTTGTGGATTCGGTTCAGGTTTTTG
shSin3b_1	TRCN0000039367	CCGGCCGTATAGACATTCCCAAGAACTCGAGTTCTTGGGAATGTCTATACGGTTTTTG
shSin3b_2	TRCN0000287547	CCGGCCGTATAGACATTCCCAAGAACTCGAGTTCTTGGGAATGTCTATACGGTTTTTG

shYy1_1	TRCN0000054553	CCGGCGACGGTTGTAATAAGAAGTTCTCGAGAACTTCTTATTACAACCGTCGTTTTTG
shYy1_2	TRCN0000054554	CCGGCCCTAAGCAACTGGCAGAATTCTCGAGAATTCTGCCAGTTGCTTAGGGTTTTTG
shYy1_3	TRCN0000054555	CCGGGCCCTCATAAAGGCTGCACAACTCGAGTTGTGCAGCCTTTATGAGGGCTTTTTG
shYy1_4	TRCN0000054556	CCGGGTGGTTGAAGAGCAGATCATTCTCGAGAATGATCTGCTCTTCAACCACTTTTTG
shYy1_5	TRCN0000054557	CCGGCACATCTTAACACACGCTAAACTCGAGTTTAGCGTGTGTTAAGATGTGTTTTTG
shRuvbl1_1	TRCN0000115241	CCGGGCTGGAGATGTGATTTACATTCTCGAGAATGTAAATCACATCTCCAGCTTTTTG
shRuvbl1_2	TRCN0000115243	CCGGGCTGGCAAAGATCAATGGCAACTCGAGTTGCCATTGATCTTTGCCAGCTTTTTG
shRuvbl1_3	TRCN0000115244	CCGGGCCACAGAGTTTGACCTTGAACTCGAGTTCAAGGTCAAACTCTGTGGCTTTTTG
shRuvbl1_4	TRCN0000115245	CCGGGCAAGATATTCTGTCTATGATCTCGAGATCATAGACAGAATATCTTGCTTTTTG
shRuvbl2_1	TRCN0000115256	CCGGCCGAGAACAGATCAATGCAAACTCGAGTTTGCATTGATCTGTTCTCGGTTTTTG
shRuvbl2_2	TRCN0000115257	CCGGTGTGACAAGAATCGAGCGAATCTCGAGATTCGCTCGATTCTTGTCACATTTTTG
shRuvbl2_3	TRCN0000115258	CCGGCCTCCATGAGATTGACGTCATCTCGAGATGACGTCAATCTCATGGAGGTTTTTG
shRuvbl2_4	TRCN0000115259	CCGGCGACACACCATTCACAGCCATCTCGAGATGGCTGTGAATGGTGTGTCGTTTTTG
shRuvbl2_5	TRCN0000115260	CCGGGCCAGCCTGGTGTGCCGGAAACTCGAGTTTCCGGCACACCAGGCTGGCTTTTTG
shSmarca5_1	TRCN0000084429	CCGGCCGAGCAAATAGATTTGAGTACTCGAGTACTCAAATCTATTTGCTCGGTTTTTG
shSmarca5_2	TRCN0000084430	CCGGGTTTGGGAAAGACACTTCAAACTCGAGTTTGAAGTGTCTTTCCCAAACTTTTTG
shSmarca5_3	TRCN0000084431	CCGGCGTCGAATTAAAGCTGATGTTCTCGAGAACATCAGCTTTAATTCGACGTTTTTG
shSmarca5_4	TRCN0000084432	CCGGCCCTTTCATCAGCTAAGAATACTCGAGTATTCTTAGCTGATGAAAGGGTTTTTG
shSmarca5_5	TRCN0000295773	CCGGTCACTAACTGGTAGTTCTTTACTCGAGTAAAGAACTACCAGTTAGTGATTTTTG
shTet1_1	TRCN0000341917	CCGGTCTAACCAGTGTGCTAATATACTCGAGTATATTAGCACACTGGTTAGATTTTTG
shTet1_2	TRCN0000341850	CCGGCCTACGGGAAGCGACCATAATCTCGAGATTATGGTCGCTTCCCGTAGGTTTTTG
shTet1_3	TRCN0000341847	CCGGCAACTTGCATCCACGATTAATCTCGAGATTAATCGTGGATGCAAGTTGTTTTTG
shTet1_4	TRCN0000341849	CCGGCTAGCTATAGAGTATAGTAAACTCGAGTTTACTATACTCTATAGCTAGTTTTTG
shTet1_5	TRCN0000341848	CCGGTTTCAACTCCGACGTAAATATCTCGAGATATTTACGTCGGAGTTGAAATTTTTG
shTet2_1	TRCN0000217530	CCGGCTTGTACTGTATAGGCATAAGCTCGAGCTTATGCCTATACAGTACAAGTTTTTTG
shTet2_2	TRCN0000192770	CCGGCCAACTCATGGGTCAATTCTTCTCGAGAAGAATTGACCCATGAGTTGGTTTTTTG
shTet2_3	TRCN0000201087	CCGGCGCTGGACATTTGTCTTGAAACTCGAGTTTCAAGACAAATGTCCAGCGTTTTTTG
shTet2_4	TRCN0000250893	CCGGTCGTGCTTTGGCCAGATTAAACTCGAGTTTAATCTGGCCAAAGCACGATTTTTG
shTet2_5	TRCN0000250895	CCGGGAGCGTTCCTCAGTATCATTTCTCGAGAAATGATACTGAGGAACGCTCTTTTTG
shTrrap_1	TRCN0000088534	CCGGCCCAGCGCATTGAACTGCTTTCTCGAGAAAGCAGTTCAATGCGCTGGGTTTTTG
shTrrap_2	TRCN0000088535	CCGGCATCAAGATCATAAGCATCATCTCGAGATGATGCTTATGATCTTGATGTTTTTG
shTrrap_3	TRCN0000088536	CCGGCGCTGAACTTTACTCTCTGTTCTCGAGAACAGAGAGTAAAGTTCAGCGTTTTTG
shTrrap_4	TRCN0000088537	CCGGGTGTCAACTCAGTGTCCATTACTCGAGTAATGGACACTGAGTTGACACTTTTTG
shSf1_1	TRCN0000109275	CCGGCCCAAGACGAATATCCAGAAACTCGAGTTTCTGGATATTCGTCTTGGGTTTTTG
shSf1_2	TRCN0000109276	CCGGGCGTAAAGATGGTCAGATGTTCTCGAGAACATCTGACCATCTTTACGCTTTTTG
shSf1_3	TRCN0000109277	CCGGCCGATGGAACCAAGACACAATCTCGAGATTGTGTCTTGGTTCCATCGGTTTTTG
shSf1_4	TRCN0000109278	CCGGTGTAGCATCGAGTGTCTTCTTCTCGAGAAGAAGACACTCGATGCTACATTTTTG
shSf1_5	TRCN0000109279	CCGGGCACGGATGGATAAAGAATATCTCGAGATATTCTTTATCCATCCGTGCTTTTTG
shSf3a1_1	TRCN0000109205	CCGGGCCAGTCTACGGAATGAATATCTCGAGATATTCATTCCGTAGACTGGCTTTTTG
shSf3a1_2	TRCN0000109206	CCGGCCGAGTAGAATGGGCCAAATTCTCGAGAATTTGGCCCATTCTACTCGGTTTTTG
shSf3a1_3	TRCN0000109207	CCGGCGGAAGGACTATGATCCCAAACTCGAGTTTGGGATCATAGTCCTTCCGTTTTTG
shSf3a1_4	TRCN0000109208	CCGGCCAGGATCAATGTGGTACCTACTCGAGTAGGTACCACATTGATCCTGGTTTTTG
shSf3a1_5	TRCN0000109209	CCGGGCCTGAATTTGAAGCTAGGATCTCGAGATCCTAGCTTCAAATTCAGGCTTTTTG
shSf3b1_1	TRCN0000109240	CCGGCCTGCTTCAATCTGATGATATCTCGAGATATCATCAGATTGAAGCAGGTTTTTG
shSf3b1_2	TRCN0000109241	CCGGGCCCACTTTCTGATGAAGAATCTCGAGATTCTTCATCAGAAAGTGGGCTTTTTG
shSf3b1_3	TRCN0000109242	CCGGCGCAGCAGATATTGACCATAACTCGAGTTATGGTCAATATCTGCTGCGTTTTTG
shSf3b1_4	TRCN0000109243	CCGGGCCGAGAGATTATTTCTAATTCTCGAGAATTAGAAATAATCTCTCGGCTTTTTG
shSf3b1_5	TRCN0000109244	CCGGGCCTGCCTTAATGAATGAATACTCGAGTATTCATTCATTAAGGCAGGCTTTTTG
shU2af1_1	TRCN0000123549	CCGGCCTCTTGAACATTTACCGTAACTCGAGTTACGGTAAATGTTCAAGAGGTTTTTG
shU2af1_2	TRCN0000123550	CCGGCGACTTGAATAACCGTTGGTTCTCGAGAACCAACGGTTATTCAAGTCGTTTTTG
shU2af1_3	TRCN0000123551	CCGGCCAACCTTTAGCCAGACCATTCTCGAGAATGGTCTGGCTAAAGGTTGGTTTTTG
shU2af1_4	TRCN0000123552	CCGGGCCCTCTTGAACATTTACCGTCTCGAGACGGTAAATGTTCAAGAGGGCTTTTTG
shU2af1_5	TRCN0000123553	CCGGCCAGTAACTGACTTCAGGGAACTCGAGTTCCCTGAAGTCAGTTACTGGTTTTTG
shZrsr2_1	TRCN0000126324	CCGGCGAGAGATACTTACCAAGTAACTCGAGTTACTTGGTAAGTATCTCTCGTTTTTG
shZrsr2_2	TRCN0000126325	CCGGCCTTTACCCTAAGTAAGTTATCTCGAGATAACTTACTTAGGGTAAAGGTTTTTG
shZrsr2_3	TRCN0000126326	CCGGGAAGAACTAGAGAGAAAGTTACTCGAGTAACTTTCTCTCTAGTTCTTCTTTTTG
shZrsr2_4	TRCN0000126327	CCGGTGGTGCAATGACAGATACCTTCTCGAGAAGGTATCTGTCATTGCACCATTTTTG
shZrsr2_5	TRCN0000126328	CCGGTGGAAACACTAGTTTCCAAATCTCGAGATTTGGAAACTAGTGTTTCCATTTTTG

Table S2. List of Primers and Taqman Probes.

Names and sequences of primers for gene expression

Gene name	Sequence (Forward)	Sequence (Reverse)
Gapdh	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA
Myh6	GCAGAACAGTAAAATTGAGGACG	CGCAGCTTCTCCACCTTAG
Tnnt2	CAGAGGAGGCCAACGTAGAAG	CTCCATCGGGGATCTTGGGT
Actc1	CTGGATTCTGGCGATGGTGTA	CGGACAATTTCACGTTCAGCA
Actn2	TGGCACCCAGATCGAGAAC	GTGGAACCGCATTTTTCCCC
Col1a1	GCTCCTCTTAGGGGCCACT	CCACGTCTCACCATTGGGG
Sf3a1	AAGAAGAAGCATCGTCAAAGGAG	GCATGGTAAGGGTCATTGGGA
Sf3b1	GTGGGCCTTGATTCCACAGG	GGCTTCTTCTGACCGAGCAA
Yy1	TCAGACCCTAAGCAACTGGC	GTGCAGCCTTTATGAGGGCAA
Smarca5	GACACCGAGATGGAGGAAGTA	CGAACAGCTCTGTCTGCTTTA
Mll2	TAAAACCGCCTATGGAGGACC	GGCGCATCAATGGGGATCT
Mll5	TTCAGACCTCCTGTAGAGAGC	AAAAGTCCTCGCATCAACACA
Tet1	ACACAGTGGTGCTAATGCAG	AGCATGAACGGGAGAATCGG
Ctcf	TTTGGATCGTCACATGAAAAGCC	ACAAAGGCCATATCGCAGTCT
Mll1	ATGAGCAGTTCTTAGGTTTTGGC	CTCCCGCGAGGTTTTCGAG
Kdm5d	TTCGGTCCCACTACGAACG	TTCCTCGTCTACTGTAGCAACT
Phf12	GGGGCTGATGGAGCAAATCC	CCACCTTCCTTGCAGCTATCG
Sin3b	GTGGAGGACGCTCTCACCTA	CGATGCTCTGGCTTTTGAACT
Bcorl1	CGCATGTGTGGCATCAACG	TCCCAACATAGTCCATTTTTGGC
Ruvbl2	GCCACCACCAAAGTCCCTG	CCCTTCTCGGATCATCTCCAG
Tet3	TGCGATTGTGTCGAACAAATAGT	TCCATACCGATCCTCCATGAG
Rad21	GCCCATGTATTTGAGTGCAACT	ATAGATGCGGACTACTCCCAG
Sf1	GAGAGTTCCGTACCCGCAAAA	CTCTGGGTCCAATTAGGAGCC
Trrap	CAACGCCCAGATCGGACTG	GAGGCTTTTGTAACAGGGCAG
U2af1	TCGGAGCATGTCGTCATGG	GGAAGAGTTTTGAGGGTTACGG
Kdm5c	GAGGCCCAGACAAGAGTGAAA	TTGGGAATCTTTAAGGATGAGCC
Phf23	CACATCATTGACGCATACTTCCC	TTTCGGTCCTTCTTTCGAGGC
Phf23	CACATCATTGACGCATACTTCCC	TTTCGGTCCTTCTTTCGAGGC
Stag2	CTACAAGCATGACCGGGACAT	GCCGTACTAACACACCAATGAAC
Ruvbl1	AGCTGGGCAGTAAAGTCCCT	CCTCCCCTTCATAAACCTCCT
Bcor	CTTTCTGCAACCCCTCTGTATG	AAGCGTCGCCATCATTCACA

Applied Biosystems Taqman probes

Gene	**Vendor**	**Product**
Gapdh	applied biosystems	Mm99999915_g1
Scn5a	applied biosystems	Mm01342518_m1
Kcnj2	applied biosystems	Mm00434616_m1
Cacna1c	applied biosystems	Mm00437917_m1
Col1a2	applied biosystems	Mm00483888_m1
Col3a1	applied biosystems	Mm01254476_m1
Postn	applied biosystems	Mm00450111_m1