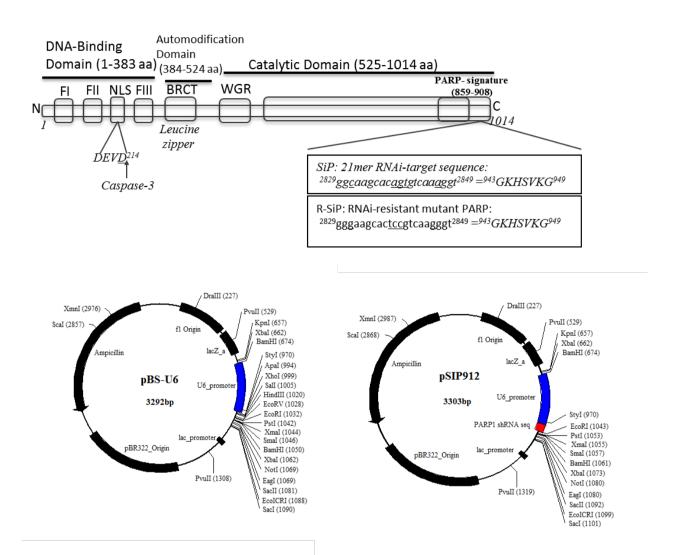
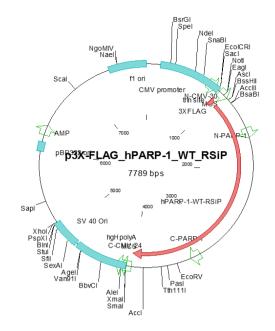
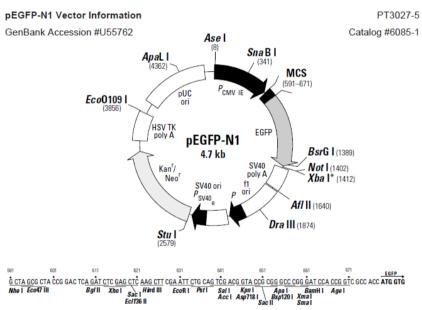


Appendix I



Appendix 1: The figure represents general structure of PARP-1 gene and site from which the shRNA sequence was cloned. Maps of pBS/U6 plasmid where PARP-1 targeted shRNA sequences 5'-GGGCAAGCACAGTGTCAAAGG-3' was introduced under the control of U6 promoter to create SiP912 shRNA against PARP-1 gene. The forward double-stranded oligo pair was cloned in pBS-U6 at ApaI (blunt)—HindIII sites, followed by cloning of the reverse oligo pair at HindIII—EcoRI sites. This DNA would direct cellular RNA polymerase III to create an RNA that would form a short hairpin (shRNA) with the two underlined complementary sequences forming double-stranded stem and intervening AAGCTT sequence (HindIII site) forming the loop of the hairpin (Rashmi G Shah et al., 2005).





Appendix 1: The figure represents general structure of PARP-1 recovery vector R-Sip:RNAi resistant mutant PARP-1 vector, as explained above. The other vector is pEGFP-N1 used for cotransfecting along with pBSU6 and pSIP912 for its selection and reporter.

Appendix II

	1	2	3	4	5	6	7	8	9	10	11	12
Α	185	HPRT1	GUSB	HNF1 B	185	HPRT 1	GUS B	HNF1 B	185	HPRT 1	GUS B	HNF1 B
В	FOXA2	REG3A	PDX1	NEU ROG 3	FOXA 2	REG3 A	PDX1	NEU ROG 3	FOXA 2	REG3 A	PDX1	NEUR OG3
С	NEURO D1	MAFA	MAFB	PAX4	NEU ROD 1	MAF A	MAF B	PAX4	NEU ROD 1	MAF A	MAF B	PAX4
D	NKX2-2	ISL1	PAX6	MMP 2	NKX2 -2	ISL1	PAX6	MMP 2	NKX2 -2	ISL1	PAX6	MMP 2
Е	MMP9	INS	INSR	GCG	MMP 9	INS	INSR	GCG	MMP 9	INS	INSR	GCG
F	ACVR1	ACVR1 B	ACVR2 A	ACVR 2B	ACVR 1	ACVR 1B	ACVR 2A	ACVR 2B	ACVR 1	ACVR 1B	ACVR 2A	ACVR 2B
G	TGFB1	TGFBR 1	PROM 1	NES	TGFB 1	TGFB R1	PRO M1	NES	TGFB 1	TGFB R1	PRO M1	NES
Н	SOX17	GATA6	PARP1	PARP 2	SOX1 7	GAT A6	PARP 1	PARP 2	SOX1 7	GAT A6	PARP 1	PARP 2

Taqman Low density Array 96 well fast plate format for transcriptome analysis during islet differentiation (specific to human)

	1	2	3	4	5	6	7	8	9	10	11	12
А	Hs999	Hs999	Hs999	Hs010	Hs999	Hs999	Hs999	Hs010	Hs999	Hs999	Hs999	Hs010
	99901	99909	99908	01602	99901	99909	99908	01602	99901	99909	99908	01602
	_s1	_m1	_m1	_m1	_s1	_m1	_m1	_m1	_s1	_m1	_m1	_m1
В	Hs002 32764 _m1	Hs001 70171 _m1	Hs002 36830 _m1	Hs018 75204 _s1	Hs002 32764 _m1		Hs002 36830 _m1	Hs018 75204 _s1	Hs002 32764 _m1	Hs001 70171 _m1	Hs002 36830 _m1	Hs018 75204 _s1
С	Hs001	Hs016	Hs005	Hs001	Hs001	Hs016	Hs005	Hs001	Hs001	Hs016	Hs005	Hs001
	59598	51425	34343	73014	59598	51425	34343	73014	59598	51425	34343	73014
	_m1	_s1	_s1	_m1	_m1	_s1	_s1	_m1	_m1	_s1	_s1	_m1
D	Hs001	Hs001	Hs002	Hs015	Hs001	Hs001	Hs002	Hs015	Hs001	Hs001	Hs002	Hs015
	59616	58126	40871	48727	59616	58126	40871	48727	59616	58126	40871	48727
	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1
E	Hs002	Hs003	Hs009	Hs001	Hs002	Hs003	Hs009	Hs001	Hs002	Hs003	Hs009	Hs001
	34579	55773	61557	74967	34579	55773	61557	74967	34579	55773	61557	74967
	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1
F	Hs001	Hs009	Hs001	Hs006	Hs001	Hs009	Hs001	Hs006	Hs001	Hs009	Hs001	Hs006
	53836	23299	55658	09603	53836	23299	55658	09603	53836	23299	55658	09603
	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1	_m1
G	Hs999	Hs006	Hs010	Hs007	Hs999	Hs006	Hs010	Hs007	Hs999	Hs006	Hs010	Hs007
	99918	10319	09250	07120	99918	10319	09250	07120	99918	10319	09250	07120
	_m1	_m1	_m1	_s1	_m1	_m1	_m1	_s1	_m1	_m1	_m1	_s1
н	Hs007	Hs002	Hs002	Hs001	Hs007	Hs002	Hs002	Hs001	Hs007	Hs002	Hs002	Hs001
	51752	32018	42302	93931	51752	32018	42302	93931	51752	32018	42302	93931
	_s1	_m1	_m1	_m1	_s1	_m1	_m1	_m1	_s1	_m1	_m1	_m1

TaqMan Array 96 - Well FAST Plate P/N: 4413259

Production Order: 2018621; Plate Name: Custom Config. 3X32; Sales Order: 0005087737 Assay IDs Gene Symbols

Appendix III

Identification of TATA box (promoter) Reg3a gene

>FP006991 Reg3a_1 :+U EU:NC; range -1000 to 100. tcttatggtcacatattcataaggattccaagagtcttctttcagaaatgattcaagctt caagaagactaaaacagggaatcataccacctggagatggttatgaattgcctgatttgt gtggtaggtaccaaagcagtacctgttaacccatgtctccagcctcctaag<mark>t</mark> tggctaaaaaaatgtaattctttaatgttaaatgggtcagtatcatcagcatgtgtcaat tacatatttgcatttgcatttggcagaat<mark>actctatttttctaa</mark>atggccttgcacttgg ${\tt tgattcgatggaataaataattgaagt} {\tt aaagacttgcctttaagca} {\tt catcttatcacagt}$ ctgtatggctgtg<mark>tg</mark> ttgaaactcagtggtcacaatatctaagactaa atgctgctcagttgttgttagtca<mark>caattttcatgcatttaaaaaatt</mark>gagaagacaa <mark>tcatct</mark>atag<mark>gaaatatggtcatatattccaaag</mark>aaataatgcct qtqaaqqaqaaaatatttaaatqttq <mark>attttactatc</mark>aacattgcagaatttcaaacg atcactggcacctgaacacagaacatgtttgctaataggaaatagccccaatgtgtgtta gtttctgtctttgccaggaagtgtcctgcaagttttgctgggaagttttctgaatgtatg ccaagcactagctatc<mark>acccagacttaaataag</mark>cattcacttaatcactttgatgccctt ccttcaaatcctatcataaaqcaqtcacctttqtcctqacAAACCATCTCAGATCTCTAC AAGAGAGGTAAGTGGGAGCTGAATGATGGTGAGAGCCTTGTGTCTCTTACTATAGAGCGA AGATACAGAAGAATCTCTGT

TATA-box	found	at:	[-707	 -691]
TATA-box	found	at:	[-674	 -658]
TATA-box	found	at:	[-515	 -494]
TATA-box	found	at:	[-490	 -474]
TATA-box	found	at:	[-441	 -425]
TATA-box	found	at:	[-369	 -346]
TATA-box	found	at:	[-330	 -314]
TATA-box	found	at:	[-311	 -290]
TATA-box	found	at:	[-265	 -249]
TATA-box	found	at:	[-83	 -67]

Primer pair	Sequence (5'->3')	Templa te strand	Lengt h	Tm	GC%	Self complementa rity	Self 3' complementa rity
Forward primer	CTGCAAGTTTTGCT GGGAAGT	Plus	21	59.5 9	47.6 2	5.00	1.00
Reverse primer	AGACACAAGGCTCT CACCATC	Minus	21	59.7 2	52.3 8	3.00	0.00
Product length	200 for -67 to -83 tat	a box					

Identification of TATA box (promoter) Pdx-1 gene

actaaagacgccaggatggtcacagatctgaaaacccggtgccaaccccttgcccaactg $\verb|ctcaaccacaaaggcaacacttctctgtgccttccgcacatttgggagtgttctgagt|$ taatcaaataagttccaatccccaaaattaaatctaataacttcaacttaagaaaaaaca taagccactgtgattccccccccccagacctaacagtcagaaggctagaagtataggga acgcagatac<mark>agataaaaataaaacg</mark>aaataaagggatagtt</mark>tgagcaataaaacaaaa acgacagettcaggettacagegetgagttctgcaagcatttctcaaaaactgtatttt tacaaaaatacaagaaaattaaaagttagacgctgtgccttacacctgcaaccccagaac gc<mark>tacaaaattagacct</mark>ccac<mark>ccctgtcttaaaaca</mark>aaaccaaaacaaacaaaaaaaca ${\tt tagcgagggggaagaggaga} {\tt tgtagacttttttttaagctc} {\tt att} {\tt gggagcggttttgta}$ aaqaqtaaaqqttctqqtatttttqtqcqccccqtttttqqaqaqctccacaqcaqcaaqc agggatcaggcgactgagagagaaaattgaaacaagtgcaggtgttcgcgggcacctaag cctccttcttaaggcagtcctccaggccaatgatggctccagggtaaaccacgtggggtg ccccagagcctatggcacggcggccggcttgtccccagccAGCCTCTGGTTCCCCAGGAG AGCAGTGGAGAACTGTCAAAGCGATCTGGGGTGGCGTAGAGAGTCCGCGAGCCACCCAGC

GCCTAAGGCCTGGCTTGTAGC

TATA-box	found	at:	[-630	 -598]
TATA-box	found	at:	[-481	 -463]
TATA-box	found	at:	[-461	 -445]
TATA-box	found	at:	[-339	 -323]
TATA-box	found	at:	[-319	 -303]
TATA-box	${\tt found}$	at:	[-255	 -239]
TATA-box	${\tt found}$	at:	[-234	 -218]
TATA-box	found	at:	[-207	 -191]

Primer pair	Sequence (5'->3')	Template strand	Length	Tm	GC%	Self complem entarity	Self 3' complem entarity
Forward primer	AGCTCATTG GGAGCGGTT T	Plus	19	59.62	52.63	4.00	0.00
Reverse primer	GTGGAGCTC TCCAAAACG GG	Minus	20	60.96	60.00	8.00	0.00
Product length	73 (tata box -	207191)					

Identification of TATA box (promoter) Neurog3 gene

AAAGGGGCAGAAAGTAGATCTGCTTTTCTCCCAGGGCCTGCACACGGAGGCATTGAAAA GACAAAAAAGGCTAGCAGAGAACAAGTCCCTCCTTGACCTTTCCCTATCACCTGCCTCTC GGGTCAGGCCTTCCCGATAGCATCCATAGTGGGGCGGGGCGTGATGAGATGCCCCCTCTG CACTCTCTACAACCACCCTCGCCTCCGGAATAGAACCCAATGTCTCGGATGAGGACTA TGGTGGGGGTTTTCAAGGTCTGGTCTGGGGGCTGGAGGGTTGGATCCCAAGGTGATATTG AACCTGGCCAAGCAATAGTTTCTGAGTAGAAAGGACTTGAGCAGGGACCGTCTCTGGTCA GACCCAACCCATAGTGGCGGAGAGCTGGATAGCACTTTGAACTAATGGGCGCTCCTCCCA GCTGCCAGCCAAGAAGACACTTGACTCCTTGATCGCTGGTTCATTTAGACAAGCCGTTTC CCTCTCTGAGCCAAAAGACCCCATGTGTAATACTCAAAGA<mark>AGAGGCCTTCCTTATATAT</mark> TATAGGCACCCCAAAACCTCCTTCATGCTACCAAGAAAGGGTCTGGACACATGCCAAAAA GCTCTTTGAGGAACCGAGAGTTGCTGGGACTGAGCCCGCGACGGGGGAGGCGTGGAGTGG GGGAACAAACAGAGTGCTGCTCCCCTCCCCGACCCCTGCCCTTTGTCCGGAATCCAGCT GTGCTCTGCGGGTGGGGGTTGTGGGGGGGAGGAGCGCGCTCGCGTGGCGCAGCCCCTGGGC TGGGTCTCATCACTGCAGCAGTGGTCGAGTACCTCCTGGAGCTTTTCTACGACTTCCAG ACGCAATTTACTCCAGGCGAGGGCGCCTGCAGTTTAGCAGAACTTCAGAGGGAGCAGAGA

ACCTGCTGCTCTATTCTTTTGAGTCGGGAGAACTAGGTAACAATTCGGAAACTCCAAA

TATA-box found at: [-485 .. -469] TATA-box found at: [-418 .. -387] TATA-box found at: [55 .. 71]

Primer pair	Sequence (5'->3')	Template strand	Length	Tm	GC%	Self complem entarity	Self 3' complem entarity
Forward primer	AGCAGAT AAAGCGT GCCAGG	Plus	20	60.75	55.00	3.00	3.00
Reverse primer	CTCGCCT GGAGTA AATTGCG	Minus	20	59.35	55.00	4.00	2.00
Product length	136 tata 5	5 to 71					

Identification of TATA box (promoter) NeuroD gene

tgaggtcattcattactccaggagcatctgaaaaccaacggagccaaggtctgctggcaa aaactagctttagacacaaaattctagggtttagagttgaagactcttagtgaagtctct ggggtaggagcaggtgaccgttaggtttacatttggagtgttcaagtgtagggtatggaa $\verb|gctgacttgcaaaggattctagaagatgctctagtcaggaaggttgagtcaaggctgtgt|\\$ ttccaga<mark>tgaggtcgtttttatatgaaat</mark>aaatgtttgcctagagaggtgatggagatta gaagccagccaccctttggtggcaataagcaaagcctctgctaagaggtagaagctaaga gatgggcctctccagagagaacaaagtcaaactgcaccaccggagaccattgtcaaggga aggacccttcagtgcacctcagtatctgggattgtgagtggttcacctctgtctacctct qctcqcctcccqcaaccccccccccccacatqtcctctqtcttctqctqccacaaaqq gttaatctctcctgcgggtaaaaacaggtccgcggagtctctaactggcgacagatgggc cactttcttctgg<mark>ccacaaaggggccgga</mark>atggagcgctc<mark>cgcggcatacaaataggca</mark>g gtcacqtqqttcccqgctcttggctggaccgggaagaccatatggcgcatgccggggagg gaaagttctggggaggggtgaatgagggcgggagtcgttcagtctggacgcgtgcgcgat caactcggctatataaccctagcgcccgcgccaccgggacACGAGGAATTCGCCCACGCA GAAGGCAAGGTGTCCCGAGGCTCCAGGGTTATGAGATCGTCACTATTCAGAACCTTTTAA CAACAGGTAATTATGATTCCT

TATA-box found at: [-751 .. -733]
TATA-box found at: [-327 .. -311]
TATA-box found at: [-301 .. -278]
TATA-box found at: [-39 .. -16]

Primer pair	Sequenc e (5'->3')	Templat e strand	Length	Tm	GC%	Self comple mentarit y	Self 3' comple mentarit Y
Forward primer	CGCTCA GCATCA GCAACT C	Plus	19	59.29	57.89	5.00	0.00
Reverse primer	GTGGGC GAATTCC TCGTGTC	Minus	20	61.36	60.00	6.00	1.00
Product length	70 FOR TA	TA BOX -16	39				

Identification of TATA box (promoter) Pax4 gene

agatatacaatggacccacaaggctttccacatctactccttcacacccttacaagcatc tattgaacctcgtctgcaatagcaacaaggtttccaaccactgtggtccacgctcacttc cagcaccctaccctacccagacactggttttctcacccttgcaatggcccagacaatctg aggtgtcttttgttcaaacaacagtatcagtttttaatctaaatgtaccaaatcccaagt ccttaga<mark>aacatgcatttctagt</mark>catcctcagacacgaattcccacccactcctcccacg gttggtgtcctgaagttcaggatagccctatttccaggcaagaactcacctcgtgtcatt tcagtcaaggaatcaacaggaggatagatgggaatcctctctggagacaactgatttatg tgacactcttctccatccattctccttctcttgaggttctagaagccaactcagtctgta ctcaatttqqctacatatcatttatcttttqtaataatacacacatqatctqqqqqttqa cttaaaagctcagatgtgtgcatgatggctgggaaacgatatcagtactcctggaatatt cttttgtgttttgatgcatgggaaactttggatacatagtctgaagtgcctcatcttcca tgttcctcattccttccaagaacactggcccatgcttgagtacattctggattgagagag cctqtctqaatqcctctatacttccttcaqqqtaqaqccacaaqqtqqactctqaaqccc cgcagaaggacacagccggtcactggctgtgggttaccctgcctcagggccagtgtcagc cctcctctgctcatggcctgtgacatcactggctactcccAGAAGGCTGCCCTCTGCTCC TGAGTGAAGGCTCTGTGAAGCTCTGGACCCCCTGGCAGGACTGAAGCAGCTGGAGGCTGT TACAAGACCAGACCACCAGCA

TATA-box found at: [-693 .. -677]
TATA-box found at: [-534 .. -518]
TATA-box found at: [-401 .. -385]

Primer pair	Sequence (5'->3')	Template strand	Length	Tm	GC%	Self complem entarity	Self 3' complem entarity
Forward primer	CACACAT GATCTGG GGGTTG A	Plus	21	60.00	52.38	5.00	1.00
Reverse primer	AGTACTG ATATCGT TTCCCAG CC	Minus	23	59.93	47.83	6.00	1.00
Product length	70 tata bo	x -401385	5				

Identification of TATA box (promoter) Nkx6.1 gene

agagcaggagacggaaagatggtgaagggtgacccttaggcctgcgaggggtttaaaaac atctacqqqcttaaqqaacaacaaatcaatttacacqattctqqaaqaqcccaqaqqq tagetecettttegeaagggteeagacacegttggaggtgggegeegegegegeggg ggaggatgacgcgagctggcgtgggcggaa<mark>gagccgcacttaaact</mark>gctttt<mark>cca</mark> <mark>gggetgga</mark>ttttcattattcctc<mark>tctttaaaaagtaatgo</mark>cctcttcgtccctgctccct aaccactcttttcgccaggcccctcccctcttggctccgcccaagtgaagctggggcggg gactaggag<mark>ggcgcgtccttatgg</mark>ctccctagtctcagccaatcaaaaggtgtggcgctc ccaggtgggcgtgttctaggagcgacgccttgcccaagctgagcgctattggaggcggtg acgtcctcgaaagttctcattttggcccccacctcccttgcgtccccagctaa agagaggcagggggggggcaaatattttattacctttgagagcttcatccgaactgtca ggcccagagggagagagagaagggaagagccgccgagagggtcagtttggccagagg acagggcttggaagagccaagcctggaaagccaaggagaaatgccagagaggcaagagaa cggcttgcagaagaggacggacgatcggaaccggccgtcAGACTTTTTCCATACTTAGG GTAGGCTCGTGGGCGCACCAA

TATA-box found at: [-885 .. -871]
TATA-box found at: [-730 .. -714]
TATA-box found at: [-708 .. -692]
TATA-box found at: [-683 .. -660]
TATA-box found at: [-633 .. -617]
TATA-box found at: [-511 .. -495]
TATA-box found at: [21 .. 37]

Primer pair	Sequence (5'->3')	Template strand	Length	Tm	GC%	Self complem entarity	Self 3' complem entarity			
Forward primer	AAGAGG ACGGAC GATCGG AA	Plus	20	60.68	55.00	6.00	1.00			
Reverse primer	CGGACTA GCCGGA TCGAAAA	Minus	20	59.90	55.00	6.00	0.00			
Product length	87 tata bo									