

Silencing the Genes Responsible for Prostate Cancer

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Abstract - Prostate cancer is one the most common cancer globally. The prostate is a small gland seen in the pelvis of men and hence prostate cancer is common in men. It develops very slowly and hence it is very difficult to see its signs for many years. If treated with chemotherapy, undesired side effects are seen. Hence a novel therapy is followed in this work, the RNA interference (RNAi). Main aim of this work is to silence the double stranded (ds) RNA sequence in prostate cancer gene receptors like ACPT,BRCA1,BRCA2,HOXB13, FGFFR4 and RNASEL using Gene silencing software siDIRECT.

Keywords: Prostate cancer, chemotherapy, gene silencing, RNA interference, geneboy

I. INTRODUCTION

Cancer is the second leading cause of death worldwide [1]. Prostate cancer exhibits tremendous differences in incidence among populations worldwide [1]. The ratio of countries with high and low rates of prostate cancer ranges from 60-fold to 100-fold [1]. Prostate cancer affects the prostate gland, the gland that produces some of the fluid in semen and plays a role in urine control Several genes and chromosomal in men [1]. regions have been found to be associated with prostate cancer in various linkage analyses, casecontrol studies, genome-wide association studies (GWAS), and ad mixture mapping studies [2]. Pathogenic variants in genes of high and moderate penetrance, such as BRCA1, BRCA2, RNASEL, ACPT, FGFR4 and HOXB13 confer modest to high lifetime risk of prostate cancer [3]. GWAS have identified more than 100 SNPs associated with the development of prostate cancer, but the clinical utility of these findings remains uncertain [4]. Several advancements are made towards treatment and control of cancer progression including chemotherapy but it is seen that undesired side effects occur during chemotherapy [5]. In recent years a novel therapy has emerged, the gene silencing therapy or RNA interference (RNAi) which is derived from nucleic acid-based molecules that is evolving from in-silico, in-vitro to clinical therapy. This involves double stranded (ds) RNAs mediate sequence-specific gene silencing. This technique finds application basic cancer research, is facilitating the identification and validation of potential therapeutic targets (the dsRNA) for

cancer, and this could be further developed into cancer therapeutics by selectively silencing the involved oncogenes [6, 7].

Genes involved in Prostate Cancer

ACPT (Acid Phosphatase, Testicular gene Protein Coding): Acid phosphatases are enzymes capable of hydrolysing ortho-phosphoric acid esters in an acid medium [8, 9]. This gene is up-regulated by androgens and is down-regulated by estrogens in the prostate cancer cell line [8]. This gene exhibits lower level of expression in testicular cancer tissues than in normal tissues [9]. The protein encoded by this gene has structural similarity to prostatic and lysosomal acid phosphatases [8, 9].

BRCA1 (Breast cancer type 1 susceptibility protein coding): This gene encodes a nuclear phosphoprotein that plays a role in maintaining genomic stability, and it also acts as a tumour suppressor. The encoded protein combines with other tumour suppressors, DNA damage sensors, and signal transducers to form a large multi-subunit protein complex known as the BRCA1-associated genome surveillance complex [10].

BRCA2: BRCA2 is considered a tumour suppressor gene, as tumours with BRCA2 mutations generally exhibit loss of heterozygosity (LOH) of the wild-type allele [10].

FGFR4 (Fibroblast Growth Factor Receptor 4 gene protein Coding): The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one

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another in their Ligand affinities and tissue distribution [11].

HOXB13 (Homeobox B13 (Gene Protein Coding): This gene encodes a transcription factor that belongs to the Homeobox gene family. Genes of this family are highly conserved among vertebrates and essential for vertebrate embryonic development [12].

RNASEL (Ribonuclease L gene protein coding): Mutations in this gene have been associated with predisposition to prostate cancer and this gene is a candidate for the hereditary prostate cancer 1 (HPC1) allele [13].

II. METHODOLOGY

In this work the following nucleotide sequences related to prostate cancer are used (Table 1).

Table 1: Genes with their NCBI Accession number.

Gene name	NCBI	Accession
	number	
ACPT	NM_033068	
BRCA1	BC106745	
BRCA2	KJ625203	
FGFR4	EU826603	
HOXB13	BC070233	
RNASEL	BC090934	

siDirect 2.0: The siDirect 2.0 is novel web server which is used for providing efficient and target-specific siRNA design for mammalian RNAi and this web server has been extensively updated to eliminate off-target silencing effects and its design algorithm is based on such mechanistic features which is combined with the reliable algorithms [14].

III. RESULTS AND DISCUSSION

The DNA sequence of the corresponding gene receptors in Table 1 was taken. Using GENEBOY software the DNA sequence was converted to its corresponding RNA sequence. Using software siDIRECT 2.2 the RNA sequence was silenced by microRNA [15].

Using siDIRECT the RNA sequence of the gene receptors in table 1 was silenced (Table 2).

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 Table 2: Effective siRNA candidates of ACPT

 a
 ACPT

	a. ACP	1						
target	target sequence	RNA oligo sequences 21nt guide	function al siRNA		seed-duplex stabilty (Tm);			
positi on	21nt target + 2nt overhang	$(5' \rightarrow 3')$ 21nt passenger $(5' \rightarrow 3')$	selectio n: <mark>U</mark> i-Tei		guide	passenger		
836- 858	CCCTCAA GATGGTC ATGTACTC A	AGUACAU GACCAUC UUGAGGG CUCAAGA UGGUCAU GUACUCA	U	0	20.4 °C	20.4 °C		
1001- 1023	CCCTCTTC TACCGCA ATGACTCC	AGUCAUU GCGGUAG AAGAGGG CUCUUCU ACCGCAA UGACUCC	U		20.5 °C	20.2 °C		

ATGGCCGGCCTGGGG	20	CACCCTGCTG	GACCTCTCCT	астастаста	50 ICTGCTGGTGG		SOGCCETOCC	90 AGAAGGACCC	CTOGTOT	1-100
TCOTGOCTCTOGTAT	120	130	CCCGCTGGCC	TCCTACCCCA	TOGACCCACA	170 CAAGGAGGT	180	190	DAGOCCT	101-200
210 BEGCCAGCTGACCAC	220 GGAGGGGGT	CCGCCAGCAG	240 CTGGAGCTGG	CCCCCTTCCT	GAGGAGCCG	270 TACGAGGCC	280	290	300 GC G G G A G	201-300
310 BAGGTGTACATCCGC	320 AGCACOGAC	330	340 COCTOGAGAG	350 T GCCCA GGCC	AACCTTOCCO	370	380 CGAGGCTGC	390 CCAGGGAGC	400 CCCGAGG	301-400
410 CCCGCTGGAGGCCGA		430					460	490	SOO TGCTGCG	401-500
S10 SAGGCCACCGAGGC	520 CGCCGAGTA	S20 CCAGGAGGCC	540 CTOGAGOGCT	GGACGGGCTT	CCTGAGTCGO	570 CTGGAGAAC	550	390	500 TOGADAD	501-600
610 CCACTOCOCAGOGCA	620	CTEGACACCO	TCATOTOCCA	GCAAGCCCAC	BOTETTCCAC	670	SBC	690	COGACTC	601-700
710	720 CTTTGDATA	730 TTGGAGCCCA	740 COTGOGCCCA	CCCCGGGCAG	750 ICAGAGAAGOO	770 CCAGCTGAC	780	790	CTATCCT	701-800
IGCAAACTTCTCCCG	SGGTCCAGCG	\$30 ECCTEGEGETE	CCCCTCAAGA	TGGTCATGTA	CTCAGCTCAT	870 FGACAGCACC	ET GCT GGCCC	890 FCCAGGGGGC	100 CCTGGGC	801-900
910 TCTATGATGGACAC	920 ACCCCGCCA		940 GCCTCGGCTT	950 TGAGTTCCGG	MO	970 BEGAATCCCO	950 CAAAGATGG	990	ACCOTOT	
1010 CCTCTTCTACCGCA		1030 ICCCACCTGCC	CCTGCCTCTC					1090 TTCTACCAGC		
1110	1120 CGCCCATGG				1160 CATCCCCCC		1180 ST GCCCCT GC			
1210 STGCTGGTGGCACTC	1220 AGCTTGGGG				1240 CTGCGGGCCT		1280 COTOTOAGCI		1300 GGCTTCC	
CTACCCCCAGCTGAC				TGC 1301-134	7					

b. BRCA1.

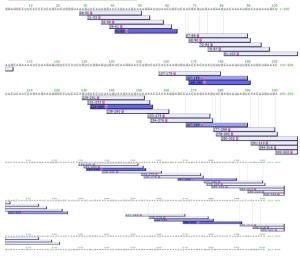
target	target sequence	RNA oligo sequences 21nt guide	fun cti ona 1 siR NA	seed-duplex stabilty (Tm);			
position	21nt target + 2nt overhang	(5'→3') 21nt passenger (5'→3')	sel ecti on: Ui- Tei	guide	passeng er		
28-50	AAGUUCA UUGGAAC AGAAAGA AA	UCUUUCUGU UCCAAUGAA CUU GUUCAUUGG AACAGAAAG AAA	U	16.6 °C	13.8 °C		
31-53	UUCAUUG GAACAGA AAGAAAU GG	AUUUCUUUC UGUUCCAAU GAA CAUUGGAAC AGAAAGAAA UGG	U	5.5 °C	20.1 °C		
36-58	UGGAACA GAAAGAA AUGGAUU UA	AAUCCAUUU CUUUCUGUU CCA GAACAGAAA GAAAUGGAU UUA	U	20.1 °C	19.2 °C		



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39-61	AACAGAA AGAAAUG GAUUUAU CU	AUAAAUCCA UUUCUUUCU GUU CAGAAAGAA AUGGAUUUA UCU	U	15.5 °C	19.1 °C
41-63	CAGAAAG AAAUGGA UUUAUCU GC	AGAUAAAUC CAUUUCUUU CUG GAAAGAAAU GGAUUUAUC UGC	U	1.8 °C	5.5 °C
67-89	UCGCGUUG AAGAAGU ACAAAAU G	UUUUGUACU UCUUCAACG CGA GCGUUGAAG AAGUACAAA AUG	U	14.7 °C	21.1 °C
68-90	CGCGUUGA AGAAGUA CAAAAUG U	AUUUUGUAC UUCUUCAAC GCG CGUUGAAGA AGUACAAAA UGU	U	7.2 °C	19.2 °C
72-94	UUGAAGA AGUACAA AAUGUCA UU	UGACAUUUU GUACUUCUU CAA GAAGAAGUA CAAAAUGUC AUU	U	14.8 °C	17.7 °C
75-97	AAGAAGU ACAAAAU GUCAUUA AU	UAAUGACAU UUUGUACUU CUU GAAGUACAA AAUGUCAUU AAU	U	20.5 °C	19.0 °C
81-103	UACAAAA UGUCAUU AAUGCUA UG	UAGCAUUAA UGACAUUUU GUA CAAAAUGUC AUUAAUGCU AUG	U	19.7 °C	5.3 °C
157-179	CACAAAGU GUGACCAC AUAUUUU	AAUAUGUGG UCACACUUU GUG CAAAGUGUG ACCACAUAU UUU	U	13.3 °C	17.8 °C
167-189	GACCACAU AUUUUGC AAAUUUU G	AAAUUUGCA AAAUAUGUG GUC CCACAUAUU UUGCAAAUU UUG	U	14.0 °C	13.3 °C
168-190	ACCACAUA UUUUGCA AAUUUUG C	AAAAUUUGC AAAAUAUGU GGU CACAUAUUU UGCAAAUUU UGC	U	-3.3 °C	6.7 °C
229-251	GUGUCCUU UAUGUAA GAAUGAU A	UCAUUCUUA CAUAAAGGA CAC GUCCUUUAU GUAAGAAUG AUA	U	12.0 °C	19.9 °C

231-253		UAUCAUUCU UACAUAAAG GAC CCUUUAUGU AAGAAUGAU AUA	U	16.2 °C	3.5 °C
232-254	GUAAGAA	AUAUCAUUC UUACAUAAA GGA CUUUAUGUA AGAAUGAUA UAA	U	8.7 °C	6.9 °C



c. BRCA2

starget	target sequence	RNA oligo sequences	func tion al siR NA	seed-duplex stabilty (Tm);			
position	21nt target + 2 overhang	21nt guide $(5' \rightarrow 3')$ 21nt passenger $(5' \rightarrow 3')$	sele ctio n: Ui- Tei		guide	passenger	
10-32	UAGUGAAGA UUCUAGUAG UUAAU	UAACUACUAG AAUCUUCAC UA GUGAAGAUU CUAGUAGUU AAU	U		17.6 °C	20.4 °C	
12-34	GUGAAGAUU CUAGUAGUU AAUGA	AUUAACUACUAGA AUCUUCAC GAAGAUUCUAGUA GUUAAUGA	U		6.6 °C	14.8 °C	
15-37	AAGAUUCUA GUAGUUAAU GAAAA	UUCAUUAACUACU AGAAUCUU GAUUCUAGUAGUU AAUGAAAA	U		8.9 °C	11.6 °C	
19-41	UUCUAGUAG UUAAUGAAA AUUUU	AAUUUUCAUUAAC UACUAGAA CUAGUAGUUAAUG AAAAUUUU	U		7.4 °C	18.8 °C	
22-44	UAGUAGUUA AUGAAAAUU	AAAAAUUUUUCAUU AACUACUA	U		-12.0 °C	6.6 °C	

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21nt guide

 $(5' \rightarrow 3')$ 21nt passenger

 $(5' \rightarrow 3')$ AAAUAUG

AGGCUAA

selection

Ui-Tei

guide

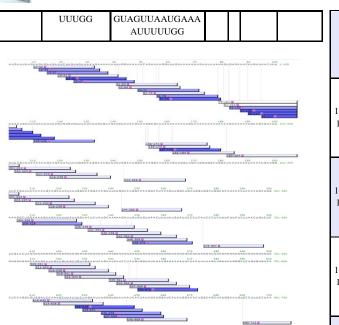
passenger

n

21nt target +

2nt overhang

AUGAUCG



d. FGFR4

target position	target sequence 21nt target + 2nt overhang	RNA oligo sequences 21nt guide $(5' \rightarrow 3')$ 21nt	functional siRNA selection:	s	seed-dup stabilty (T	
		passenger $(5' \rightarrow 3')$	<mark>U</mark> i-Tei		guide	pass enge r
329-351	UGCAGAAUC UCACCUUGA UUACA	UAAUCAA GGUGAGA UUCUGCA CAGAAUC UCACCUU GAUUACA	U		12.0 °C	19.1 °C
331-353	CAGAAUCUC ACCUUGAUU ACAGG	UGUAAUC AAGGUGA GAUUCUG GAAUCUC ACCUUGA UUACAGG	U		16.1 °C	20.4 °C

uacaocuacuacu	aacccuquue	aasauccuad	40 UOA 0U 0U 0C	SUGGOCCUCC	-aucuusucci	70 0000400CCUC		MANDENUQAQ	CCCUOCC 1-1	00
110 DEGCUCCCAGCCUG	GAGCAGCAAS	AGCAGGAGCU	GACAGUAGC	150 COUNSECAS	cueueceuci	170 Jougeugugaga	160 SCGGGCUGAGO	sussussee	ACUGGUA 101	-300
ZAAGGAGGGCAGUC	accusscace	uacuaaccau	240 QUACODOOC	250	SCCUAGAGAU	270	UACCUGAGOA	uacusacca	CUACCUC 201	1-300
310 VOCCUOBCACGAGG	CUCCAUGAUC	329-351		and the second se	J60 UBACUCCUUBA	370 ACCUCCABCAA	360 360	250 IGACCCCAAGI	400 JCCCAUA 301	1-400
410 GGACCCCUCGAAU	AGGCACAGUU	ACCCCCAGCA	AGCACCOUA	CUQGACACACI	CCCCAGCGCAI	470 JGGAGAAGAAA	CUSCAUGCAG	WACCUSCOOI	500	1-500
SUCAAGUUCCGCU	SUCCASCUSC		ACOCCCACC	SSO SSO	SEO	570 CAGGCCUUUC	100 AUGGGGAGAA	CCGCAUUGG	400CAUU 301	-400
COCUDCOCCAUCA	CACUERA DU	630 CUCQUGAUGO	640	UGCCCUCOGAI	COCOCACAI	670	680		ADCAUCE SOL	1.700
TIO TIO	CUAGAUGUGO	130 UEGA GC GEUC	CCCBCACCO	SCCCAUCCUS	750	270	ACCACAGCCO	750	800 701	
SAGCUSCUGUSCA	AGGUGUACAG	CGAUGCCCAG	CCCCACAUC	CAGUGGCUGA		AUCAACOGCA	GCAGCUUCGO	AGCCGACGG		-908
BLO BLO	S20	DACAUCAAUA	SHD OCUCADADD	SSO SSO	BUACCUGCOG	970	980 CGAGGACOCA	990 GGCGAGUACI	1000 HOL	L+100
1010 COCAGOCAAUUCC	1030 AUCOSCUCU	1030 CCUACCAGUO	1040	1050 CACGGUGCUG	1060 CAQQUGAQCA	1070 ACCUGA46600	1060 CAOGAQAUGO	1090	1100 100	01-11
ISSCCAGCAGUGGG	1120 66CUBUGGCC	1130	1140 UCAGUCUCU	1150	1160	1170 UGGGGGGGCAG	IL60	1190	1200 110	51-13
UGACAGCCCUCU	SUGCCUCUCC	ACACOUGOCO	SUCCAUGUS	1250	1260		1200			01-13

1310 CCCACAUAUGUUGGGAGCUGGGAGGGGACUGAGUUAG 1301-

e. HOXB13

target positio	target sequence	RNA oligo sequences	functional siRNA	seed-duplex stabilty (Tm);
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1241-UUAGCCU CGAUCAU U 8.7 °C 16.5 °C CAUAUUU GAUCGUU 1263 AGCCUCA UC UAUUUUC UCUAGAU GCCUCAU AGAAAAU 1251-AUUUUCU AUGAGGC 13.0 8.7 °C U 1273 AUCUAGA CUCAUAU °C GC UUUCUAU CUAGAGC AUAAUUA UUCAUGA GCUCAAU 1299-AUUGAGC UCAUGAA -2.3 U 7.2 °C °C UAAUUAU CAUGAAU 1321 GA UGAGCUA AUUAUGA AUCAUAA AUGAAUU UUAGCUC 1302-GAGCUAA AAUUCAU 8.7 °C 12.0 °C U UUAUGAU 1324 GAAUUGA AA GCUAAUU AUGAUAA AAUUUAU UUGAGCU CAUAAUU 1307-AAUUAUG AGCUCAA U 1.8 °C 18.3 °C 1329 AUAAAUU GAGCUAA UG UUAUGAU AAAUUUG UUUUUUU CAGGGAA UUUUUUU 1346-AAAAAAA UUCCCUG -11.3 14.3 °C U 1368 AAAAAAA GGGAAAA °C AA AAAAAAA AAAAAAA UUUUUUU AGGGAAA UUUUUUU 1347-AAAAAAA UUUCCCU -11.3 0.7 °C U AAAAAAA GGAAAAA 1369 °C AAAAAAA AA AAAAAAA UUUUUUU GGGAAAA UUUUUUU 1348-AAAAAAA UUUUCCC -11.3 U -11.3 °C 1370 AAAAAAA GAAAAAA °C AA AAAAAAA ААААААА UUUUUUU AACCAAA UUUUUUU 1406-AAAAAAA UUUGGUU -11.3 -2.9 °C U 1428 AAAAAAA CCAAAAA °C АААААА AA AAAAAAA UUUUUUU UUUUUUU ACCAAAA 1407-AAAAAAA UUUUGGU -11.3 U -11.3 °C 1429 ААААААА CAAAAAA °C AA AAAAAAA AAAAAAA



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10 GCUUUGGAUUCCCC	20 31 CGGCCUGGGUGGGGA	40 50 AGCGAGCUGGGUGCCCCCUAGAU	60 UCCCCGCCCCGCAC	70 80 CUCAUGAGCCGACCCU	90 100 CGGCUCCAUGGAGCCC	1-100
110 GGCAAUUAUGCCAC	120 13 CUUGGAUGGAGCCAAC	140 150 GAUAUCGAAGGCUUGCUGGGAGC	160 GGGA GGGGGGGCGGA A	170 180 UCUGGUCGCCCACUCC	190 200 CCUCUGACCAGCCACC	101-20
210 CAGCGGCGCCUACG	220 231 CUGAUGCCUGCUGUCA	240 250 ACUAUGCCCCCUUGGAUCUGCCA		270 280 SCCAAAGCAAUGCCACC	290 300 CAUGCCCUGGGGUGCC	201-30
310 CCAGGGGACGUCCC	320 330 CAGCUCCCGUGCCUUA	340 350 UGGUUACUUUGGAGGCGGGUACU	360 ACUCCUGCCGAGUGU	370 380 ICCCGGAGCUCGCUGAA	390 400 ACCCUGUGCCCAGGCA	301-40
410 GCCACCCUGGCCGC	420 430 SUACCCCGCGGGAGACU	440 450 CCCACGGCCGGGGAAGAGUACCC		470 480 GUUUGCCUUCUAUCCG	490 500 GGAUAUCCGGGAACCU	401-50
510 ACCAGCCUAUGGCC	520 531 A GUUA CCUGGA CGUGU	540 550 CUGUGGUGCAGACUCUGGGUGCU	560 CCUGGAGAACCGCGA	570 580 CAUGACUCCCUGUUGC	590 600 CUGUGGACAGUUACCA	501-60
610 GUCUUGGGCUCUCG	620 631 CUGGUGGCUGGAACAC	640 650 CCAGAUGUGUUGCCAGGGAGAAC		670 680 CCUUUUGGAAGGCAGC	690 700 AUUUGCAGACUCCAGC	601-70
500CAGCACCCUCC	720 73	740 750 CGUCGCGGCCGCAAGAAACGCAU		770 780 SGCAGUUGCGGGAGCUG	790 800 GAGCGGGAGUAUGCGG	701-80
810 CUAACAAGUUCAUC	820 83	840 GCAAGAUCUCGGCAGCCACCAGC		870 880 AUUACCAUCUGGUUUC	890 900 AGAACCGCCGGGUCAA	801-90
910 AGAGAAGAAGGUUC	920 93 UCGCCAAGGUGAAGAA	540 950 CAGCGCUACCCCUUAAGAGAUCU		970 980 BAGGAGCGAAAGUGGGG	990 1000 SUGUCCUGGGGAGACC	901-10
1010 AGGAACCUGCCAAG	1020 103 CCCAGGCUGGGGGCCAA	1040 1050 GGACUCUGCUGAGAGGCCCCUAG		070 1080 CAGGCCACUGGCUGCU	1090 1100 GGACUGUUCCUCAGGA	1001-1
1110 GCGGCCUGGGUACC	1120 113 CAGUAUGUGCAGGGAG	1140 1150 ACGGAACCCCAUGUGACAGCCCA		170 1180 CAAAGAACCUGGCCCA	1190 1200 GUCAUAAUCAUUCAUC	1101-1
		ACUAGCUGCCAUGAUCGUUAGCC 1241-1263 U 1231	-1273 U			9-1321
1310 CAUGAAUUGAGCUA 2302-1324 U 2307-1329 U	1320 133 2004064044400060	1340 AAGGCGAUCCCUUUGCAGGGAAA 1344-1346-1346-1 1344-1346-1347	1260 1 11111111111111111111111111111111111		1390 1400	1301-1
1410 AAAAAAACCAAAAAA 2405-1425 U	1420 1430	AAAAAAA 1401-1437				
f.	RNAS	SEL				
		RNA oligo	functi onal ciPN	seed	-duplex	

target position	target sequence 21nt target + 2nt overhang	RNA oligo sequences 21nt guide $(5' \rightarrow 3')$ 21nt passenger	functi onal siRN A select ion:	seed-duplex stabilty (Tm);		
		(5′→3′)	<mark>U</mark> i- Tei		guide	passenger
96-118	GAGAACAU UGUUCCUUC UUCAUA	UGAAGAAGG AACAAUGUU CUC GAACAUUGU UCCUUCUUC AUA	D		19.1 °C	12.1 °C
132-154	GCCAGAGA AUCCCAAUU UACACU	UGUAAAUUG GGAUUCUCU GGC CAGAGAAUC CCAAUUUAC ACU	D		-0.3 °C	19.1 °C
149-171	UACACUCAA AGCUUCUU UGAUUA	AUCAAAGAA GCUUUGAGU GUA CACUCAAAG CUUCUUUGA UUA	U		20.4 °C	19.2 °C
177-199	UAGGAGAU AAAUUUGC AUUUUCU	AAAAUGCAA AUUUAUCUC CUA GGAGAUAAA UUUGCAUUU UCU	U		20.0 °C	16.0 °C
198-220	CUCAAGGA AAAGGCUA AAAGUGG	ACUUUUAGC CUUUUCCUU GAG CAAGGAAAA GGCUAAAAG UGG	U		1.3 °C	18.7 °C
314-336	GACAAUCAC UUGCUGAU UAAAGC	UUUAAUCAG CAAGUGAUU GUC CAAUCACUU GCUGAUUAA AGC	U		8.9 °C	19.2 °C

324-346	UGCUGAUU AAAGCUGU UCAAAAC	UUUGAACAG CUUUAAUCA GCA CUGAUUAAA GCUGUUCAA AAC	U	20.5 °C	8.9 °C
334-356	AGCUGUUC AAAACGAA GAUGUUG	ACAUCUUCG UUUUGAACA GCU CUGUUCAAA ACGAAGAUG UUG	U	20.4 °C	20.5 °C
426-448	CUCUGCAUA ACGCAGUAC AAAUG	UUUGUACUG CGUUAUGCA GAG CUGCAUAAC GCAGUACAA AUG	U	19.0 °C	21.1 °C
563-585	CUGAAACU UUUCCUUUC UAAAGG	UUUAGAAAG GAAAAGUUU CAG GAAACUUUU CCUUUCUAA AGG	U	7.1 °C	3.2 °C
593-615	GUCAAUGA GUGUGAUU UUUAUGG	AUAAAAAUC ACACUCAUU GAC CAAUGAGUG UGAUUUUUA UGG	U	-9.7 °C	19.2 °C
658-680	AGCCCUAAA AUUCCUUU AUAAGA	UUAUAAAGG AAUUUUAGG GCU CCCUAAAAU UCCUUUAUA AGA	U	-2.3 °C	11.0 °C
660-682	CCCUAAAAU UCCUUUAU AAGAGA	UCUUAUAAA GGAAUUUUA GGG CUAAAAUUC CUUUAUAAG AGA	U	-2.3 °C	-9.7 °C
692-714	GUGAAUUU GAGGCGAA AGACAAA	UGUCUUUCG CCUCAAAUU CAC GAAUUUGAG GCGAAAGAC AAA	U	21.5 °C	7.4 °C
935-957	GUCAAUGU GAGGGGAG AAAGAGG	UCUUUCUCC CCUCACAUU GAC CAAUGUGAG GGGAGAAAG AGG	U	19.1 °C	20.5 °C
1026- 1048	AGCACAUA GAGAUUAA UGACACA	UGUCAUUAA UCUCUAUGU GCU CACAUAGAG AUUAAUGAC ACA	U	16.1 °C	20.3 °C
1078- 1100	UGCUGUUG AACUCAAAC UGAAGA	UUCAGUUUG AGUUCAACA GCA CUGUUGAAC UCAAACUGA AGA	U	19.2 °C	20.5 °C

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Graphical view of effective siRNA candidates

start- end	Functional, off-target reduced siRNA (seed duplex Tm < 10 °C)
start- end	Functional, off-target reduced siRNA (seed duplex Tm < 15 °C)
start- end	Functional, off-target reduced siRNA (seed duplex Tm < 21.5 °C)
start- end	Functional siRNA

IV. CONCLUSION

The ds RNA sequence of the prostate cancer gene receptors viz. BRCA1, BRCA2, RNASEL, ACPT, FGFR4 and HOXB13 are silenced using siRNA technique.

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