CHARACTERIZATION AND CLONING OF THE HUMAN PERLECAN PROMOTER REGION

by

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A thesis submitted to the Faculty of the University of Delaware in partial fulfillment of the requirements for the degree of Honors Bachelor of Science in Biological Sciences with Distinction.

Spring 2009

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ACKNOWLEDGMENTS

I would like to thank Benjamin Rohe for teaching me for the past two years. Your patience helped me persevere and your knowledge motivated me to study the science behind the protocols. Thank you.

I would also like to thank Dr. Mary C. Farach-Carson. Your support and optimism inspired me to keep looking for answers. Thank you for inspiring me to continue working towards the solution.

Thank you to Dr. Daniel D. Carson, for continued support during the difficult search for answers

Thank you to Lynn Opdenaker for beginning my education in the laboratory

Mark Sausen: thank you for finding the key to the reaction.

Thank you to everyone in the Carson Lab who was helped me over the past two years

This research was supported by the P01 CA098912 grant to Dr. Mary C. Farach-Carson and in part by The Howard Hughes Medical Institute.

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Bp	base pair
BSA	bovine serum albumin
C4-2B	bone metastatic, androgen independent prostate cancer cell line
cDNA	complementary deoxyribonucleic acid
CREB	cAMP response element binding
DMEM	Dulbecco's Modified Eagle's Medium
DMSO	dimethyl sulfoxide
DNA	deoxyribonucleic acid
E. coli	*Escherichia coli*
ECM	extracellular matrix
EDTA	ethylenediaminetetraacetic acid
EMT	epithelial- mesenchymal transition
FBS	fetal bovine serum
FGF-2	fibroblast growth factor 2
HS	heparan sulfate
HSPG	heparan sulfate proteoglycan
HS27A	immortalized normal human bone marrow stromal cell line
IFN-γ	interferon gamma

NF-κB	nuclear factor kappa b
PCR	polymerase chain reaction
Pln	perlecan
QPCR	quantitative polymerase chain reaction
RE	restriction enzyme
RNA	ribonucleic acid
RT-PCR	real-time polymerase chain reaction
SHH	Sonic Hedgehog signal pathway
SMAD	similar to mothers against decapentaplegic
TAE	tris-acetate-EDTA
TGF-β	transforming growth factor beta
TNF-α	tumor necrosis factor alpha
UTR	untranslated region
WIDR	colon adenocarcinoma-derived cell line

ABSTRACT

Prostate cancer metastasizes preferentially to bone. The bone microenvironment presents the invading cells with a rich supply of growth and angiogenic factors. Because trabecular bone is in a state of resorption and deposition, the mineralized matrix is degraded and reformed constantly. This process also releases important growth factors, such as TGF-β, which may aid the survival of metastatic prostate cancer cells. Unpublished data from members of this lab group shows a large upregulation of a heparan sulfate proteoglycan, called perlecan, in the reactive stroma surrounding prostate epithelial cells. Perlecan is a structural protein located in the basement membranes and the matrix surrounding endothelial, mesenchymal and stromal cells. Among other properties, perlecan, through the heparan sulfate side chains, can bind growth factors. This property of perlecan identifies it as a protein that may help promote prostate cancer metastasis by providing the mobile cells with a scaffold to store growth and angiogenic factors in close proximity to their receptors. My project was concerned with the large upregulation of perlecan in the reactive stroma. I began my project by characterizing the promoter region for perlecan and identifying conserved transcription factor binding sites that could participate in transcriptionally regulating perlecan in prostate cancer. I identified several transcription factor binding sites of interest for further study, including NFκB [-2410 to -2398], CREB ([-1797 to -1777] and [-709 to -689]), Smad3 ([-1301 to -1293] and [-187 to -179]), Elk-1 [-1699 to -1679], c-Jun ([-2453 to -2441] and [-2496

to -2476]) and TCF/LEF-1 ([-1521 to -1505] and [-1247 to -1231]). I then attempted to clone the promoter region from genomic DNA using polymerase chain reaction, and encountered several issues. I attempted to alter the reaction conditions and to try different kits to correct the problems. I found that addition of dimethyl sulfoxide to the reaction increased the specificity of the reaction and allowed for the successful cloning of the perlecan promoter region into a plasmid vector. Following the cloning of the vector, I began testing the effects of two growth factors, TGF-β and TNF-α, on perlecan transcription. Following treatment for 24 hours, RNA was extracted from HS27a bone marrow stromal cells and used to conduct quantitative PCR in order to test the levels of perlecan transcript. Although the data have not yet been analyzed, the cell cultures showed growth changes, namely the formation of a cobblestone growth pattern, which indicated that the growth factors affected some cellular processes. Further research needs to be conducted in order to determine if this effect indicates a change in perlecan transcription in order to determine whether perlecan could be a viable target for new therapies.

Chapter 1

INTRODUCTION

1.1 Biology of Prostate Cancer

Excluding skin cancers, prostate cancer is the most commonly diagnosed cancer in men in the United States. The American Cancer Society estimates that about 186,320 new cases of prostate cancer will be diagnosed and that about 28,660 men will die from it in 2008. On a larger scale, the American Cancer Society estimates that about one man in thirty five in the United States will die from prostate cancer (American Cancer Society, 2009). It is the most commonly diagnosed non-skin cancer in the U.S. and is also one of the leading causes of cancer-related deaths in American men, second only to lung cancer. Overall, prostate cancer in the seventh leading cause of death in the United States (Porth and Kunert, 2002).

Prostate cancer is described clinically by using stages. There are four general stages that are the result of scores in two common staging systems. The first system is the Gleason score, which describes the organization of the cancerous tissue and how similar it appears to normal tissue (American Cancer Society 2009). The second system is based on clinical and surgical exams. It is called the TNM system and it serves as a descriptor of tumor size and the extent of close or distant metastasis to lymph nodes or other tissues (Porth and Kunert, 2002). The scores assigned in each system are then grouped into stages, with stage I representing a prostate-confined tumor in the early stages of development and stage IV representing a more aggressive,

less-differentiated tumor with metastasis to surrounding tissue or to distant sites in the body. The first three stages can be treated utilizing standard options, including a prostatectomy, radiation therapy, and hormone therapy. However, stage IV prostate cancer with metastases to surrounding or distant tissues is not considered curable and current treatments are limited to managing the symptoms (Buijs and van der Pluijm, 2009; Keller and Brown, 2004; Msaouel et al., 2008; Ye et al., 2007).

Initial treatments of prostate cancer tumors generally include androgen-deprivation. Prostate cancer cells are initially hormone-sensitive and respond to androgen withdrawal by initiation of apoptosis (Dorkin and Neal, 1997). Androgen-deprivation therapy may slow progression, but many tumors, especially at metastatic sites, will develop an androgen-independent phenotype following androgen-ablation therapy (Dorkin and Neal, 1997; Msaouel et al., 2008). The mechanisms of this switch to a hormone-refractory disease are not fully understood, but the difficulties associated with treatment underscore the importance of prostate cancer screens to identify the tumor earlier since early stage prostate cancer is generally asymptomatic. The manifestation of more obvious symptoms is generally indicative of cancer metastasis (Porth and Kunert, 2002). Additionally, many men diagnosed with cancer that seemingly localized to the prostate will relapse with metastases following a prostatectomy, suggesting that many metastases initially go undetected. These metastases will be susceptible to hormone therapy at first, but will eventually transform to incurable androgen-independent secondary tumors (Gopalkrishnan et al., 2001).

The struggle associated with stage IV prostate cancer is that prostate cancer cells preferentially metastasize to the axial skeleton and other bones. Various

studies have reported that up to 90% of patients dying from prostate carcinoma have skeletal metastases (Buijs and van der Pluijm, 2009; Bussard et al., 2008; Gopalkrishnan et al., 2001; Keller and Brown, 2004; Msaouel et al., 2008; Porth and Kunert, 2002). Despite of the high prevalence of skeletal metastases, the process of metastasis is very dangerous for the individual prostate cancer cells. After invading the stroma and escaping into the blood stream by intravasation, most cells will die. It has been estimated that fewer than 0.1% of cells will successfully metastasize following intravasation (Gopalkrishnan et al., 2001). Should the cell survive, it theoretically has access to most tissues in the body. However, prostate cancer cells show a clear preference for trabecular bone. The exact mechanism behind this preference is not clearly understood, but a commonly accepted hypothesis was proposed by Stephen Paget in 1889, known as the 'seed and soil' hypothesis (Bussard et al., 2008; Msaouel et al., 2008).

The seed and soil hypothesis states that the circulating prostate cancer cells, the seeds, will prefer a host tissue, the soil, with specific factors that aid in survival and growth. This hypothesis is generally combined with another hypothesis related to blood flow because vasculature of the prostate is connected to the network of veins that drains the pelvic girdle. This network, Baston's plexus, is directly connected to the marrow spaces of the lower vertebral column, providing a direct route from the prostate to the marrow of the axial skeleton (Msaouel et al., 2008). In reality, both hypotheses may work in concert to explain the preferential metastasis of prostate cancer cells. The vasculature of the bone marrow spaces consists of sinusoids, which act as a series of lakes in a line of faster flowing rivers. The circulating prostate cancer cells have more time to settle, bind and extravasate into the bone environment due to

slowed blood flow. At the same time, factors both in the cancer cells and the bone microenvironment allow for more efficient binding and extravasation in bone than in other tissues (Buijs and van der Pluijm, 2009; Bussard et al., 2008; Msaouel et al., 2008).

Although it is very important to study and understand the mechanisms behind this preferential metastasis, the proposed molecular mechanisms are beyond the scope of this report. Following metastasis to bone, the bone microenvironment presents surviving prostate cancer cells a fertile soil to establish secondary tumors. Once established, these tumors will inevitably become hormone refractory and create tumors resistant to standard treatment options. Ultimately, the prostate cancer cells and bone will interact to drastically change the homeostasis to create a bone microenvironment that is even more favorable to prostate cancer cell growth and survival.

1.2 Prostate cancer cells in Bone

As previously discussed, the bone environment serves as a fertile 'soil' containing many factors that aid in cancer cell growth and proliferation. Healthy bone is a mineralized collagen network containing many growth factors. In healthy bone, degradation of old bone (osteolysis) and formation of new bone (osteogenesis) is in a dynamic state of homeostasis. Due to this constant remodeling, the mineralized bone is broken down and growth factors are released, creating the fertile soil needed for metastasis (Buijs and van der Pluijm, 2009; Ye et al., 2007). Interestingly, trabecular bone, the preferred site of metastasis for prostate cancer cells, exhibits a higher rate of turnover than cortical bone (Bussard et al., 2008). The more metabolically active bone

will have a higher rate of osteolysis and therefore may have more growth factors available to the prostate cancer cells.

Osteolysis is widely considered to be necessary for prostate cancer metastasis (Buijs and van der Pluijm, 2009; Keller and Brown, 2004; Ye et al., 2007). Osteoclasts, the cells responsible for osteolysis, are stimulated by factors released by prostate cancer cells. However, bone production eventually increases and bone remodeling is increased. Most cancers that metastasize to bone will usually shift this homeostasis to favor bone resorption. In these osteolytic lesions, the result is weakened bone due to net bone loss, as in osteoporosis (Bussard et al., 2008). Prostate cancer cells in bone are different. Initially, prostate cancer cells will induce osteoclast-mediated bone resorption which results in the release of factors stored in the bone (Msaouel et al., 2008). This initial osteolytic phase, in terms of the seed and soil analogy, basically stirs up soil and releases nutrients to help the seed grow. Once established, the prostate cancer metastases will begin to produce and release their own factors into the bone. These factors and the factors released from bone create a cross-talk that shifts the homeostatic environment to favor osteoblastic bone deposition. This new bone, however, is not organized in the same manner as the bone it replaces. Bone in non-diseased state, lamellar bone, is characterized by a much more organized, layered structure that lends more strength to adult bone. The bone deposited by the osteoblastic lesions, called woven bone, is characterized by random orientation of fibers. This type of bone, generally seen at growth plates and the fetal skeleton, is weaker than lamellar bone and therefore more prone to fractures (Vela et al., 2007).

There is still some osteoclastic activity in the bone environment, but the osteoblasts and prostate cancer cells create a ‘vicious cycle’ interaction that supports

both bone deposition and tumor survival. (Msaouel et al., 2008; Sato et al., 2008; Ye et al., 2007). The factors released by osteoblasts, including transforming growth factor beta (TGF-β), support growth and survival of prostate cancer cells, which, in turn, secrete factors that activate osteoblasts and inhibit function of osteoclasts (Buijs and van der Pluijm, 2009; Vela et al., 2007). This situation results in an environment rich in growth and angiogenic factors that aids in the growth and survival of prostate cancer cells in bone.

It has been reported that the metastatic cells are affected by, and affect, the bone microenvironment (Festuccia et al., 1999; Sung et al., 2008). Specifically, cytokines, such as tumor necrosis factor alpha (TNF-α), are produced by various cells in bone as part of an inflammatory immune response. TNF-α, in turn, can activate osteoclasts and therefore increase bone resorption, resulting in the release of TGF-β from bone. These factors can stimulate signaling cascades in the prostate cancer cells that result in increased growth and proliferation (Bussard et al., 2008). Initially, TGF-β is an inducer of epithelial-mesenchymal transition, or EMT. In bone, it can promote osteoblast activity and prostate cancer cell survival (Buijs and van der Pluijm, 2009). Additional studies have shown that in prostate cancer, overexpression of TGF-β actually promotes tumor survival (Bierie and Moses, 2006; Padua and Massague, 2009). As part of the 'seed and soil' hypothesis, these factors that are very prevalent in bone act like fertilizers for the metastatic cancer cells, and it is thought that these factors act to transcriptionally control various genes in the invading cancer cells.

Of interest is also β2-Microglobulin signaling because it is released by prostate cancer, prostate and bone stromal cells. In the prostate cancer cells, it is responsible for altering gene expression so that the prostate cells mimic the expression

profiles of bone cells (Huang et al., 2008). One study has shown that inhibition of this signal pathway results in greatly increased apoptosis while not affecting normal prostate cells (Huang et al., 2008). Many of these signaling pathways may be identified as potential therapeutic targets to regulate the production of key factors aiding prostate cancer cell survival and growth.

1.3 Perlecan

One factor that may promote prostate cancer survival and growth is perlecan (Pln). Pln is a heparan sulfate proteoglycan expressed in nearly all vascularized tissues in the body and it can also be found in the matrix surrounding epithelial, mesenchymal and stromal cells. In normal tissue, Pln is primarily restricted to the basement membranes. The protein is very large, with an estimated size of 400-470 kDa without the heparan sulfate (HS) side chains (Iozzo, 2005). This core is comprised of 5 domains, 4 of which show homology to other proteins, including the Ig superfamily and the low density lipoprotein receptor. Each domain carries a set of proposed functions. For example, it is believed that domain I, the only domain unique to Pln, contains glycosylation sites for attachment of the HS side chains (Cohen et al., 1993; Iozzo et al., 1994). In addition to the wide distribution of Pln within the body, its biological importance can be seen by a very high degree of conservation of each of the five domains and the observation that mutations in the gene cause abnormal development (Cohen et al., 1993; Iozzo, 2005). Its distribution also indicates that Pln may be important for development of bone marrow (Iozzo et al., 1997).

The function of Pln has been studied, but it is still not fully understood. Besides forming dimeric or multimeric forms, Pln is capable of binding various growth and angiogenic factors, including TGF-β and fibroblast growth factor (FGF-2),

and depends on the presence of HS side chains. This binding capacity is important in cancer because these factors can aid in angiogenesis and also trigger survival pathways (Iozzo et al., 1994; Smith et al., 2007). In conjunction with the pro-angiogenic functions of Pln, the protein is important as a scaffolding for metastatic cells on which the neovasculature can develop (Savore et al., 2005). Additionally, when the protein is digested, a functional 85 kDa fragment of domain V is produced. This fragment, called endorepellin, has anti-angiogenic properties which can activate the cAMP-response element binding protein (CREB) via protein kinase A (Datta et al., 2006b; Iozzo, 2005). Pln also has been implicated in increased Sonic Hedgehog (SHH) pathway, which is important in prostate cancer metastasis, and may be important in response to other growth factors, such as FGF-2 (Datta et al., 2006b). In fact, this regulation may be important in prostate cancer metastasis to bone.

Because Pln is prevalent in bone and important to prostate cancer metastasis, it may represent a possible therapeutic target that can be used in conjunction with current prostate cancer treatments (Datta et al., 2006a). It is adhesive for fibroblasts, endothelial cells and chondrocytes (Iozzo et al., 1997). Additionally, Pln has been shown to be greatly upregulated in the reactive stroma of the prostate (figure 1). This large increase in Pln levels outside of the basement membranes and surrounding neovasculature further supports the thought that Pln is important to tumor growth, survival and metastasis because of its interaction with growth and angiogenic factors.

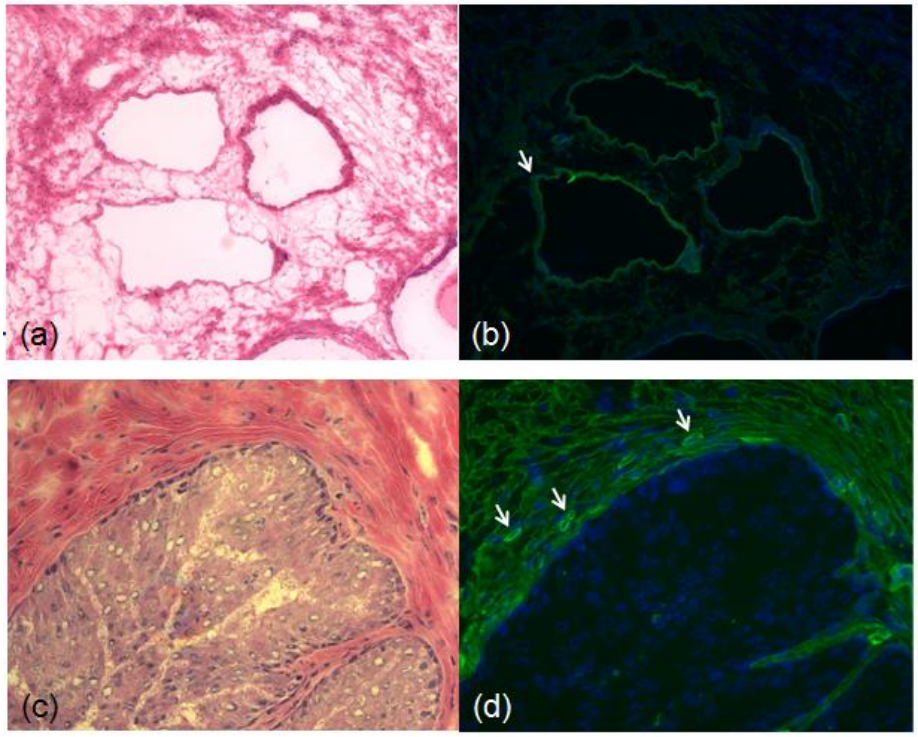


Figure 1 **Upregulation of Pln in reactive stroma in prostate cancer.** (a) Normal prostate tissue stained to show Pln in green (b). Pln is generally confined to the basement membranes (arrow) surrounding the lumen. In prostate where the tumor begins to invade the stroma (c), Pln is found to be greatly upregulated in the stroma and around new blood vessels (arrows, d).

Due to this large and unexamined upregulation of Pln in prostate cancer, I decided to study potential signaling pathways that control transcription of Pln. Previous studies involving Pln have focused largely on the protein core or the modifications of the side chains. However, one study focused on the promoter region for Pln. This study noted that the promoter region is a GC rich region, with areas of up to 80% GC pairs (Iozzo et al., 1997). Based on deletion analyses with a 2500 bp region at the 5′ end of the gene as the standard, functional activity is largely located in

the region proximal to the start site of transcription, although activity is decreased without the 5′ end of the promoter region (Iozzo et al., 1997). TGF-β was found to increase transcription of Pln, but this effect also could be blocked by addition of interferon-γ (IFN-γ). This effect was found to be entirely reversible and the result was a growth suppression without cell death (Sharma and Iozzo, 1998). The functional TGF-β response element was found to be located in the region of -461 and -285 bp (Iozzo et al., 1997). This result is significant because a different study indicates that bone-derived TGF-β can increase prostate cancer cell proliferation while simultaneously activating osteoclast activity. As previously mentioned, this releases additional growth factors, feeding into a 'vicious cycle' of tumor growth in bone (Sato et al., 2008).

Based on the prevalence of Pln in the reactive stroma of the prostate tumor and the functional activity of the promoter region in response to TGF-β, I believe that Pln could potentially be used as a therapeutic target. When the metastatic prostate cancer cells reach bone, they find an environment rich in growth and angiogenic factors. It is clear that the cancer cells and bone stromal cells exert effects on each other to create an ideal environment for the growth of a secondary tumor. It is possible that controlling specific signaling pathways to decrease or halt production of Pln in the metastatic prostate tumor cells could slow tumor growth or allow current therapies to be more effective. I propose to study the transcriptional control of Pln to identify pathways that could be targeted by further studies. Understanding of the control of Pln regulation would allow future studies to examine the importance of this protein to tumor growth and metastasis.

Chapter 2

MATERIALS AND METHODS

2.1 Promoter analysis

Mouse and human gene sequences for the Pln promoter region (labeled HSPG2 in the online databases) were identified using online databases including NCBI (www.ncbi.nih.gov), MGI (www.informatics.jax.org) and OMIM (www.ncbi.nlm.nih.gov/sites/entrez?db=omim). Once the location was determined, the human sequence was cross-checked on GeneCards (www.genecards.org/index.shtml). The sequences for the mouse and the human promoter regions were located and exported from the Ensembl database (www.ensembl.org). Based on the previously published sequence, the 2570 bp DNA sequence 5' of the start site was exported for each sequence and stored online at the SDSC Biology Workbench (workbench.sdsc.edu). The published Iozzo sequence was transcribed manually and checked against the Ensembl sequence for accuracy. The exported genomic regions were analyzed to determine the locations of potential transcription factor response elements using the online MatInspector program (www.genomatix.de/cgi-bin/matinspector/matinspector.pl). The data, provided in the Appendix, were manually compared. Transcription factor response elements that were not present in both mouse and human sequences were eliminated first. In order to further reduce the number of results, the remaining factors were researched and evaluated based on their relevance to bone or prostate cancer.

2.2 Genomic DNA extraction

The first extraction was performed on C4-2B cells on passage 18 (p18) provided by Lynn Opdenaker (University of Delaware, Biological Sciences) at about 80% confluence in a petri dish. The second extraction was performed on a different culture of C4-2B cells provided by Lynn Opdenaker at 80% confluence. Both extractions were performed using the Qiagen DNeasy Blood & Tissue kit and protocol. The elutions were performed twice using 200 µL Barnstead deionized water each time. Each elution was collected in a separate tube. The results were quantified by finding the absorbance at a wavelength of 260 nm using a BioRad SmartSpec™ 3000 spectrophotometer. The final extraction used WIDR colon adenocarcinoma cells provided by Benjamin Rohe (University of Delaware, Biological Sciences). This cell line was chosen because they produce high levels of Pln, and therefore the genome should be open and unsilenced in the Pln promoter region. This extraction was also performed using the Qiagen DNeasy Blood & Tissue Kit, but both elutions were collected in the same tube and the second elution was completed using 100 µL Barnstead deionized water instead of 200 µL of Barnstead deionized water.

2.3 Polymerase Chain Reaction

Unless otherwise stated, all thermocycling reactions were performed using either the PTC-100™ Programmable Thermal Controller (MJ Research, Inc.; Waltham, MA) or the GeneAmp® PCR system 9700 (Applied Biosystems; Foster City, CA). All imaging was completed using a MultiImage™ Light Cabinet (Alpha Innotech Corporation; San Leandro, CA) and the images were manipulated using AlphaImager software v.5.5. The results of all extractions were quantified by

spectrophotometry (wavelength = 260nm) on a BioRad SmartSpec™ 3000 spectrophotometer.

2.3.1 Primer Design

Primers initially were made manually by examining the Pln promoter sequence and checking the stability of the primer sequence online using the IDT OligoAnalyzer 3.1 (http://www.idtdna.com/analyzer/Applications/OligoAnalyzer/).

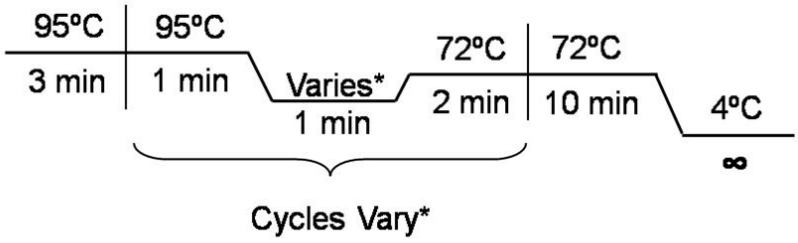
Sets A and B were designed manually and the reverse complement set (set C) was made using the REVCOMP feature on SDSC Biology Workbench. The remaining primer sequences were designed using Primer3 on SDSC Biology Workbench. All sequences were checked with the OligoAnalyzer 3.1 program and also by using BLAST to confirm sequence specificity. All primer sequences referenced in this paper can be found in table 2.1. Note: primer set C is the reverse complement of primer set A.

Table 2.1 **Primer Sets.** This table lists sequences and information for every primer set ordered for promoter analysis.

Set Designation	Product location	Sequences	Product size (bp)	T_M (°C)
A	-2565 to 0	**F:** 5'- CATGGACAGGCAAGGCCT -3' **R:** 5'- AGCTCGGGACAGCGCGGC -3'	2500	58.1 66.6
B	-1500 to 0	**F:** 5'- CCTCTCCACCCATCAGCCTCGGG -3' **R:** 5'- AGCTCGGGACAGCGCGGC -3'	1492	65.4 66.6
C	-2565 to 0	**F:** 5'- GCCGCGCTGTCCCGAGCT -3' **R:** 5'- AGGCCTTGCCTGTCCATG -3'	N/A	66.6 58.1
1	-800 to -167	**F:** 5'- GCATGTAGGCAATGATGTGG -3' **R:** 5'- TACTAGGCCTTTGTCTGGGC -3'	633	54.2 56.6
2	-715 to -167	**F:** 5'-CTTGTTGGGATGTATGCGTG -3' **R:** 5'- TACTAGGCCTTTGTCTGGGC -3'	548	54.1 56.6
3	-2390 to -1083	**F:** 5'- TGTGGAGGCTGCTCCTCTAT -3' **R:** 5'- ATTACAGGCATTGAGCCACC -3'	1307	57.7 55.4
4	-2432 to -1083	**F:** 5'- CCTGGTGTACTCTCCCCTCA -3' **R:** 5'- ATTACAGGCATTGAGCCACC -3'	1349	57.9 55.4
5	-2390 to-880	**F:** 5'- TGTGGAGGCTGCTCCTCTAT -3' **R:** 5'- ATCTTGGCTCACTGCAACCT -3'	1510	57.7 56.9
6	-1495 to -1083	**F:** 5'- TTTTCCTCTCCACCCATCAG -3' **R:** 5'- ATTACAGGCATTGAGCCACC -3'	412	54.3 55.4
7	-1613 to -1083	**F:** 5'- AACCCAGCCATGAGTTTCTG -3' **R:** 5'- ATTACAGGCATTGAGCCACC -3'	530	55.3 55.4
8	-1495 to -880	**F:** 5'- TTTTCCTCTCCACCCATCAG -3' **R:** 5'- ATCTTGGCTCACTGCAACCT -3'	615	54.3 56.9
9	-1613 to -880	**F:** 5'- AACCCAGCCATGAGTTTCTG -3' **R:** 5'- ATCTTGGCTCACTGCAACCT -3'	733	55.3 56.9
10	-2466 to -1620	**F:** 5'- CTTTCTCATCGGACAGGGAG -3' **R:** 5'- CAGGAGTGAGGTGAGCTGTG -3'	846	54.8 57.5
11	-2474 to -1620	**F:** 5'- TTTGAAGCCTTTCTCATCGG -3' **R:** 5'- CAGGAGTGAGGTGAGCTGTG -3'	854	52.9 57.5
QPCR	Pln domain V	**F:** 5'-ACCATCGAGCTGGAGGTTC -3' **R:** 5'- GAGGCTGATGAAGTCCTTGC -3'	102	56.9 55.9

2.3.2 GoTaq® Green Master Mix

Polymerase chain reaction (PCR) was performed using a GoTaq® Green Master Mix kit and protocol (Promega; Madison, WI). Primer set A was used with each primer at a final concentration of 0.8 μM in a 25 μL reaction. Two hundred and two nanograms of C4-2B genomic DNA from the first extraction were used in the reactions. The same reaction was conducted using various thermocycling conditions, which can be found in figure 3.1. PCR products were electrophoresed through a 2.0% (w/v) agarose/TAE gel containing 2 μL ethidium bromide. The voltage and duration of electrophoresis also varied and the data are included in figure 2.1. The correctly sized products from trials 3 and 4 were extracted from the gel using the QIAquick Gel Extraction Kit and protocol (QIAGEN; Valencia, CA). The extracted products then were inserted into a TOPO 2.1 vector using One Shot® Mach1™-T1R chemically competent *Escherichia coli* (*E. coli*) cells and the protocol as described in section 2.4 (Invitrogen; Carlsbad, CA).



Trial number	Annealing temperature (°C)	Number of Cycles	Gel Voltage (V)	Duration of electrophoresis (minutes)
1	53	35	150	20
2	56	33	117	30
3	59	35	80	60
4	56	35	130	30

Figure 2.1 Thermocycling and electrophoresis conditions for GoTaq® Green PCR reactions. The diagram above the table details the thermocycling conditions for the GoTaq® Green PCR reactions using C4-2B genomic DNA from extraction 1. The annealing temperature and the cycle numbers were varied in order to determine the optimal conditions for this PCR reaction. The gel electrophoresis conditions were varied based on desired separation.

2.3.3 Platinum® Taq DNA Polymerase

PCR also was performed using the Platinum® Taq DNA Polymerase and protocol (Invitrogen). Two hundred and two nanograms of C4-2B genomic DNA from the first extraction were used for these reactions with primer set A at a final concentration of 0.2 μM each, as directed in the protocol. The thermocycling conditions consisted of 2 minutes at 94ºC followed by 35 cycles (trial 1) or 42 cycles (trial 2) of 30 seconds at 94ºC, 30 seconds at 55ºC and 2 minutes and 30 seconds at 72ºC, followed by 10 minutes at 72ºC and ending with a hold at 4ºC. PCR products were electrophoresed through a 1.5% (w/v) agarose/TAE gel containing 2 μL ethidium bromide at 117 V for about 1 hour. The correctly sized products were extracted from the gel using the QIAquick Gel Extraction Kit and protocol (QIAGEN).

2.3.4 Gradient PCR

A Gradient PCR reaction was performed using the HotStarTaq DNA Polymerase kit (QIAGEN). Two reaction sets of four samples each were performed simultaneously. One set used the kit's special buffer (buffer Q: intended to increase specificity and affinity of primers) included in the HotStarTaq kit while the other set used $MgCl_2$ instead. Four hundred and five nanograms of C4-2B genomic DNA were used in each sample with primer set A added to a final concentration of 0.4 μM each. The thermocycling conditions included an initial 10 minutes at 94ºC followed by 40 cycles of 1 minute at 94ºC, 1 minute at the varied temperature and 3 minutes at 72ºC, followed by 10 minutes at 72ºC and ending with a 4ºC hold. The four annealing temperatures were 49.0ºC, 53.8ºC, 61.0ºC and 65.0ºC. This reaction was conducted using an MG-96G MyGene™ Series Peltier Thermal Cycler (LongGene Scientific

Instruments Co., Ltd.). PCR products were electrophoresed through a 1.25% (w/v) agarose/TAE gel with 2 μL ethidium bromide at 117V for about 1 hour. Products of the correct size were extracted from the gel using the QIAquick Gel Extraction Kit and protocol (QIAGEN). The extracted products then were inserted into a TOPO 2.1 vector using DH5-α T1R chemically competent *E. coli* cells (Invitrogen) and the protocol as described in section 2.4.

2.3.5 HotStarTaq PCR

PCR with the HotStarTaq kit was conducted using set C to a final concentration of 0.4 μM each with $MgCl_2$ instead of buffer Q. Three different DNA templates were used in three different reaction sets: Four hundred and five nanograms of C4-2B genomic DNA, and two separate 2500 bp products (inside a TOPO 2.1 vector) from the Gradient PCR reaction at about 350 nanograms each. The thermocycling conditions included a 10 minute heating period at 94ºC followed by the 40 cycles of 1 minute at 94ºC, 1 minute at 61ºC and 3 minutes at 72ºC, followed by 10 minutes at 72ºC and ending with a hold period at 4ºC. The products were electrophoresed through a 1.5% (w/v) agarose/TAE gel with 2 μL ethidium bromide at 130V for 40 minutes. The same thermocycling conditions and DNA template samples were used for a separate PCR using primer set B at a final concentration of 0.4 μM each. These samples were electrophoresed through a 1.5% (w/v) agarose/TAE gel with 2 μL ethidium bromide at 100 V for 1 hour.

PCR was also conducted using WIDR genomic DNA as template for all three sets of primers: the A set, B set and C set. In each reaction, each primer was added to a final concentration of 0.4 μM. The samples were electrophoresed through a 1.5% agarose/TAE gel with 3 μL ethidium bromide at about 90V for 1 hour. Products

of the correct size were extracted from the gel using the QIAquick Gel Extraction Kit and protocol (QIAGEN). The extracted products then were inserted into a TOPO 2.1 vector using DH5-α T1R chemically competent *E. coli* cells and the protocol as described in section 2.4 (Invitrogen).

PCR using the HotStarTaq kit also was used to test primer sets 1, 5, 9 and 11. In each reaction, primers were added to a final concentration of 0.4 μM each. Four master mixes, one for each primer set, were made according to the HotStarTaq protocol, and each set was tested against both WIDR genomic DNA and C4-2B genomic DNA. For WIDR, 600 nanograms of DNA were added to the samples. For C4-2B, 220 nanograms of DNA template were added to each sample. The thermocycling conditions were chosen based on the highest and lowest melting temperature (T_M) for all primers used. The program included 15 minutes at 95ºC followed by 35 cycles of 94ºC for 1 minute, 50ºC for 1 minute and 72ºC for 2 minutes. The set of cycles was followed by 10 minutes at 72ºC and a final hold at 4ºC. The products were electrophoresed through a 1.25% (w/v) agarose/TAE gel containing 2 μL ethidium bromide for 75 minutes at 80V. Products of the correct sizes derived from WIDR genomic DNA for sets 1 and 11 were extracted from the gel using a QIAquick Gel Extraction Kit and protocol (QIAGEN), eluting with 30 μL Barnstead water. The same protocol was repeated, including the gel extraction, using only primer sets 1 and 11 and increasing the number of cycles from 35 to 38. The gel extractions from the repeat trial were ligated into a TOPO 2.1 vector (Invitrogen) using DH5-α T1R chemically competent *E. coli* cells as described in section 2.4

2.3.6 HotStarTaq kit and Restriction Enzyme Digest

The Pln promoter sequence was analyzed on SDSC Biology Workbench to identify restriction enzyme (RE) cut sites within and around the region. Enzymes that cut within the promoter region were eliminated, leaving a list of enzymes that cut near the region. An area $\pm$ 1000 bp of each end of the promoter region was examined to find any RE that cut a small segment of DNA around the promoter region. A sample of C4-2B genomic DNA and a sample of WIDR genomic DNA were then treated with XhoI using 1 µL of RE, 1 µL RE buffer and 10 µL Barnstead water. 1.2 µg of WIDR genomic DNA was added to one reaction while 0.8 µg of C4-2B genomic DNA was added to the other reaction. Both RE digests were incubated at 37ºC in a water bath for 1 hour and stored overnight at -20ºC. The samples were electrophoresed through a 1.5% (w/v) agarose/TAE gel with 2 µL ethidium bromide at 80V for 75 minutes. DNA fragments matching the predicted fragment size were then extracted from the gel using a QIAquick Gel Extraction Kit and protocol (QIAGEN).

The XhoI digest was repeated using 3.0 µg of WIDR genomic DNA and 3.2 µg of C4-2B genomic DNA using the following mix: 4 µL RE 10x buffer, 29.1 µL Barnstead water, 0.4 µL acetylated bovine serum albumin (BSA) and 1.5 µL RE. Two additional digests were run using FspI and either 4.8 µg WIDR genomic DNA or 3.2 µg C4-2B genomic DNA. The mix for FspI included 4 µL RE buffer, 3µL RE (WIDR samples) or 2 µL RE (C4-2B samples) and Barnstead water to make a final reaction volume of 40 µL. Both RE digest sets were allowed to incubate in a 37ºC water bath overnight for about 24 hours. Following the incubation, all four samples (one sample of each RE digest for both sets of genomic DNA) were electrophoresed through a 0.5% (w/v) agarose/TAE gel with 3 µL ethidium bromide at 80V for 1 hour. Negative controls used WIDR genomic DNA without either RE added. The bands of DNA at

the correct size for the XhoI digest then were extracted using the QIAEX II Agarose Gel Extraction Kit and protocol (QIAGEN) while the FspI digest product from C4-2B genomic DNA was extracted using the QIAquick Gel Extraction Kit and protocol (QIAGEN).

PCR was conducted using the HotStarTaq kit with primer set A, with each primer having a final concentration of 0.4 μM each. Three different templates were tested: Both XhoI digest gel extraction products and the FspI digest gel extraction product. About 600 nanograms of XhoI digested WIDR DNA was used, while 450 nanograms each of the XhoI C4-2B DNA digest and the FspI C4-2B extract were used. The thermocycling conditions are the same as described in the other HotStarTaq kit reactions. The products were electrophoresed through a 1.25% (w/v) agarose/TAE gel with 2.5 μL ethidium bromide at 80V for 90 minutes.

2.3.7 Dual Restriction Enzyme Digest and PCR

Genomic DNA was digested by XhoI and FspI simultaneously. One sample of 4.8 μg of WIDR genomic DNA was digested with 3 μL each of XhoI and FspI and 4 μL of the FspI reaction buffer. Barnstead water was added to a final reaction volume of 40 μL. Another sample of 3.2 μg C4-2B genomic DNA was digested with 2 μL each of XhoI and FspI in 4μL of the FspI reaction buffer with Barnstead water to a final reaction volume of 40 μL. Both samples were allowed to incubate overnight in a 37ºC water bath. Following incubation, the samples were rapidly heated to about 95ºC and allowed to cool slowly to room temperature in order to deactivate both enzymes. This was performed by heating a flask of water to 95ºC, floating the samples in the bath and allowing the entire setup cool down to room temperature.

PCR was conducted for each digest sample using the HotStarTaq kit and protocol with primer set A. For each reaction, 10 µL of one of the deactivated digest reactions was added to the mixture to make a final reaction volume of 50 µL. The thermocycling conditions for the reactions included an initial 95ºC hot start for 10 minutes followed by 35 cycles of 94ºC for 1 minute, 61ºC for one minute and 72ºC for 2 minutes and 40 seconds. The program ended with 10 minutes at 72ºC followed by a hold at 4ºC. The products were electrophoresed through a 1.25% (w/v) agarose/TAE gel containing 2 µL ethidium bromide at 80V for about 90 minutes. The DNA area of the gel that represents the location of 2500bp products was extracted using the QIAquick Gel Extraction Kit and protocol (QIAGEN), skipping the optional wash. Next, 25 µL of each products from this extraction was run in a PCR using the HotStarTaq kit and protocol and primer set A. The thermocycling conditions were set the same as the previous reaction. The products were electrophoresed through a 1.25% (w/v) agarose/TAE gel containing 2 µL ethidium bromide for about 110 minutes at 80V. Products were extracted from the gel using the QIAquick Gel Extraction Kit and protocol (QIAGEN). The extracted products then were inserted into a TOPO 2.1 vector using DH5-α T1R chemically competent *E. coli* cells and the protocol as described in section 2.4 (Invitrogen).

2.3.8 Dimethyl Sulfoxide as a PCR Additive

5% (v/v) final concentration dimethyl sulfoxide (DMSO) was used in PCR with the GoTaq® Green Master mix kit and protocol and primer set 1. Each primer was added to a final concentration of 0.4 µM in the 50 µL reaction. Only C4-2B genomic DNA was used: 160 nanograms of template were added to each sample. Several control samples also were set up in addition to the 5% DMSO sample: a water

blank without genomic DNA or DMSO, DNA water instead of DMSO, water with a very low concentration of DMSO (0.25% (v/v) final concentration) and DNA with the low concentration of DMSO. The thermocycling conditions included a 2 minute initial heating at 94ºC followed by 30 cycles of 1 minute at 94ºC, 1 minute at 53ºC and 1 minute 30 seconds at 68ºC. The program was ended with a final 10 minutes at 68ºC followed by a 4ºC hold. The products were electrophoresed through a 1.25% (w/v) agarose/TAE gel containing 2 µL ethidium bromide at 80V for about 90 minutes. Products of the correct size were extracted using the QIAquick Gel Extraction Kit and protocol (QIAGEN).

PCR using the GoTaq® Green Master Kit and protocol with DMSO added to a final concentration of 5% (v/v) also was conducted using primer set A with 160 nanograms of C4-2B genomic DNA. The thermocycling conditions included a 2 minute initial heating at 94ºC followed by 30 cycles of 1 minute at 94ºC, 1 minute at 58ºC and 2 minutes 45 seconds at 72ºC. The program was ended with a final 10 minutes at 72ºC followed by a 4ºC hold. The products were electrophoresed through a 1.25% (w/v) agarose/TAE gel containing 2 µL ethidium bromide at 80V for about 90 minutes. Any product of the correct size was extracted using the QIAquick Gel Extraction Kit and protocol (QIAGEN). The extracted product then was inserted into a TOPO 2.1 vector using DH5-α T1R chemically competent *E. coli* cells and the protocol as described in section 2.4 (Invitrogen).

A final trial PCR was executed using two mixed sets of primers with the GoTaq® Green Master Kit and protocol with DMSO added to a final concentration of 5% (v/v). The first set included primer 1R with primer 11F, while the second included 1R with 4F. Each primer was added to a final concentration of 0.4 µM in the 50 µL

reaction. The thermocycling conditions included a 2 minute initial heating at 94ºC followed by 30 cycles of 1 minute at 94ºC, 1 minute at 53ºC and 2 minutes 45 seconds at 68ºC. The program was ended with a final 10 minutes at 68ºC followed by a 4ºC hold. The reaction products were electrophoresed through a 1.25% (w/v) agarose/TAE gel containing 2 μL ethidium bromide at 80V for about 90 minutes. The raw PCR product was ligated into a TOPO 2.1 vector (Invitrogen) using One Shot® TOP10 chemically competent *E. coli* cells as described in section 2.4.

2.4 TOPO TA Cloning® Reactions

All TOPO® cloning reactions were carried out using the pCR®2.1-TOPO® vector (Invitrogen) and chemically competent *E. coli* cells (either DH5-α T1R cells, One Shot® TOP10 cells or One Shot® Mach1™-T1R cells). The kit protocol was used, and the cells were streaked on LB agar plates containing either ampicillin or kanamycin. Plates were incubated for 12 to 16 hours at 37ºC. Overnight cultures were grown from colonies on the agar plates. These cultures consisted of 5 ml liquid LB media containing 50 μg/ml of the same antibiotic that was used on the agar plates. The cultures were incubated overnight at 37ºC while being shaken at 200 rpm. The plasmids were extracted using the QIAprep Spin Miniprep Kit protocol using a microcentrifuge. The results of all plasmid extractions were quantified by spectrophotometry on a BioRad SmartSpec™ 3000 spectrophotometer. A sample of the extracted plasmid then was digested with EcoRI in a 37ºC water bath for about 1 hour. The product from the RE digest was electrophoresed through a 1-2% agarose/TAE gel containing 2 μL ethidium bromide. The voltage and the duration of electrophoresis varied depending on the size of the gel and the extent of separation desired. Any plasmids containing an insert of the correct size were sequenced using

the Pre-Mixed DNA Sequencing protocol from Genewiz, Inc. (South Plainfield, NJ) and the results were checked with the Ensembl sequence online using tools available via the SDSC Biology Workbench. Glycerol stocks were made of all cultures that were sequenced. The glycerol stocks included 750 µL of the overnight culture in liquid LB media mixed with 750 µL 80% (v/v) glycerol in an Eppendorf tube. This mixture was then frozen rapidly in 100% (v/v) ethanol mixed with dry ice. The samples then were stored in the -80ºC freezer.

2.5 Cell culture

An HS27a cell line, p8, was cultured from a freeze-down stock stored in liquid nitrogen. This cell line was selected to model the prostate cancer stromal cells showing the large upregulation of Pln (figure 1). The cells were grown in high glucose Dulbecco's modified Eagle's medium (DMEM) with no sodium pyruvate (Gibco) and 10% fetal bovine serum (FBS). At p14, the media was switched to low glucose DMEM with GlutaMAX™ (Gibco) plus 10% fetal bovine serum (FBS) and 1% penicillin-streptomycin. Cells were passaged at about 80% confluency, by visual inspection, and cultured in T75 flasks. Flasks were trypsinized for 5 minutes, incubated at 37ºC and pelleted. The cell pellet was resuspended in 5ml media and 1ml of the suspension was added to 11ml of media in each flask. For the individual treatments, cells were plated in each well of a six-well plate. They were grown in low glucose DMEM with GlutaMAX™ with 10% FBS and 1% penicillin-streptomycin until they reached 70-80% confluency. Once the cells reached 70-80% confluency, the media was replaced with serum free low glucose DMEM with GlutaMAX™ containing 1% penicillin-streptomycin and grown for 24 hours. After serum-starving for 24 hours, the media was replaced with glucose DMEM with GlutaMAX™ containing 1%

penicillin-streptomycin and either TGF-β [at 0, 1, 5 or 10 ng/ml] or TNF-α [at 0, 0.5, 1, 5 ng/ml] (Sigma-Aldrich; Saint Louis, MO) and grown for an additional 24 hours.

2.6 Ribonucleic acid extraction and complementary DNA reaction

Total ribonucleic acid (RNA) was extracted from the HS27a cells following a 24 hour treatment with either TNF-α or TGF-β. The cells were lysed directly on the plate and the RNA was collected and purified using the RNeasy® Mini Kit and protocol (QIAGEN). Following lysis, the suspension was homogenized using the QIAshredder™ microcentrifuge tubes (QIAGEN). Once the RNA was eluted from the kit, the eluate was treated with DNase to eliminate possible DNA contamination. This step was completed using the DNA-*free*™ DNase Treatment & Removal kit (Ambion Inc; Austin, TX), incubating for 30 minutes at 37ºC. The RNA was then quantified by spectrophotometry at wavelength 260 nm, as described for the DNA extraction.

After quantifying the RNA samples, a reverse-transcription PCR (RT-PCR) was conducted to make complementary DNA (cDNA). All RT-PCR reactions were conducted using the Omniscript® RT Kit (QIAGEN) and 0.5-1 μg RNA in a final volume of 20 μL. Each reaction set consisted of the cDNA reactions and control reactions lacking the reverse transcriptase, in order to ensure that the RNA samples were not contaminated with DNA. The samples were incubated at 37ºC for 1 hour, followed by heat-inactivation of the reverse transcriptase by heating the samples to 93ºC for 3 minutes. The cDNA were stored at -20ºC.

2.7 Quantitative PCR

Quantitative PCR (QPCR) was used to quantify the effects of signaling pathways on Pln transcription. Reactions were mixed using the SYBR® Green PCR Master Mix (Applied Biosystems) to a final reaction volume of 25 μL. The samples were then analyzed using an ABI Prism 7000 Sequence Detection System (Applied Biosystems). The thermocycling conditions consisted of 10 minutes at 95ºC followed by 45 cycles of 15 seconds at 95ºC and 1 minute at 58ºC.

Chapter 3

COMPUTATIONAL ANALYSIS OF THE HUMAN PERLECAN PROMOTER: RESULTS AND DISCUSSION

3.1 The Human Pln promoter region is located on the minus strand

The Pln gene in mouse DNA was found to be located on chromosome 4 on the plus strand from 136,740,845 – 136,842,706 bp. In order to obtain the promoter region, 2565 bp of DNA sequence 5′ of the start of the gene region (136,738,280 – 136,842,706) was downloaded from Ensembl and saved online. The human Pln gene, however, is located on chromosome 1 from bp 22,021,325 to bp 22,136,377 on the minus strand. Therefore, two regions of DNA were tested. The first region that was tested was the 2565 bp segment before the start of the gene region (starting at 22,018,760). This was found to be the incorrect promoter sequence when it was aligned with the previously published sequence (Iozzo et al., 1997). I confirmed this by including exon 1 at the end of the downloaded sequence. When I ran analysis on this sequence on SDSC Biology Workbench, the amino acid sequence generated by what was thought to be exon 1 did not match the known Pln protein code.

However, when Pln exon 1 was downloaded from Ensembl, I found that the reverse complement of the downloaded sequence generated an amino acid sequence that matched the known Pln protein sequence. Interestingly, the generated sequence matched a fragment of the protein sequence from Pln domain V at the 3′ end of the gene. Therefore, the promoter region was downloaded from Ensembl from bp

22,136,377 to bp 22,138,942, saved to the Biology Workbench and converted to the reverse complement sequence using a program available through the Biology Workbench. This sequence was aligned with the previously published sequence (Iozzo et al., 1997) and the two sequences differed only slightly (data not shown). Therefore, I determined that the correct sequence is on the minus strand of DNA, as noted on Ensemble, but that the sequence that is provided is the plus strand.

When the human and mouse promoter sequences were aligned, there was significantly less agreement than between the two human sequences. The human Pln promoter sequence was further examined and found to have a 56.6% GC content. Also noted was a region of 23 adenosine nucleotide repeats located about 800 bp before the 5′ UTR. Finally, alignment information indicated that due to gaps and disagreements between the published promoter sequence and the Ensembl sequence, the lengths of the promoters were slightly different. In order for the 5′ ends to match, the Ensembl sequence had 16 bp clipped from the 5′ end, making it only 2549 bp long. Because of these differences, I expected that there would be minor discrepancies in presence or location of some transcription factor binding sites.

As a result of the difficulties with the human Pln promoter sequence, the mouse promoter was checked by extracting the exon 1 sequence and comparing the theoretical amino acid sequence to the known sequence. This analysis confirmed the downloaded mouse Pln sequence was the correct region of DNA.

3.2 Pln promoter region contains many highly conserved transcription factor response elements

Despite the low level of agreement in nucleotide sequence between mouse and human sequences, the transcription factor response element analysis was

completed using the online MatInspector (Genomatix) program. The raw results from the program were sorted manually and are provided in tables A1 – A3 (appendix). A short list of 22 transcription factors was created from highly conserved elements across all three promoter sequences (table A4 in the appendix). While many factors were ruled out simply because they were not found to be conserved between human and mouse, other factors had to be researched to determine their relevance to prostate cancer cell metastasis to bone. From the short list, four transcription factors were chosen for further study: NFκB, Smad3, Elk-1 and CREB. The locations of these four factors were determined within each promoter region. The results can be found in figure 3.1.

Figure 3.1 **Human and Mouse Pln promoter region maps** Aligned map that depicts the conservation of the four transcription factor response elements of interest in the Pln promoter region. The response elements were aligned to match the results for the human Pln sequence from Ensembl (top line) in order to demonstrate conservation. The middle line represents the promoter region sequence as published by Iozzo (1997), and the bottom line represents the mouse sequence from Ensembl. Bar colors: red = NFκB; green = Elk 1; blue = CREB; and orange = Smad3.

The response elements were found to be spread all throughout the 2565 bp region of the Pln promoter. Although the mouse sequence showed higher numbers of potential binding sites, the conserved sites were highly conserved in position as well (data available in table A4) suggesting an evolutionary importance for these sites. In addition to the high degree of conservation, all four of these transcription factors have been implicated in disease states, either through inflammatory response or through aberrant signaling in cancer, as discussed in the introduction. For these reasons, it was decided to attempt to extract the entire 2565 bp from genomic DNA. Figure 3.2 shows the signal pathways that I propose to study. All of the pathways pictured are simplified, and they may overlap through crosstalk mechanisms.

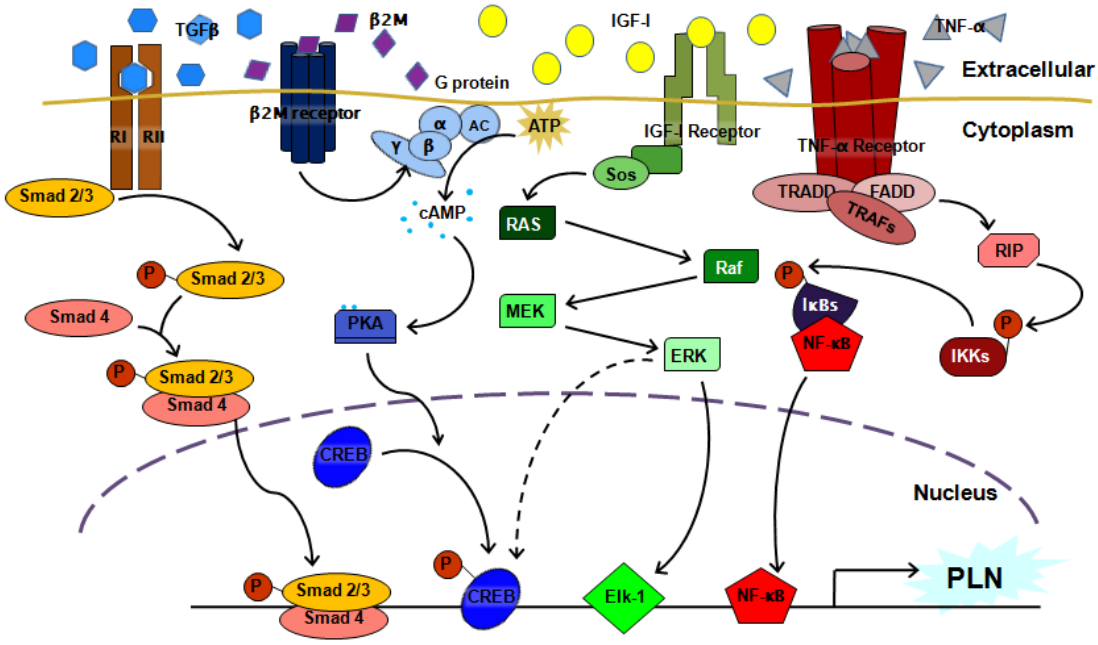


Figure 3.2 **Schematic drawing of signaling pathways of interest.** The figure illustrates the four signaling pathways of interest. Each pathway is more complicated than drawn and there is greater crosstalk between them.

Chapter 4

CLONING AND PRELIMINARY FUNCTIONAL ANALYSIS OF THE HUMAN PLN PROMOTER REGION: RESULTS AND DISCUSSION

4.1 Extracting the promoter region from genomic DNA using PCR: optimization of reaction conditions

4.1.1 Primer design

Because the transcription factor response elements were spread throughout the Pln promoter region, I designed PCR primers that target the entire promoter region. The first primer set I designed was primer set A (see table 2.1). Eventually the reverse complement set A was tested (set C), followed by a truncated set that utilized the same reverse primer as set A but had a new forward primer to target only 1500 bp of the promoter region. As will be discussed, these primers were not optimal, and therefore new sets of primers were designed. The online Biology Workbench could not produce any primer sets based on the full 2549 bp of the Pln promoter region. Because of this, I had to split the promoter into three pieces, with the 3′ segment expanded to include the 5′ UTR. This generated several small segments of the promoter that could be spliced together to build the full promoter region. The target regions of each primer set can be found in figure 4.1.

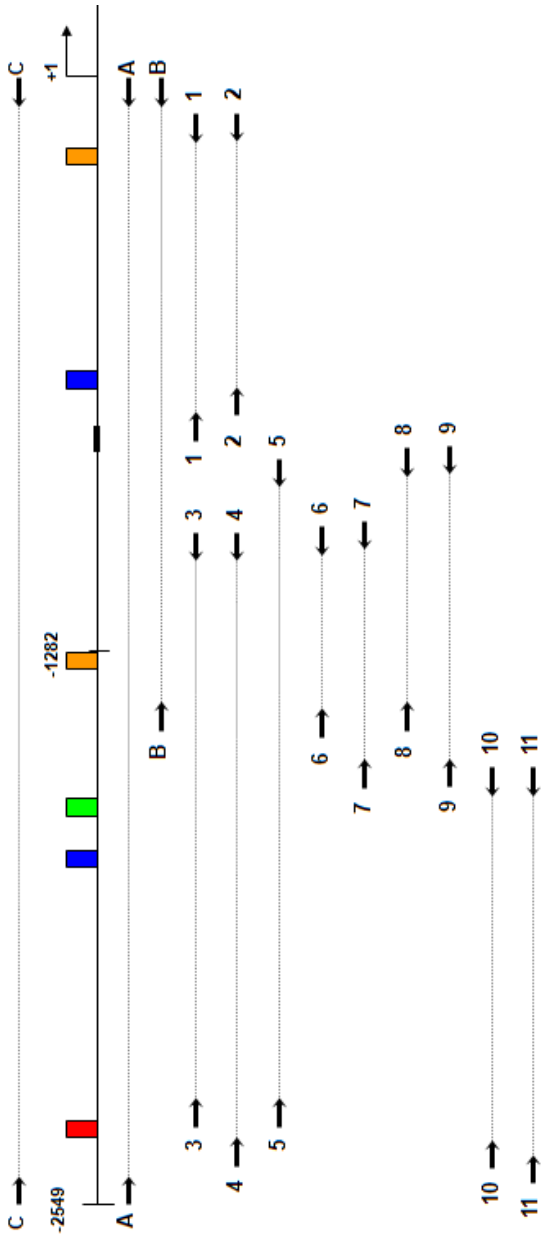


Figure 4.1 **Map of the primer targets within the human Pln promoter region.** Detailed information about each primer set can be found in table 2.1. This map shows the location and relative length of each primer product within the promoter region

4.1.2 GoTaq® Green Master Mix and primer set A

The results of each gel electrophoresis can be seen below in figure 4.2.

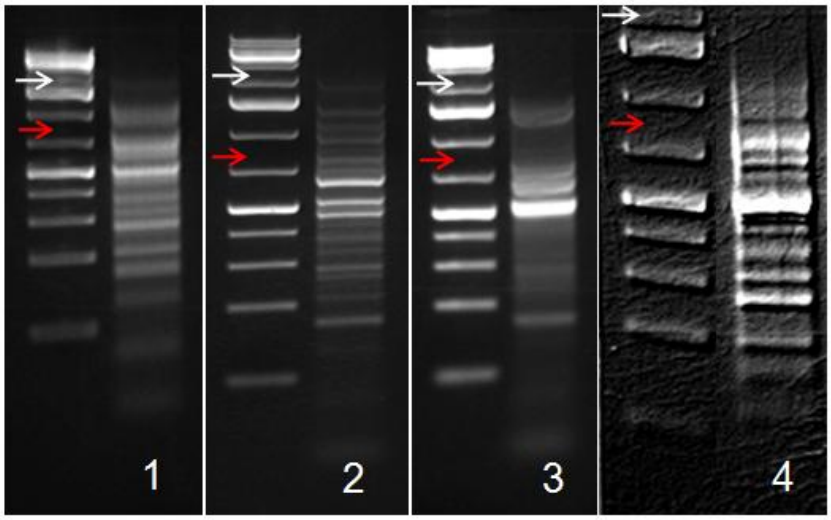


Figure 4.2 Gel electrophoresis of PCR products using GoTaq® Green kit. Trials 1 and 3 demonstrate the problem with smearing. All four trials show the extent of non-specific binding. Red arrows indicate the location I thought the ladder identified as 2500 bp. White arrows indicate actual site of 2500 bp product.

In addition to nonspecific primer binding (indicated by multiple bands), there was smearing in trials 1 and 3, which may be indicative of problems with the thermocycling conditions. At first it was thought that the thermocycling conditions were not ideal, which was causing the primers to release from the template early. Because there was product present where I had expected to see it (red arrows in figure 4.2), I performed a gel extraction on trials 3 and 4. After extracting the band of DNA at the red arrows, I ligated the products into a TOPO 2.1 vector. Inserting the product into this vector would allow me to make a glycerol stock of the *E. coli* containing the

promoter region. In addition to lending more stability to the stock, it could facilitate cloning the product into a reporter plasmid. When the vectors were sequenced, it was discovered that the inserted products did not align to the human Pln promoter sequences saved on Biology Workbench. The sequences were shortened and the reverse complements were generated in order to test possible sequencing errors. However, these manipulations did not show any positive results and when the product sequences were run through BLAST, the program was able to match the sequences to over 100 genes or coding regions. This, in addition to the fact that the sequences were shorter than expected forced me to the conclusion that they were not the correct products.

It was later discovered that the wrong ladder key was being used and that the site that was thought to signify a 2500 bp product actually only represented an 850 bp product, which is consistent with the length of the product that was sequenced. Seen in figure 4.2, the white arrow indicates the correct location of the Pln promoter region in the gel. Of note is that there is little to no DNA present at the correct size. For this reason, I believed that the GoTaq® Green taq polymerase may be releasing from the DNA before the full product could be produced. As a result, I decided to try to use the Platinum® Taq kit, which was designed for use with longer PCR products.

4.1.3 Platinum® Taq PCR with primer set A

The Platinum® Taq (Invitrogen) kit is designed for use with large products. Because I had been seeing multiple bands with the GoTaq® Green Master mix, I thought that the Taq polymerase may have been releasing the DNA template before the product was completed. The results of the PCR trials using the Platinum® Taq kit can be seen in figure 4.3

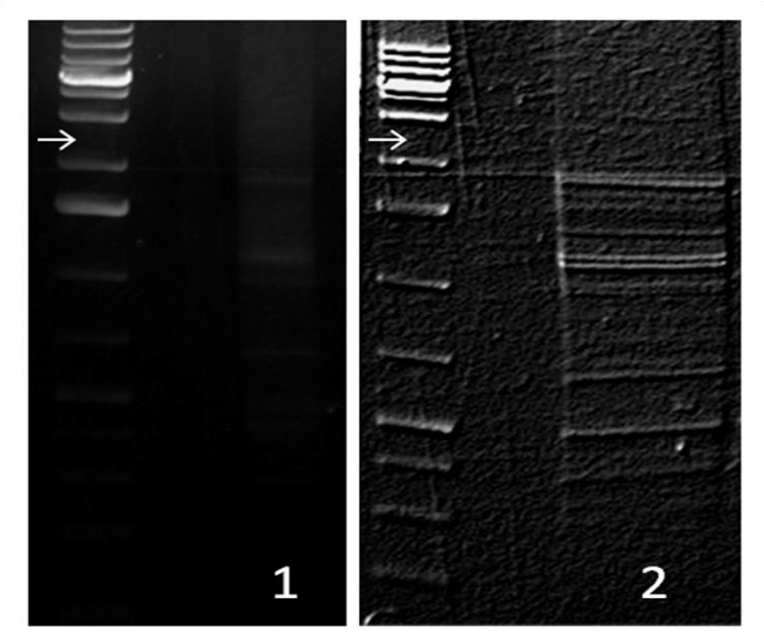


Figure 4.3 Gel electrophoresis of PCR products using Platinum® Taq. Both images show PCR products using Platinum® Taq kit (Invitrogen) electrophoresed through 1.5% (w/v) agarose/TAE gel. Both images are 8/30 exposures, showing that very little product is present. Arrows represent the correct location for the human Pln promoter (about 2500 bp).

The largest product present in the gel was extracted and analyzed by spectrophotometric analysis. I found that very little product was present, so the product could not be ligated into the TOPO 2.1 vector. When the reaction was repeated, the same results were seen. The bands in the gel were very faint both in the pictures and when the gel was inspected visually. Because the product was barely present in the first trial, the number of cycles was increased from 35 (figure 4.3 panel 2) to 42 (figure 4.3 panel 1) in order to try to increase the amount of product. As seen in figure 4.3, there was no increase in product.

Because there was not enough product present to extract and the product size was slightly smaller than expected, I did not ligate the product into TOPO 2.1 vector. Also of note is that the PCR was not specific. There were smaller products present in both trials, indicating that the problems encountered with the GoTaq® Green Master Mix were probably due to non-specific primer binding than issues with the taq polymerase. As a result of the difficulties with the Platinum® Taq kit, I tried a different PCR kit that was designed for increased specificity.

4.1.4 PCR with the HotStarTaq Kit and protocol

The gradient PCR was set up using primer set A and the HotStarTaq kit and protocol (Invitrogen) in order to try to optimize the annealing temperature for the primer set. The results, shown in figure 4.4, demonstrated the same problems seen with the other PCR kits. Primarily, there was nonspecific binding of the primers when $MgCl_2$ was used in place of the special buffer, Buffer Q, included in the HotStarTaq kit. This can be seen in figure 4.4, lanes 5-7, in the multiple bands present and the smearing in lanes 5 and 6. Because these problems were far more severe in lanes 5 and 6, these two lanes were disregarded. However, lane 7 showed a band at the correct size. This product was created at an annealing temperature of 61ºC, which also showed the most specificity. The product band at the correct size was extracted and ligated into the TOPO 2.1 vector. The plasmids that showed a product of a correct size following RE digest were sent to Genewiz, Inc. for sequencing. The returned sequences were aligned against the Ensembl sequence on the Biology Workbench. Although I broke the experimental sequences into smaller sections and tried the reverse complement of the sequence, they did not match the Ensembl sequence.

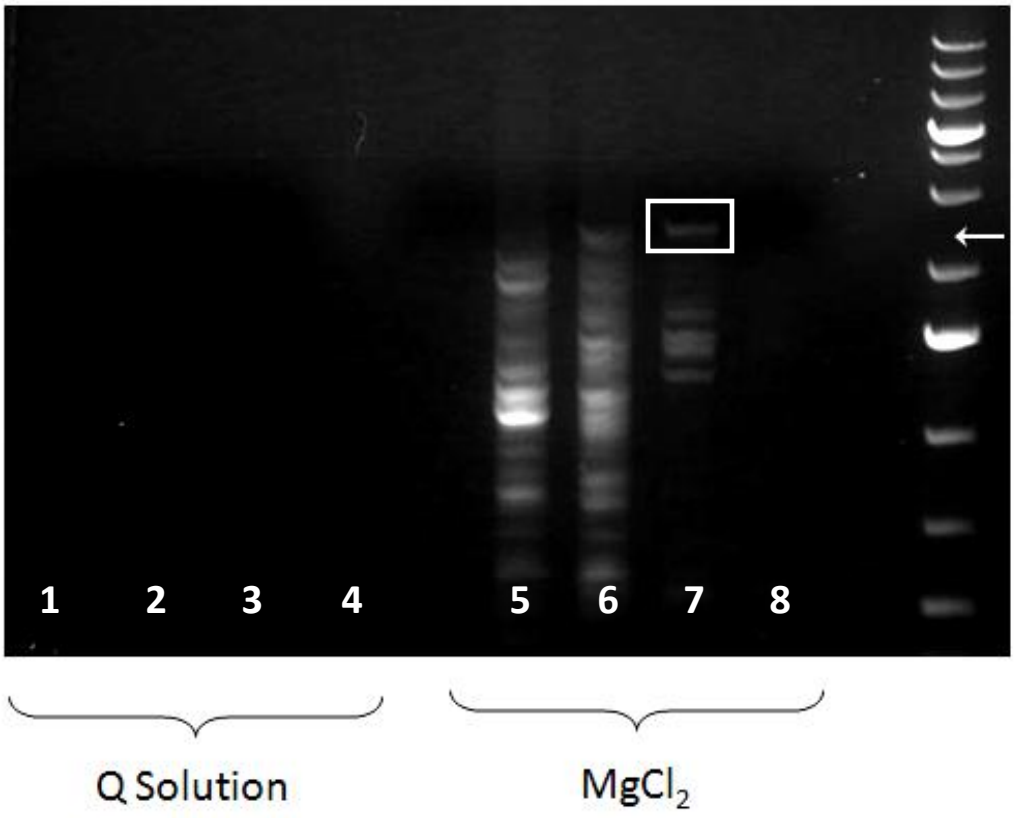


Figure 4.4 **Gel electrophoresis results of gradient PCR using HotStarTaq kit.** The figure shows the results of the HotStarTaq gradient PCR. Lanes 1-4 and lane 8 showed no product formation, while lanes 5, 6 and 7 showed multiple products and smearing. There were no products at the correct size (arrow) in either lane 5 or 6. The product band at the 2500 bp location was extracted (box).

Additionally, one of the sequences was degraded and did not sequence. When the fragments of the experimental sequences were tested using BLAST, over 100 results with at least 84% specificity were returned, none of which were located in the human Pln promoter region. This indicated that the experimental sequences were not correct. This information, in addition to the gel results, indicated that the problem may have been with the primers. Since the buffer that is designed to increase the specificity of the primers showed absolutely no product formation and the one product of the correct size did not match the Ensemble sequence, I tried new primers.

The first primer set I decided to try was set C. It was thought that the orientation of the gene within the region may be different than what was seen online. The orientation found online was not very clear, and not all of the databases agreed. Therefore, primer set B was used with HotStarTaq kit and protocol. There was no product formed with genomic C4-2B DNA used as template, and two of the reactions using the extracted gradient PCR product as template created products that were twice as large as expected. One product formed from this template showed two bands, while another showed a product of the correct size (results not pictured). This sample was not sequenced because it was concluded that it was either the same product or a fragment of the TOPO 2.1 vector plasmid. This conclusion was based on the reasoning that the old product was used as template and no products were seen in the genomic DNA lanes. The same protocol was attempted using WIDR genomic DNA as template. No products were found in the lane using buffer Q. While product was found in the lane using $MgCl_2$, it showed the same problems encountered before. Primarily, there were multiple, nonspecific products. There was one product around

the 3000 bp marker in the gel. However, since the product was barely visible and too large, it was not sequenced.

Based on the difficulties encountered with trying to copy the full 2549 bp of the promoter region, I opted to study the shorter 1500 bp proximal to the start of transcription, as shown in figure 4.1. This primer set was run with the HotStarTaq kit using genomic C4-2B DNA as a template as well as two old 2500 bp experimental products that did not match the promoter region. None of the three templates showed a product of the correct size. Because of this disappointing result, I tried using WIDR genomic DNA as template. The reason for this was because WIDR has been shown to produce large amounts of Pln. Because the gene is so active in WIDR cells, this region of the genome should be open so that the transcription proteins have access. A PCR reaction was carried out using this new genomic DNA template with both primer set A and primer set B, the 1500 bp product set. Products were found and extracted for both sets of primers. However, there was also contamination and non-specific primer binding (results not pictured). Nevertheless, the products of the correct size were sequenced and found to match the experimental products obtained when using C4-2B genomic DNA as template.

In order to try to increase the specificity of the primers, I tried to digest the genomic DNA, separate the fragments and use the fragment containing the promoter region as template for PCR with the HotStarTaq kit and primer set A. In addition to reducing the number of sequences that the primers could bind to, this procedure may also open up the DNA in the area of the Pln promoter region. I found that FspI cut a fragment of DNA of about 9700 bp that included the promoter region and XhoI cut a fragment of about 16,300 bp. Because of the size of the XhoI fragment, I had to use a

different kit to extract the fragment from the gel. In the first trial, DNA was digested and the fragments were separated using gel electrophoresis. Once the desired fragments were removed from the gel, they were used as templates in a second PCR using the HotStarTaq kit and protocol and primer set A. However, this method did not generate any product. In the next trial, I decided to combine both XhoI and FspI in a single RE digest. This should generate a fragment of DNA of about 9400bp around the Pln promoter region. Instead of separating fragments through a gel, I decided to use the DNA directly from the RE digest so that I did not lose any template during the extraction. This did not generate any results.

I tried the above technique a second time. The results can be found in figure 4.5. This time I repeated the PCR and then ran the products through a 1.25% (w/v) agarose/TAE gel. This time, I extracted any DNA in the region of the gel around the 2500 bp region. I then used this as template in a second PCR using the HotStarTaq kit. No difference was seen between WIDR and C4-2B genomic DNA as starting material. The results from the second PCR showed that a small product was targeted by the primers and no product was seen in the 2500 bp region of the gel. I extracted the small product and ligated into a TOPO 2.1 vector, but the protocol did not work and the *E. coli* did not grow after the first night. Because this protocol, designed to create a template that is highly specific to the Pln promoter region, did not work, I decided to design a new set of primers.

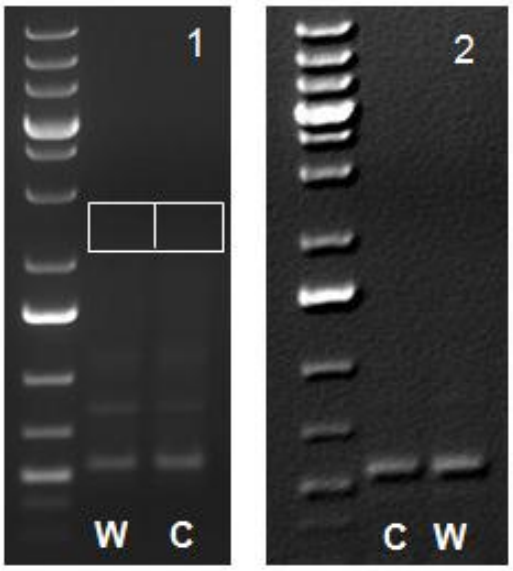


Figure 4.5 **PCR and double RE digest of genomic DNA.** Image 1 shows the gel results of the first PCR using DNA that had been digested with FspI and XhoI. The box indicates the region of DNA that was extracted from the gel. Image 2 shows the results of the PCR using the gel extraction products as template. C = C4-2B genomic DNA starting material; W = WIDR genomic DNA starting material.

4.1.5 PCR using various primer sets

Following the RE digest and PCR protocol detailed in section 4.1.4, I designed new primers using the primer3 application available on Biology Workbench. This program did not find any possible primer sets when I used the full 2549 bp promoter region, so I divided the region into three pieces. I also expanded the region beyond the 5′ end of the region and into the 5′ UTR. The results of this analysis can be found in table 2.1. I found 11 potential sets, many with common primers and I tried to select primer sets that overlapped. Overall, the sets span the entire promoter region (figure 4.1).

I first set up four simultaneous reactions to test primer sets 1, 5, 9 and 11. I used the HotStarTaq kit and protocol with samples both C4-2B and WIDR genomic used for each primer set, although no difference was seen between the two templates. The results, shown in figure 4.6, varied by primer set. Primer sets 5 and 9 showed less specificity and more smearing, indicating that the thermocycling conditions were not optimal for these sets. Because I had set the thermocycling conditions according to the four sets of primers together, I may have set the annealing temperature too low for sets 5 and 9. However, because I saw distinct bands at the correct sizes for sets 1 and 11, I repeated the previous reaction with sets 1 and 11 only.

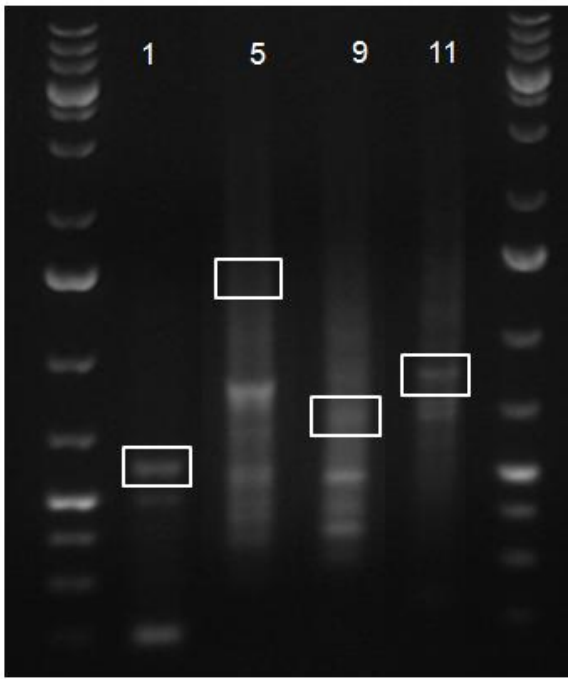


Figure 4.6 Gel electrophoresis of PCR products using primer sets 1, 5, 9 and 11. The boxes indicate the location of the desired product for each primer set. Sets 1 and 11 showed distinct bands in the expected regions

The bands in the repeated reaction were much more distinct, and they were extracted and ligated into the TOPO 2.1 vector and prepared for sequencing. However, I noted that the gel extraction had a very low yield, and that I likely had lost most of the product. After the TOPO plasmid preparation, there were no plasmids that showed a product insert of the correct size, so set 11 was not sequenced. The sequencing results for set 1 did not match the Pln promoter region. Because of the low yield from the gel extraction and the difficulties with ligating the product into the TOPO 2.1 vector, I proposed that I was losing the promoter sequence in the gel extraction process.

In order to bypass the gel extraction, I needed to increase the specificity of the PCR so that I could ligate the product directly into the TOPO 2.1 vector. Fortunately, a member of the laboratory sent me a protocol that used DMSO to increase the specificity of PCR for difficult products, such as GC rich regions (Frackman 1998). This additive, which functions by interfering with hydrogen bonds in the DNA helix, thereby facilitating strand separation, was added to a final concentration of 5% (v/v) in a PCR mix using the GoTaq® Green Master Mix kit and protocol.

I tested this protocol first with primer set 1 and found that it eliminated all products other than the target product. Following these results, I tried the protocol with primer set A, but no product was seen. I extracted the product from primer set 1 and the DMSO protocol to check that it was the correct fragment of the promoter region. Although the extraction resulted in a low yield again, the sequencing confirmed that it was the correct product. After confirming that the DMSO protocol did help increase specificity, I mixed primers in order to copy the full 2549 bp of the

Pln promoter region. I initially tried two sets: 1 REV and 11 FOR; and 1 REV and 4 FOR. These sets were used in amplification using the GoTaq® Green Master Mix with DMSO added to a final concentration of 5% (v/v). The results were checked using gel electrophoresis (figure 4.7). The product was ligated into the TOPO 2.1 vector using raw PCR product instead of gel-extracted product. This was sent for sequencing.

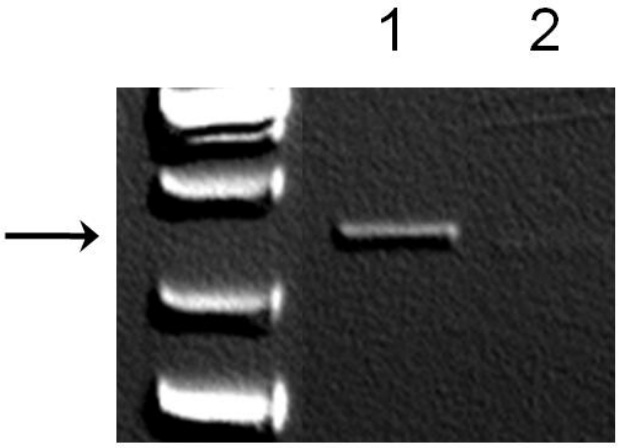


Figure 4.7 Gel electrophoresis results of PCR with mixed primer sets and DMSO. Lane 1 shows a distinct band in the area of the gel representing a 2500 bp product (arrow). No other product was seen in this lane. Lane 2 shows a very slight product, more visible to the naked eye, but also showed evidence of primer dimer formation (not shown).

Genewiz, Inc. reported that the template provided could not be sequenced using the standard protocol. Therefore, I sent the same samples a second time to be sequenced using the GC-rich protocol. The results from this sequencing protocol were aligned with the Ensembl sequence on Biology Workbench, and the experimental products were found to match. The results of this sequencing can be found in figure 4.8. Because the product was so long, the middle portion was not sequenced.

Figure 4.8 **Human Pln promoter region with transcription factor binding sites and experimental sequences identified.** The underlined regions of sequence indicate regions of the experimental promoter region that either were not sequenced, that were not copied or that did not match the Ensembl sequence. Black bold/italic regions indicate primer binding sites. Red = NFκB binding site; green = Elk-1 binding site; blue = CREB binding site; orange = Smad 3 binding site.

4.1.6 DMSO aided the successful copying and cloning of the human Pln promoter region

Although a portion of the product was not sequenced, the high degree of agreement in the sequenced areas indicated that this product was indeed the human Pln product. Therefore, I concluded that mixed primer set 1 REV/11 FOR used in conjunction with GoTaq® Green Master Mix with 5% DMSO was successful in extracting the Pln promoter region from genomic DNA. I have ligated this product successfully into a TOPO 2.1 vector and made glycerol stocks of the *E. coli* colonies containing the plasmid + product construct.

4.2 Cell culture treatments

The HS27a cells grew slowly for the first few passages after they were grown out of the stock stored in liquid nitrogen. However, following the change in media from high glucose DMEM to low glucose DMEM, the doubling time appeared to decrease. Serum-starving the cells did not have visible effects after the first 48 hours. However, treatment with TGF-β resulted in a change in culture formation. It is reported that the HS27a cell line can support a cobblestone growth pattern (Graf et al., 2002; Torok-Storb et al., 1999). I saw the cells begin to adopt this pattern of growth after 24 hours of treatment with TGF-β (figure 4.9).

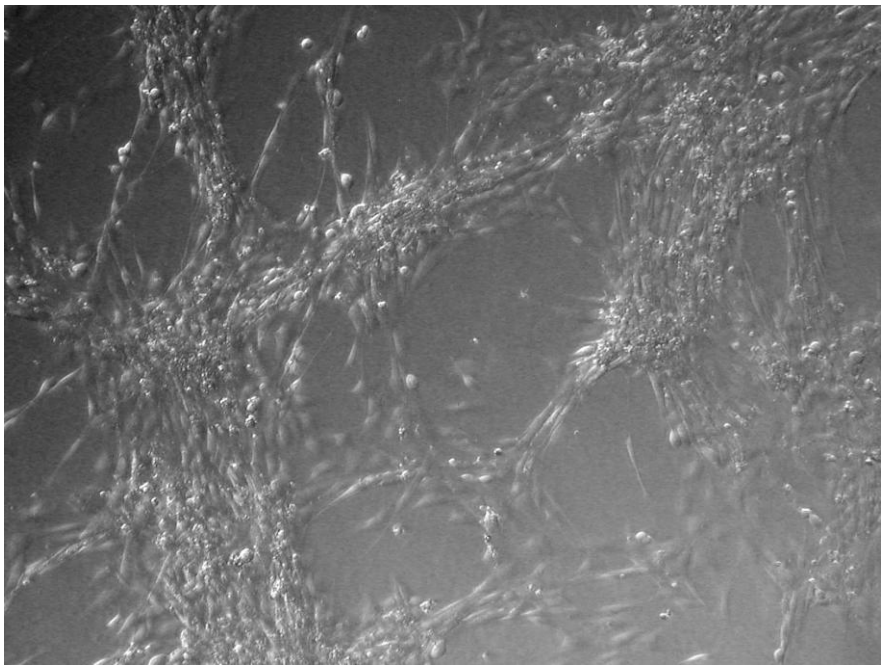


Figure 4.9 Cobblestone growth of HS27a cells Following a 24 hour serum-starving and an addition 24 hours treatment with TGF-β, these cells were found to organize into this cobblestone pattern, creating a lattice of cells

Interestingly, these results were only seen when the cells were treated after they reached 70% confluency. When a culture of HS27a cells was treated with TGF-β before it reached 70% confluency, this patterning of cells was not observed. Additionally, there was slight cobblestone formation present in the cultures treated with TNF-α, but it was not as clearly organized as the TGF-β-treated cultures.

Following treatment, the RNA from each sample was collected and analyzed by spectrophotometry. The RNA concentrations were fairly low, ranging from 25 μg/ml to over 200 μg/ml. Despite these results, I proceeded with the cDNA reaction and then utilized the cDNA in a QPCR reaction. The results from the QPCR were gathered but the data have not yet been fully analyzed.

Due to time constraints, I was only able to obtain preliminary results. However, based on the effects the treatments had on cell growth, it is clear that the treatments affect cell processes. The cobblestone growth response to TGF-β seen indicates that the growth factor may have altered cell processes, including extracellular matrix (ECM) proteins. Although this effect is very pronounced when the cell concentration is high, there was significantly less response when the cells were treated at about 60% confluency. Finally, TNF-α showed no changes in growth of the cultures. It may have slowed cell proliferation and resulted in cell death, but these results were not quantified. As a future direction of this work, it would be recommended to test the CREB and the Elk-1 pathways as well and to attempt to quantify and categorize their effects on cell growth and proliferation.

4.3 Conclusions

- The properties of the promoter region, including the high GC content, produced many difficulties in PCR
- DMSO stabilized the promoter region and allowed the primers to preferentially bind to that region of DNA
- The difficulties encountered in PCR do not necessarily translate to low biological activity of the promoter region. Various cell factors, such as histones, may stabilize this region and allow transcription factors to bind. The large upregulation seen in the prostate cancer stromal cells seems to indicate that some mechanism promotes this stabilization of the DNA.
- Preliminary observations of cell culture indicate that TGF-β and TNF-α affect cell growth and proliferation *in vitro*. QPCR data

will be needed to show whether these effects manifest in changes in Pln transcription.

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APPENDIX

Table A.1 Genomatix Analysis of the Mouse Perlecan Promoter Region

GEMS Launcher Task: *MatInspector*: Search for transcription factor binding sites
working on MouseHSPG2_Ensembl (2566 bp)

Please be aware:

Individual binding sites in a promoter are NEVER sufficient to indicate transcriptional function. Functional assessment of binding sites can be carried out by our other tools, e.g. ModelInspector, Comparative Genomics, FrameWorker, BiblioSphere

If MatInspector does **not** identify a known site, please send an email to support@genomatix.de citing the corresponding paper!

Search Results (440 matches)

MatInspector Release professional 7.4.8, May 2007 **Mon Jun 11 20:06:51 2007**

Solution parameters:

Sequence file: MouseHSPG2_Ensembl (2566 bp)
Family matches: yes
MatInspector library: Matrix Family Library Version 6.3 (March 2007)
Selected groups (core/matrix sim)
- ALL vertebrates.lib (0.75/Optimized)

Family/matrix	Further Information	Opt.	Position from - to	Str.	Core sim.	Matrix sim.	Sequence (red: ci-value > 60 capitals: core sequence)
V$GKLF/GKLF.01	Gut-enriched Krueppel-like factor	0.86	1 - 13	(-)	1.000	0.934	gaagaaaaaAGGG
V$EVI1/EVI1.06	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.83	18 - 34	(+)	1.000	0.847	gagacaAGATcttaggt
V$RXRF/RAR_RXR.03	Retinoic acid receptor / retinoid X receptor heterodimer, DR5 sites	0.81	20 - 44	(+)	0.883	0.811	gacaaGATCttaggtagttcaagct
V$GATA/GATA3.02	GATA-binding factor 3	0.91	21 - 33	(+)	1.000	0.955	acaAGATcttagg
V$NR2F/TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	0.76	22 - 46	(+)	0.829	0.802	caagatcttaggtaGTTCaagctgg
V$RORA/RORA2.01	RAR-related orphan receptor alpha2	0.82	27 - 49	(+)	0.750	0.831	tcttaggtaGTTCaagctggttt
V$GRHL/GRHL3.01	Grainyhead-like 3 (sister-of-mammalian grainyhead - SOM)	0.82	39 - 51	(+)	1.000	0.833	caagctGGTTttg
V$CHRF/CHR.01	Cell cycle gene homology region (CDE/CHR tandem elements regulate cell cycle dependent repression)	0.92	45 - 57	(+)	1.000	0.952	ggttTTGAattta
V$SNAP/PSE.02	Proximal sequence element (PSE) of RNA polymerase III-transcribed genes	0.73	46 - 64	(-)	0.892	0.835	attgcCATAaattcaaaac
V$SORY/HMGA.01	HMGA family of architectural transcription factors (HMGA1, HMGA2)	0.88	49 - 65	(+)	1.000	0.892	ttgAATTtatggcaatc
V$THAP/THAP1.01	THAP domain containing, apoptosis associated protein	0.90	53 - 63	(+)	1.000	0.902	atttatGGCAa
V$OCT1/OCT1.04	Octamer-binding factor 1	0.80	54 - 68	(+)	1.000	0.838	ttTATGgcaatcctc
V$RBPF/RBPJK.02	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.94	74 - 88	(-)	1.000	0.940	aactTGGGaagctga
V$ETSF/ELK1.02	Elk-1	0.91	78 - 98	(-)	1.000	0.955	agaatcccGGAActtgggaag
V$NRSF/NRSE.01	Neural-restrictive-silencer-element	0.67	81 - 101	(-)	1.000	0.674	cctagaatccCGGAacttggg
V$STAT/STAT1.01	Signal transducer and activator of transcription 1	0.77	81 - 99	(-)	1.000	0.807	tagaatcccGGAActtggg
V$STAT/STAT3.01	Signal transducer and activator of transcription 3	0.75	83 - 101	(+)	1.000	0.750	caagTTCCgggattctagg
V$STAT/STAT5.01	STAT5: signal transducer and activator of transcription 5	0.89	89 - 107	(-)	0.945	0.945	tactTTCCtagaatcccgg
V$BCL6/BCL6.02	POZ/zinc finger protein, transcriptional repressor, translocations observed in diffuse large cell lymphoma	0.77	90 - 106	(-)	1.000	0.901	actttccTAGAatcccg
V$STAT/STAT5.01	STAT5: signal transducer and activator of transcription 5	0.89	91 - 109	(+)	1.000	0.949	gggaTTCTaggaaagtacc
V$NFKB/NFKAPPAB.02	NF-kappaB	0.82	99 - 111	(-)	0.750	0.862	gtGGTActttcct
V$RU49/RU49.01	Zinc finger transcription factor RU49 (zinc finger proliferation 1 - Zipro 1). RU49 exhibits a strong preference for binding to tandem repeats of the minimal RU49 consensus binding site.	0.98	103 - 109	(+)	1.000	1.000	aAGTAcc
V$CLOX/CDPCR3.01	Cut-like homeodomain protein	0.73	106 - 124	(+)	1.000	0.896	taccactcatttctATGGt
V$PLZF/PLZF.01	Promyelocytic leukemia zink finger (TF with nine Krueppel-like zink fingers)	0.86	138 - 152	(-)	1.000	0.913	acaTACAgtcctggg
V$TEAF/TEF1.01	TEF-1 related muscle factor	0.84	138 - 150	(-)	0.750	0.840	ataCAGTcctggg
V$GREF/ARE.01	Androgene receptor binding site, IR3 sites	0.80	139 - 157	(+)	1.000	0.814	ccaggactgtaTGTTatgc
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	139 - 157	(-)	0.956	0.902	gcataacatacaGTCCtgg
V$BRNF/BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS-1)	0.74	142 - 160	(-)	1.000	0.778	atagCATAacatacagtcc
V$PARF/DBP.01	Albumin D-box binding protein	0.84	147 - 163	(+)	1.000	0.902	gtatgTTATgctatgca
V$OCT1/OCT1.02	Octamer-binding factor 1	0.85	156 - 170	(+)	1.000	0.857	gctATGCaagcactc
V$RXRF/LXRE.02	Highly conserved DR1 element selected by LXRbeta/RXR heterodimers	0.69	162 - 186	(-)	0.826	0.692	atgtaGTTCaatggtagagtgcttg
V$RORA/RORA2.01	RAR-related orphan receptor alpha2	0.82	168 - 190	(-)	0.750	0.847	ggagatgtaGTTCaatggtagag
V$BARB/BARBIE.01	Barbiturate-inducible element	0.88	186 - 200	(-)	1.000	0.919	ttcaAAAGctggaga
V$CHRF/CHR.01	Cell cycle gene homology region (CDE/CHR tandem elements regulate cell cycle dependent repression)	0.92	192 - 204	(+)	1.000	0.934	gcttTTGAacttc

V$ETSF/ELK1.01	Elk-1	0.81	193 - 213	(-)	1.000	0.810	ttcttaaaGGAAgttcaaaag
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	196 - 214	(-)	1.000	0.914	attcttaaaGGAAgttcaa
V$GKLF/GKLF.02	Gut-enriched Krueppel-like factor	0.96	199 - 211	(-)	1.000	0.971	cttAAAGGaagtt
V$HOXF/HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	0.88	200 - 216	(-)	1.000	0.898	atattctTAAAggaagt
V$FKHD/FHXB.01	Fork head homologous X binds DNA with a dual sequence specificity (FHXA and FHXB)	0.83	204 - 220	(+)	0.818	0.849	cctttaAGAAtatttat
V$OCTP/OCT1P.01	Octamer-binding factor 1, POU-specific domain	0.86	207 - 219	(-)	1.000	0.910	taaATATtcttaa
V$FKHD/HNF3B.01	Hepatocyte nuclear factor 3beta (FOXA2)	0.94	209 - 225	(-)	1.000	0.986	gtaaaataAATAttctt
V$NKXH/NKX31.01	Prostate-specific homeodomain protein NKX3.1	0.84	210 - 224	(-)	0.760	0.844	taaaatAAATattct
V$EVI1/EVI1.03	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.79	212 - 228	(-)	0.750	0.795	aaggtAAAAtaatatt
V$MYBL/VMYB.01	v-Myb	0.88	224 - 236	(-)	0.865	0.882	cacAACTgaaggt
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	239 - 253	(-)	0.750	0.884	acaTCCCcccacata
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	244 - 252	(+)	1.000	0.995	ggGGGGatg
V$TEAF/TEF1.01	TEF-1 related muscle factor	0.84	255 - 267	(-)	0.750	0.840	ctaCACTcctgtg
V$OAZF/ROAZ.01	Rat C2H2 Zn finger protein involved in olfactory neuronal differentiation	0.73	265 - 281	(+)	1.000	0.764	taGCACcctcagatgtg
V$AP1R/BACH2.01	Bach2 bound TRE	0.89	269 - 293	(+)	0.813	0.916	accctcagaTGTGtcatatcccca
V$RP58/RP58.01	Zinc finger protein RP58 (ZNF238), associated preferentially with heterochromatin	0.84	271 - 283	(-)	1.000	0.880	gacaCATCtgagg
V$SRFF/SRF.02	Serum response factor	0.84	286 - 304	(-)	0.822	0.857	aactcCAGAtctgggggat
V$SRFF/SRF.02	Serum response factor	0.84	287 - 305	(+)	0.822	0.883	tccccCAGAtctggagtta
V$RXRF/VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	0.79	296 - 320	(+)	0.952	0.808	tctGGAGttacaggaggttgtgagc
V$PARF/VBP.01	PAR-type chicken vitellogenin promoter-binding protein	0.86	299 - 315	(-)	1.000	0.866	caacctcctGTAActcc
V$NF1F/NF1.03	Non-palindromic nuclear factor I binding sites	0.92	309 - 329	(+)	1.000	0.978	gaggttgtgagctGCCAagta
V$SRFF/SRF.02	Serum response factor	0.84	318 - 336	(-)	1.000	0.898	gcaccCATActtggcagct
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	327 - 349	(-)	1.000	0.918	ggctttcCCCCcagcacccatac
V$NR2F/HPF1.01	HepG2-specific P450 2C factor-1, DR1 sites	0.78	333 - 357	(+)	1.000	0.802	gtgctgggggggAAAGcccaggctcc
V$INSM/INSM1.01	Zinc finger protein insulinoma-associated 1 (IA-1) functions as a transcriptional repressor	0.90	334 - 346	(+)	1.000	0.921	tgctgGGGGgaaa
V$IKRS/IK3.01	Ikaros 3, potential regulator of lymphocyte differentiation	0.84	337 - 349	(+)	1.000	0.846	tggggGGAAagcc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	338 - 346	(+)	1.000	0.995	ggGGGGaaa
V$NFKB/NFKAPPAB.01	NF-kappaB	0.89	339 - 351	(+)	1.000	0.906	ggGGGAaagccca
V$NFKB/CREL.01	c-Rel	0.91	341 - 353	(-)	1.000	0.988	cctgggctTTCCc
V$PERO/PPAR_RXR.02	PPAR/RXR heterodimers, DR1 sites	0.69	351 - 373	(+)	1.000	0.717	aggctccctgtaAAAGatcattg
V$TBPF/TATA.02	Mammalian C-type LTR TATA box	0.89	356 - 372	(+)	1.000	0.904	cctgTAAAagatcatt
V$SORY/SOX5.01	Sox-5	0.87	363 - 379	(-)	1.000	0.991	cttaaaCAATgatcttt
V$FKHD/FREAC2.01	Fork head related activator-2 (FOXF2)	0.84	367 - 383	(-)	1.000	0.912	gctgctTAAAcaatgat
V$TBPF/ATATA.01	Avian C-type LTR TATA box	0.78	369 - 385	(+)	1.000	0.795	cattgttTAAGcagcat
V$AP4R/PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class B bHLH factors, forms heterodimers with E12	0.86	378 - 394	(+)	0.882	0.917	agcAGCAtatgtgtggc
V$NR2F/HNF4.03	Hepatic nuclear factor 4, DR1 sites	0.83	388 - 412	(+)	0.833	0.901	gtgtggcggtCAGAggacaactttg
V$RXRF/RAR_RXR.01	Retinoic acid receptor / retinoid X receptor heterodimer, DR1 sites	0.78	390 - 414	(+)	0.769	0.850	gtggcggtcagAGGAcaactttggg
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	400 - 422	(-)	1.000	0.836	accaacTCCCcaaagttgtcctc
V$MYT1/MYT1.02	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.88	401 - 413	(-)	1.000	0.893	ccaAAGTtgtcct
V$LEFF/LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.86	428 - 444	(-)	1.000	0.880	ggtcctaCAAAggtaga
V$RXRF/LXRE.02	Highly conserved DR1 element selected by LXRbeta/RXR heterodimers	0.69	444 - 468	(-)	0.782	0.755	cttgaGATCagagctctatctctgg

V$EREF/ER.02	Canonical palindromic estrogen response element (ERE), IR3 sites	0.81	677 - 695	(+)	1.000	0.872	aaagGTCAgcatggcctt
V$EREF/ER.02	Canonical palindromic estrogen response element (ERE), IR3 sites	0.81	677 - 695	(-)	0.767	0.816	aaggGCCAtgctgacttt
V$ETSF/ELF2.01	Ets - family member ELF-2 (NERF1a)	0.90	689 - 709	(-)	1.000	0.939	tccgttcaGGAAgcaagggcc
V$HEAT/HSF1.01	Heat shock factor 1	0.84	690 - 714	(+)	0.857	0.842	gcccttgcttccTGAAcggaggcag
V$GKLF/GKLF.01	Gut-enriched Krueppel-like factor	0.86	691 - 703	(-)	1.000	0.914	caggaagcaAGGG
V$MYBL/VMYB.05	v-Myb, variant of AMV v-myb	0.90	701 - 713	(+)	1.000	0.932	ctgAACGgaggca
V$BRAC/BRACH.01	Brachyury	0.66	742 - 762	(-)	0.750	0.790	ctaccatctAGCTgtgaagtc
V$BRAC/BRACH.01	Brachyury	0.66	745 - 765	(+)	0.750	0.715	ttcacagctAGATggtagagg
V$HOXH/MEIS1A_HOXA9.01	Meis1a and Hoxa9 form heterodimeric binding complexes on target DNA	0.77	746 - 760	(+)	0.760	0.770	TCACagctagatggt
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	751 - 761	(-)	1.000	0.963	taCCATctagc
V$ZFIA/ZID.01	Zinc finger with interaction domain	0.85	755 - 767	(-)	0.770	0.853	tgCCTCtaccatc
V$HESF/HELT.01	Hey-like bHLH-transcriptional repressor	0.91	789 - 803	(+)	1.000	0.925	atagCACGaggcagg
V$EBOX/MYCMAX.03	MYC-MAX binding sites	0.91	790 - 802	(-)	0.982	0.917	ctgcctCGTGcta
V$CHRE/CHREBP_MLX.01	Carbohydrate response element binding protein (CHREBP) and Max-like protein X (Mlx) bind as heterodimers to glucose-responsive promoters	0.83	793 - 809	(+)	1.000	0.877	CACGaggcaggattgtg
V$RXRF/CAR_RXR.01	Constitutive androstane receptor / retinoid X receptor heterodimer, DR4 sites	0.75	803 - 827	(-)	0.750	0.764	aaaggGGACaaaggaggacacaatc
V$NR2F/HNF4.01	Hepatic nuclear factor 4, DR1 sites	0.82	805 - 829	(-)	1.000	0.870	ctaaagggaCAAAggaggacacaa
V$PERO/PPAR_RXR.02	PPAR/RXR heterodimers, DR1 sites	0.69	808 - 830	(-)	1.000	0.693	gctaaaggggacAAAGgaggaca
V$LEFF/LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.86	810 - 826	(-)	1.000	0.867	aaggggaCAAAggagga
V$SNAP/PSE.01	Proximal sequence element (PSE) of RNA polymerase II-transcribed snRNA genes	0.75	819 - 837	(+)	0.838	0.819	gTCCCctttagcagaacag
V$GREF/GRE.01	Glucocorticoid receptor, C2C2 zinc finger protein binds glucocorticoid dependent to GREs, IR3 sites	0.85	829 - 847	(-)	1.000	0.872	tcagtggtccctGTTCtgc
V$P53F/P53.02	Tumor suppressor p53 (5' half site)	0.91	847 - 869	(+)	1.000	0.948	aggaccacaactgggCATGcctt
V$SRFF/SRF.02	Serum response factor	0.84	847 - 865	(+)	0.866	0.865	aggacCACAactgggcatg
V$P53F/P53.01	Tumor suppressor p53	0.73	848 - 870	(-)	1.000	0.746	gaaggCATGcccagttgtggtcc
V$CP2F/CP2.02	LBP-1c (leader-binding protein-1c), LSF (late SV40 factor), CP2, SEF (SAA3 enhancer factor)	0.84	855 - 873	(+)	1.000	0.843	aACTGggcatgccttctct
V$P53F/P53.02	Tumor suppressor p53 (5' half site)	0.91	858 - 880	(-)	1.000	0.959	gacagacagagaaggCATGccca
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	866 - 884	(+)	0.956	0.897	ccttctctgtctGTCCcat
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	871 - 891	(+)	0.750	0.721	tctgtcTGTCccatcccccctg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	889 - 901	(+)	1.000	0.900	ctgcGAGGagcag
V$AP4R/PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class B bHLH factors, forms heterodimers with E12	0.86	894 - 910	(+)	0.882	0.872	aggAGCAgatgcaggcc
V$SRFF/SRF.03	Serum response factor	0.79	904 - 922	(-)	0.868	0.875	agcacctaatAAGGcctgc
V$SRFF/SRF.03	Serum response factor	0.79	905 - 923	(+)	0.754	0.851	caggccttatTAGGtgcta
V$RBPF/RBPJK.01	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.84	923 - 937	(+)	1.000	0.843	atgcTGGGagcctgg
V$THAP/THAP1.01	THAP domain containing, apoptosis associated protein	0.90	949 - 959	(+)	1.000	0.937	agtgttGGCAg
V$NKXH/HMX3.01	H6 homeodomain HMX3/Nkx5.1 transcription factor	0.89	959 - 973	(-)	1.000	0.945	acatccAAGTgggcc
V$NR2F/HPF1.01	HepG2-specific P450 2C factor-1, DR1 sites	0.78	965 - 989	(-)	1.000	0.846	atgaagagcagAAAGtacatccaag
V$GREF/ARE.01	Androgene receptor binding site, IR3 sites	0.80	969 - 987	(+)	0.750	0.834	gatgtactttcTGCTcttc
V$GCMF/GCM1.01	Glial cells missing homolog 1, chorion-specific transcription factor GCMa	0.85	1001 - 1011	(+)	1.000	0.925	gtCCCTcatag
V$RXRF/RAR_RXR.01	Retinoic acid receptor / retinoid X receptor heterodimer, DR1 sites	0.78	1011 - 1035	(+)	0.807	0.780	gttatgcccacAGGGcagagaagag
V$YY1F/YY1.02	Yin and Yang 1 repressor sites	0.94	1041 - 1059	(-)	1.000	0.945	agacaCCATctccaaaaga
V$PAX5/PAX5.03	PAX5 paired domain protein	0.80	1052 - 1080	(+)	0.789	0.833	tggtgTCTCtgtggaatagggtcaggatg

V$SNAP/PSE.02	Proximal sequence element (PSE) of RNA polymerase III-transcribed genes	0.73	1058 - 1076	(-)	1.000	0.732	ctgacCCTAttccacagag
V$RORA/REV-ERBA.01	Orphan nuclear receptor rev-erb alpha (NR1D1)	0.88	1062 - 1084	(+)	1.000	0.919	gtggaataggGTCAggatgtcag
V$EREF/ER.01	Estrogen receptor, IR3 sites	0.83	1068 - 1086	(+)	1.000	0.853	taggGTCAggatgtcagtg
V$ETSF/PDEF.01	Prostate-derived Ets factor	0.93	1068 - 1088	(+)	1.000	0.937	tagggtcaGGATgtcagtgtt
V$MEF3/MEF3.01	MEF3 binding site, present in skeletal muscle-specific transcriptional enhancers	0.89	1070 - 1082	(+)	1.000	0.899	gggTCAGgatgtc
V$TALE/TGIF.01	TG-interacting factor belonging to TALE class of homeodomain factors	1.00	1076 - 1086	(+)	1.000	1.000	ggatGTCAgtg
V$CSEN/DREAM.01	Downstream regulatory element-antagonist modulator, Ca2+-binding protein of the neuronal calcium sensors family that binds DRE (downstream regulatory element) sites as a tetramer	0.95	1078 - 1088	(+)	1.000	0.964	atGTCAgtgtt
V$FKHD/FREAC4.01	Fork head related activator-4 (FOXD1)	0.78	1080 - 1096	(-)	1.000	0.824	cctgagaaAACActgac
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	1095 - 1113	(+)	0.944	0.856	ggtCCCCaagtgtctggct
V$NKXH/HMX3.01	H6 homeodomain HMX3/Nkx5.1 transcription factor	0.89	1096 - 1110	(+)	1.000	0.890	gtccccAAGTgtctg
V$EBOX/USF.04	Upstream stimulating factor 1/2	0.90	1098 - 1110	(-)	0.851	0.935	cagaCACTtgggg
V$AP4R/TH1E47.01	Thing1/E47 heterodimer, TH1 bHLH member specific expression in a variety of embryonic tissues	0.93	1102 - 1118	(-)	1.000	0.949	ataggagCCAGacactt
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	1106 - 1114	(+)	1.000	0.994	GTCTggctc
V$GATA/GATA1.01	GATA-binding factor 1	0.96	1111 - 1123	(-)	1.000	0.968	ctgtGATAggagc
V$EVI1/EVI1.05	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.81	1121 - 1137	(+)	0.750	0.813	cagagaaCATActttcc
V$GREF/PRE.01	Progesterone receptor binding site, IR3 sites	0.84	1122 - 1140	(-)	1.000	0.904	tccggaaagtaTGTTctct
V$ETSF/ELK1.02	Elk-1	0.91	1125 - 1145	(-)	1.000	0.955	ccctgtccGGAAagtatgttc
V$HOXF/NANOG.01	Homeobox transcription factor Nanog	0.94	1145 - 1161	(-)	1.000	0.952	cactgAATGgcgccagc
V$CAAT/NFY.02	Nuclear factor Y (Y-box binding factor)	0.83	1148 - 1162	(+)	0.750	0.833	ggcgCCATtcagtga
V$SORY/HBP1.01	HMG box-containing protein 1	0.86	1148 - 1164	(-)	1.000	0.880	gttcactgAATGgcgcc
V$STAT/STAT5.01	STAT5: signal transducer and activator of transcription 5	0.89	1149 - 1167	(-)	0.845	0.890	ccagTTCActgaatggcgc
V$STAT/STAT5.01	STAT5: signal transducer and activator of transcription 5	0.89	1151 - 1169	(+)	0.845	0.890	gccaTTCAgtgaactgggc
V$NR2F/TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	0.76	1154 - 1178	(-)	0.829	0.775	gaaggaaatgcccaGTTCactgaat
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	1154 - 1172	(-)	0.777	0.831	aatGCCCagttcactgaat
V$NFKB/CREL.01	c-Rel	0.91	1164 - 1176	(+)	1.000	0.969	ctgggcatTTCCt
V$BRAC/BRACH.01	Brachyury	0.66	1190 - 1210	(-)	0.750	0.677	tttgcagccAGGAgttaggtg
V$PAX6/PAX4_PD.01	PAX4 paired domain binding site	0.91	1192 - 1210	(-)	0.965	0.916	tttGCAGccaggagttagg
V$HEAT/HSF2.02	Heat shock factor 2	0.95	1216 - 1240	(-)	1.000	0.965	ttgctaggttccAGAAaactcctag
V$HEAT/HSF1.01	Heat shock factor 1	0.84	1217 - 1241	(+)	0.952	0.878	taggagttttctGGAAcctagcaac
V$STAT/STAT1.01	Signal transducer and activator of transcription 1	0.77	1218 - 1236	(-)	0.767	0.779	taggttccaGAAAactcct
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	1220 - 1238	(+)	1.000	0.895	gagttttctGGAAcctagc
V$XBBF/RFX1.01	X-box binding protein RFX1	0.89	1227 - 1245	(+)	1.000	0.942	ctggaacctaGCAActcac
V$ETSF/CETS1P54.01	c-Ets-1(p54)	0.92	1239 - 1259	(+)	0.901	0.920	aactcaCAGGaaacaatggaa
V$CLOX/CDPCR3.01	Cut-like homeodomain protein	0.73	1240 - 1258	(+)	1.000	0.730	actcacaggaaacaATGGa
V$FKHD/FKHRL1.01	Fkh-domain factor FKHRL1 (FOXO)	0.83	1242 - 1258	(+)	1.000	0.846	tcacaggaAACAatgga
V$SORY/SOX5.01	Sox-5	0.87	1246 - 1262	(+)	1.000	0.988	aggaaaCAATggaaact
V$XBBF/RFX1.02	X-box binding protein RFX1	0.90	1246 - 1264	(+)	0.881	0.919	aggaaacaatgGAAActtg
V$IRFF/ISRE.01	Interferon-stimulated response element	0.81	1247 - 1267	(+)	1.000	0.849	ggaaacaatgGAAActtgggt
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1251 - 1269	(+)	1.000	0.810	acaatgGAAActtgggttt

V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	1253 - 1271	(+)	1.000	0.842	aatGGAAAacttgggtttgt
V$AP1F/AP1.02	Activator protein 1	0.87	1290 - 1300	(-)	1.000	0.905	tttGAGTgatg
V$EKLF/EKLF.01	Erythroid krueppel like factor (EKLF)	0.89	1294 - 1310	(+)	1.000	0.911	actcaaaGGGGTtttcct
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	1294 - 1312	(-)	1.000	0.976	tgaGGAAAaacccttgagt
V$GKLF/GKLF.02	Gut-enriched Krueppel-like factor	0.96	1295 - 1307	(+)	1.000	0.986	ctcAAAGggtttt
V$NFKB/CREL.01	c-Rel	0.91	1298 - 1310	(+)	1.000	0.970	aaagggttTTCCt
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	1300 - 1318	(-)	1.000	0.882	tgcctttgaGGAAaaccct
V$BCL6/BCL6.01	POZ/zinc finger protein, transcriptional repressor, translocations observed in diffuse large cell lymphoma	0.76	1303 - 1319	(+)	1.000	0.762	gttTTCCtcaaaggcac
V$LEFF/LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.94	1304 - 1320	(+)	1.000	0.943	ttttcctCAAAggcaca
V$GKLF/GKLF.02	Gut-enriched Krueppel-like factor	0.96	1309 - 1321	(+)	1.000	0.970	ctcAAAGgcacac
V$MOKF/MOK2.02	Ribonucleoprotein associated zinc finger protein MOK-2 (human)	0.98	1309 - 1329	(-)	1.000	0.991	aagtatgtgtgtgCCTTtgag
V$MYBL/CMYB.02	c-Myb, important in hematopoesis, cellular equivalent to avian myoblastosis virus oncogene v-myb	0.96	1325 - 1337	(-)	1.000	0.963	aaTAACtgaagta
V$MEF2/MEF2.06	Myocyte-specific enhancer factor 2	0.87	1327 - 1349	(-)	1.000	0.898	ggtggagagaaAAATaactgaag
V$HNF1/HNF1.01	Hepatic nuclear factor 1	0.80	1331 - 1347	(+)	1.000	0.814	aGTTAttttttctctcca
V$E2FF/E2F.01	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.75	1334 - 1350	(-)	1.000	0.790	gggtggagaGAAAaata
V$DICE/DICE.01	Downstream Immunoglobulin Control Element, interacting factor: BEN (also termed Mus-TRD1 and WBSCR11)	0.80	1337 - 1351	(+)	1.000	0.802	ttttCTCTccaccca
V$HOXF/GSH2.01	Homeodomain transcription factor Gsh-2	0.95	1342 - 1358	(-)	1.000	0.976	aggcTAATgggtggaga
V$PDX1/ISL1.01	Pancreatic and intestinal lim-homeodomain factor	0.82	1343 - 1363	(-)	1.000	0.828	gccccaggcTAATgggtggag
V$AP2F/AP2.01	Activator protein 2	0.90	1352 - 1366	(+)	1.000	0.975	ttaGCCTggggcttc
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	1352 - 1366	(-)	0.905	0.921	gaaGCCCcaggctaa
V$CP2F/CP2.02	LBP-1c (leader-binding protein-1c), LSF (late SV40 factor), CP2, SEF (SAA3 enhancer factor)	0.84	1355 - 1373	(+)	0.833	0.853	gCCTGgggcttcctggaaa
V$ETSF/ETS1.01	c-Ets-1 binding site	0.92	1355 - 1375	(-)	1.000	0.937	aatttccaGGAAgccccaggc
V$NFKB/CREL.01	c-Rel	0.91	1356 - 1368	(+)	1.000	0.937	cctggggcTTCCt
V$HEAT/HSF1.01	Heat shock factor 1	0.84	1357 - 1381	(+)	0.952	0.869	ctggggcttcctGGAAattttcagt
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	1358 - 1376	(-)	1.000	0.967	aaatttccaGGAAgcccca
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	1360 - 1378	(+)	1.000	0.951	gggcttcctGGAAattttc
V$BCL6/BCL6.02	POZ/zinc finger protein, transcriptional repressor, translocations observed in diffuse large cell lymphoma	0.77	1361 - 1377	(+)	0.800	0.888	ggcttccTGGAaatttt
V$SORY/HMGIY.01	HMGI(Y) high-mobility-group protein I (Y), architectural transcription factor organizing the framework of a nuclear protein-DNA transcriptional complex	0.92	1363 - 1379	(-)	1.000	0.944	tgaaAATTtccaggaag
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	1366 - 1384	(+)	1.000	0.853	cctGGAAattttcagtcaa
V$SORY/HMGIY.01	HMGI(Y) high-mobility-group protein I (Y), architectural transcription factor organizing the framework of a nuclear protein-DNA transcriptional complex	0.92	1368 - 1384	(+)	1.000	0.954	tggaAATTttcagtcaa
V$FKHD/XFD3.01	Xenopus fork head domain factor 3 (FoxA2a)	0.82	1375 - 1391	(+)	0.782	0.869	tttcagtcAAAAaagg
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	1395 - 1411	(+)	0.766	0.834	ccctGGGTaggtggtaa
V$HOXF/HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	0.88	1402 - 1418	(+)	1.000	0.927	taggtggTAAAgacaca
V$FKHD/FREAC3.01	Fork head related activator-3 (FOXC1)	0.84	1403 - 1419	(+)	1.000	0.855	aggtgGTAAagacacac
V$EKLF/BKLF.01	Basic krueppel-like factor (KLF3)	0.95	1407 - 1423	(-)	1.000	0.953	tgGGGTgtgtctttacc
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	1411 - 1425	(-)	1.000	1.000	gctGGGGtgtgtctt
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	1412 - 1428	(-)	1.000	0.943	ggagctGGGGtgtgtct
V$P53F/P53.05	Tumor suppressor p53	0.78	1417 - 1439	(-)	1.000	0.802	cacaCAAGcctggagctggggtg

V$AHRR/AHRARNT.02	Aryl hydrocarbon / Arnt heterodimers, fixed core	0.77	1425 - 1449	(+)	0.750	0.784	ctccaggcttGTGTgtctgcccctg
V$ZNFP/SZF1.01	SZF1, hematopoietic progenitor-restricted KRAB-zinc finger protein	0.82	1446 - 1470	(+)	0.875	0.824	cctGGGAtgcagcagggttgcctca
V$PAX6/PAX4_PD.01	PAX4 paired domain binding site	0.91	1454 - 1472	(+)	0.965	0.935	gcaGCAGggttgcctcaat
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	1460 - 1480	(-)	1.000	0.854	tcacTGGCattgaggcaaccc
V$NF1F/NF1.03	Non-palindromic nuclear factor I binding sites	0.92	1460 - 1480	(+)	1.000	0.962	gggttgcctcaatGCCAgtga
V$AP1R/TCF11MAFG.01	TCF11/MafG heterodimers, binding to subclass of AP1 sites	0.81	1469 - 1493	(+)	1.000	0.861	caatgccagTGACttggcaagaaca
V$XBBF/MIF1.01	MIBP-1 / RFX1 complex	0.76	1473 - 1491	(-)	0.800	0.782	ttcttgccaaGTCActggc
V$GREF/GRE.01	Glucocorticoid receptor, C2C2 zinc finger protein binds glucocorticoid dependent to GREs, IR3 sites	0.85	1486 - 1504	(-)	1.000	0.905	tcagtctcaggtGTTCttg
V$MYOD/E47.02	E47 homodimer	0.93	1486 - 1502	(-)	1.000	0.953	agtctcaGGTGttcttg
V$AP4R/PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class B bHLH factors, forms heterodimers with E12	0.86	1487 - 1503	(+)	1.000	0.863	aagAACAcctgagactg
V$ETSF/GABP.01	GABP: GA binding protein	0.86	1503 - 1523	(+)	1.000	0.897	gaggctctGGAAgagccttgt
V$MOKF/MOK2.02	Ribonucleoprotein associated zinc finger protein MOK-2 (human)	0.98	1505 - 1525	(+)	1.000	0.990	ggctctggaagagCCTTgtct
V$P53F/P53.05	Tumor suppressor p53	0.78	1515 - 1537	(-)	0.760	0.798	atacCCAGgttcagacaaggctc
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	1516 - 1536	(+)	0.750	0.795	agccttgtctgaaCCTGggta
V$FKHD/FREAC4.01	Fork head related activator-4 (FOXD1)	0.78	1529 - 1545	(+)	0.750	0.808	cctgggtaTACAaagtg
V$HOXC/HOX_PBX.01	HOX/PBX binding sites	0.81	1557 - 1573	(+)	1.000	0.893	ggacTGATgtatgtgaa
V$AP1R/NFE2.01	NF-E2 p45	0.85	1561 - 1585	(-)	1.000	0.868	gacccactCTGAttcacatacatca
V$OCT1/OCT.01	Octamer binding site (OCT1/OCT2)	0.78	1564 - 1578	(+)	0.795	0.867	tgtATGTgaatcaga
V$PBXC/PBX1_MEIS1.02	Binding site for a Pbx1/Meis1 heterodimer	0.77	1564 - 1580	(-)	1.000	0.845	actcTGATtcacataca
V$AP1F/AP1.01	Activator protein 1	0.94	1568 - 1578	(+)	0.880	0.961	tgtgAATCaga
V$GFI1/GFI1.02	Growth factor independence 1	0.90	1569 - 1583	(+)	1.000	0.905	gtgAATCagagtggg
V$AP1R/BACH1.01	BTB/POZ-bZIP transcription factor BACH1 forms heterodimers with the small Maf protein family	0.82	1579 - 1603	(+)	1.000	0.844	gtgggtctaTGAGtgattcagatcg
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	1580 - 1600	(-)	0.750	0.718	tctgaaTCACtcatagaccca
V$AP1R/NFE2.01	NF-E2 p45	0.85	1583 - 1607	(-)	1.000	0.868	cagacgatCTGAatcactcatagac
V$AP1F/AP1.02	Activator protein 1	0.87	1586 - 1596	(+)	1.000	0.900	tatGAGTgatt
V$AP1F/AP1.01	Activator protein 1	0.94	1590 - 1600	(+)	0.833	0.950	agtgATTCaga
V$EVI1/EVI1.06	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.83	1622 - 1638	(-)	1.000	0.860	tggacaAGATggtgctc
V$GATA/GATA1.01	GATA-binding factor 1	0.96	1635 - 1647	(-)	1.000	0.961	gcgtGATActgga
V$HOXC/HOX_PBX.01	HOX/PBX binding sites	0.81	1648 - 1664	(+)	0.944	0.839	actgGGATgaatgtgtg
V$SORY/HBP1.01	HMG box-containing protein 1	0.86	1649 - 1665	(+)	1.000	0.878	ctgggatgAATGtgtgg
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	1650 - 1668	(-)	1.000	0.840	cctCCACacattcatccca
V$TEAF/TEF1.01	TEF-1 related muscle factor	0.84	1651 - 1663	(-)	1.000	0.866	acaCATTcatccc
V$HOXF/NANOG.01	Homeobox transcription factor Nanog	0.94	1652 - 1668	(+)	1.000	0.964	ggatgAATGtgtggagg
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	1664 - 1682	(+)	1.000	0.994	ggaGGAAaaatgtagaaca
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	1675 - 1693	(-)	1.000	0.911	accagcctatatGTTCtac
V$AP1R/TCF11MAFG.01	TCF11/MafG heterodimers, binding to subclass of AP1 sites	0.81	1692 - 1716	(+)	0.777	0.827	gtgagtgtgTGAAaaagcacataag
V$FKHD/XFD3.01	Xenopus fork head domain factor 3 (FoxA2a)	0.82	1695 - 1711	(+)	0.782	0.828	agtgtgtgAAAAagcac
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	1719 - 1737	(-)	0.869	0.926	ctcacacattttGTGCtag
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	1729 - 1749	(+)	1.000	0.972	atgtgtgaGGAActgggtgtg
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	1739 - 1753	(+)	0.750	0.878	aacTGGGtgtgtgat
V$CAAT/NFY.01	Nuclear factor Y (Y-box binding factor)	0.90	1746 - 1760	(-)	1.000	0.928	cacaCCAAtcacaca

V$HOXC/PBX1.01	Homeo domain factor Pbx-1	0.78	1746 - 1762	(+)	1.000	0.815	tgtgtGATTggtgtgtg
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	1762 - 1770	(-)	1.000	1.000	GTCTggatc
V$RBPF/RBPJK.02	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.94	1783 - 1797	(+)	1.000	0.950	tcagTGGGaagagat
V$HMTB/MTBF.01	Muscle-specific Mt binding site	0.90	1794 - 1802	(+)	1.000	0.900	agatATTTg
V$ZNFP/ZBRK1.01	Transcription factor with 8 central zinc fingers and an N-terminal KRAB domain	0.77	1800 - 1824	(-)	0.898	0.796	ctcaggtaACAGagctttgtggcaa
V$NR2F/TR4.02	TR4 homodimer, DR1 site	0.75	1803 - 1827	(-)	1.000	0.761	caactcAGGTaacagagctttgtgg
V$CREB/E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	0.80	1809 - 1829	(-)	1.000	0.822	tccaactcagGTAAcagagct
V$PARF/VBP.01	PAR-type chicken vitellogenin promoter-binding protein	0.86	1812 - 1828	(-)	1.000	0.890	ccaactcagGTAAcaga
V$ZFHX/AREB6.01	AREB6 (Atp1a1 regulatory element binding factor 6)	0.93	1813 - 1825	(+)	1.000	0.955	ctgttACCTgagt
V$STAT/STAT1.01	Signal transducer and activator of transcription 1	0.77	1825 - 1843	(+)	1.000	0.778	ttggatcccGGAAcccaca
V$ETSF/ELK1.02	Elk-1	0.91	1826 - 1846	(+)	1.000	0.950	tggatcccGGAAcccacatgc
V$GCMF/GCM1.01	Glial cells missing homolog 1, chorion-specific transcription factor GCMa	0.85	1836 - 1846	(+)	0.789	0.902	aaCCCAcatgc
V$PDX1/ISL1.01	Pancreatic and intestinal lim-homeodomain factor	0.82	1848 - 1868	(-)	1.000	0.883	tttggaaagTAATggtctcct
V$HOXF/GSH1.01	Homeobox transcription factor Gsh-1	0.85	1850 - 1866	(-)	1.000	0.885	tggaaagTAATggtctc
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	1850 - 1868	(-)	1.000	0.865	tttGGAAagtaatggtctc
V$RXRF/LXRE.02	Highly conserved DR1 element selected by LXRbeta/RXR heterodimers	0.69	1861 - 1885	(-)	0.782	0.720	gtggaGCTCagaggtgttttggaaa
V$NR2F/TR4.01	TR4 homodimer, DR1 site	0.72	1863 - 1887	(-)	1.000	0.722	atgtggagctcagAGGTgttttgga
V$MITF/MIT.01	MIT (microphthalmia transcription factor) and TFE3	0.81	1878 - 1896	(+)	1.000	0.820	agctccaCATGtgcactgg
V$HESF/DEC2.01	Basic helix-loop-helix protein known as Dec2 or Sharp2	0.96	1880 - 1894	(-)	0.903	0.965	agtgcaCATGtggag
V$RP58/RP58.01	Zinc finger protein RP58 (ZNF238), associated preferentially with heterochromatin	0.84	1880 - 1892	(-)	0.757	0.845	tgcaCATGtggag
V$PAX6/PAX4_PD.01	PAX4 paired domain binding site	0.91	1887 - 1905	(+)	1.000	0.917	tgtGCACtggggcatgtat
V$P53F/P53.02	Tumor suppressor p53 (5' half site)	0.91	1895 - 1917	(-)	1.000	0.919	gcgtgcgcctacataCATGcccc
V$TBPF/ATATA.01	Avian C-type LTR TATA box	0.78	1900 - 1916	(+)	0.750	0.781	atgtatgTAGGcgcacg
V$GZF1/GZF1.01	GDNF-inducible zinc finger protein 1 (ZNF336)	0.73	1902 - 1914	(-)	1.000	0.878	TGCGcctacatac
V$AHRR/AHRARNT.01	Aryl hydrocarbon receptor / Arnt heterodimers	0.92	1903 - 1927	(-)	1.000	0.926	gcgcgcgcgcgCGTGcgcctacata
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1906 - 1922	(-)	1.000	0.941	cgcGCGCgtgcgcctac
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1907 - 1923	(+)	1.000	0.912	tagGCGCacgcgcgcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1907 - 1917	(-)	1.000	0.960	gcgtGCGCcta
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1908 - 1924	(-)	1.000	0.847	cgcGCGCgcgtgcgcct
V$HESF/HELT.01	Hey-like bHLH-transcriptional repressor	0.91	1909 - 1923	(+)	1.000	0.957	ggcgCACGcgcgcgc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1909 - 1925	(+)	0.750	0.843	ggcGCACgcgcgcgcgc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1910 - 1926	(-)	1.000	0.838	cgcGCGCgcgcgtgcgc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1911 - 1927	(+)	0.750	0.838	cgcACGCgcgcgcgcgc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1912 - 1928	(-)	1.000	0.936	cgcGCGCgcgcgcgtgc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1913 - 1929	(+)	1.000	0.936	cacGCGCgcgcgcgcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1913 - 1923	(-)	1.000	0.966	gcgcGCGCgtg

V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1914 - 1930	(-)	1.000	0.942	cgcGCGCgcgcgcgcgt
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1915 - 1931	(+)	1.000	0.942	cgcGCGCgcgcgcgcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1915 - 1925	(-)	1.000	0.968	gcgcGCGCgcg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1916 - 1932	(-)	1.000	0.933	tgcGCGCgcgcgcgcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1916 - 1926	(+)	1.000	0.968	gcgcGCGCgcg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1917 - 1933	(+)	1.000	0.942	cgcGCGCgcgcgcgcac
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1917 - 1927	(-)	1.000	0.968	gcgcGCGCgcg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1918 - 1934	(-)	1.000	0.900	tgtGCGCgcgcgcgcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1918 - 1928	(+)	1.000	0.968	gcgcGCGCgcg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1919 - 1935	(+)	1.000	0.942	cgcGCGCgcgcgcacac
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1919 - 1929	(-)	1.000	0.968	gcgcGCGCgcg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1920 - 1936	(-)	0.750	0.796	tgtGTGCgcgcgcgcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1920 - 1930	(+)	1.000	0.968	gcgcGCGCgcg
V$E2FF/E2F.03	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.85	1921 - 1937	(+)	1.000	0.865	cgcgcGCGCgcacacac
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	1921 - 1937	(+)	1.000	0.838	cgcGCGCgcgcacacac
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1921 - 1931	(-)	1.000	0.968	gcgcGCGCgcg
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1922 - 1932	(+)	1.000	0.968	gcgcGCGCgca
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1923 - 1933	(-)	1.000	1.000	gtgcGCGCgcg
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1924 - 1934	(+)	1.000	0.952	gcgcGCGCaca
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	1925 - 1935	(-)	1.000	0.997	gtgtGCGCgcg
V$DICE/DICE.01	Downstream Immunoglobulin Control Element, interacting factor: BEN (also termed Mus-TRD1 and WBSCR11)	0.80	1975 - 1989	(-)	0.891	0.817	tgttTTCTgtacctc
V$FKHD/ILF1.01	Winged-helix transcription factor IL-2 enhancer binding factor (ILF), forkhead box K2 (FOXK2)	0.98	1978 - 1994	(+)	1.000	0.988	gtacagaaAACAaacac
V$FKHD/HFH3.01	HNF-3/Fkh Homolog 3 (FOXI1, Freac-6)	0.97	1982 - 1998	(+)	1.000	0.977	agaaaacAAACacaata
V$CABL/CABL.01	Multifunctional c-Abl src type tyrosine kinase	0.97	1984 - 1994	(+)	1.000	0.973	aaAACAaacac
V$FKHD/FHXB.01	Fork head homologous X binds DNA with a dual sequence specificity (FHXA and FHXB)	0.83	1987 - 2003	(+)	0.909	0.844	acaaacACAAtaaataa
V$HOXF/HOXA9.01	Member of the vertebrate HOX - cluster of homeobox factors	0.87	1990 - 2006	(+)	0.780	0.890	aacacaataAATAaaag
V$FAST/FAST1.01	FAST-1 SMAD interacting protein	0.81	1991 - 2005	(-)	1.000	0.829	ttttattTATTgtgt
V$ATBF/ATBF1.01	AT-binding transcription factor 1	0.79	1995 - 2011	(-)	0.782	0.807	agtggctttttATTTatt
V$TBPF/TATA.01	Cellular and viral TATA box elements	0.90	2003 - 2019	(-)	1.000	0.936	agctaTAAAgtggcttt
V$NKXH/TTF1.01	Thyroid transcription factor-1 (TTF1) binding site	0.92	2024 - 2038	(-)	1.000	0.939	agactCAAGcatccc
V$CEBP/CEBP.02	CCAAT/enhancer binding protein	0.92	2034 - 2048	(+)	0.885	0.926	agtctgtaGAAAggt
V$FKHD/FREAC2.01	Fork head related activator-2 (FOXF2)	0.84	2042 - 2058	(+)	1.000	0.991	gaaaggTAAAcaaaaag
V$SORY/SRY.01	Sex-determining region Y gene product	0.93	2046 - 2062	(+)	1.000	0.940	ggtaaACAAaaaggtaa
V$NBRE/NBRE.01	Monomers of the nur subfamily of nuclear receptors (nur77, nurr1, nor-1)	0.86	2052 - 2066	(+)	1.000	0.867	caaaAAGGtaaacag
V$RXRF/VDR_RXR.04	Bipartite binding site of VDR/RXR heterodimers, DR3 sites	0.79	2052 - 2076	(+)	0.750	0.814	caaaaaGGTAaacaggtacatggag
V$FKHD/ILF1.01	Winged-helix transcription factor IL-2 enhancer binding factor (ILF), forkhead box K2 (FOXK2)	0.98	2054 - 2070	(+)	1.000	0.981	aaaaggtaAACAggtac
V$ZFHX/AREB6.01	AREB6 (Atp1a1 regulatory element binding factor 6)	0.93	2061 - 2073	(-)	1.000	0.953	catgtACCTgttt

V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	2066 - 2076	(-)	1.000	0.967	ctCCATgtacc
V$HEN1/HEN1.01	HEN1	0.82	2079 - 2099	(-)	1.000	0.830	atgcactCAGCtgctcacatc
V$AP4R/AP4.02	Activator protein 4	0.92	2081 - 2097	(-)	1.000	0.962	gcactcAGCTgctcaca
V$MITF/MIT.01	MIT (microphthalmia transcription factor) and TFE3	0.81	2090 - 2108	(+)	1.000	0.818	ctgagtgCATGtgagatcc
V$CHRE/CHREBP_MLX.01	Carbohydrate response element binding protein (CHREBP) and Max-like protein X (Mlx) bind as heterodimers to glucose-responsive promoters	0.83	2097 - 2113	(+)	0.944	0.831	CATGtgagatcccc
V$SNAP/PSE.01	Proximal sequence element (PSE) of RNA polymerase II-transcribed snRNA genes	0.75	2105 - 2123	(+)	0.838	0.778	aTCCCcctctctcgaaaac
V$E2FF/E2F.01	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.75	2109 - 2125	(+)	1.000	0.810	ccctctctcGAAAactg
V$DICE/DICE.01	Downstream Immunoglobulin Control Element, interacting factor: BEN (also termed Mus-TRD1 and WBSCR11)	0.80	2134 - 2148	(-)	0.783	0.816	cgtgCTCCacacgga
V$CREB/XBP1.01	X-box-binding protein 1	0.88	2138 - 2158	(+)	1.000	0.886	tgtggagcACGTggtgtgaag
V$AP4R/PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class B bHLH factors, forms heterodimers with E12	0.86	2140 - 2156	(+)	0.882	0.860	tggAGCAcgtggtgtga
V$HIFF/ARNT.01	AhR nuclear translocator homodimers	0.89	2140 - 2152	(+)	1.000	0.959	tggagcaCGTGgt
V$EBOX/MYCMAX.02	c-Myc/Max heterodimer	0.92	2141 - 2153	(+)	1.000	0.997	ggagcaCGTGgtg
V$HESF/HELT.01	Hey-like bHLH-transcriptional repressor	0.91	2141 - 2155	(+)	1.000	0.918	ggagCACGtggtgtg
V$EBOX/MYCMAX.02	c-Myc/Max heterodimer	0.92	2142 - 2154	(-)	1.000	0.990	acaccaCGTGctc
V$HIFF/ARNT.01	AhR nuclear translocator homodimers	0.89	2143 - 2155	(-)	1.000	0.946	cacaccaCGTGct
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	2145 - 2159	(-)	1.000	0.838	cctTCACaccacgtg
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2149 - 2171	(-)	1.000	0.877	gcacacgCCGCtccttcacacca
V$EGRF/EGR3.01	Early growth response gene 3 product	0.77	2160 - 2176	(+)	1.000	0.839	agcgGCGTgtgcggagg
V$RXRF/VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	0.79	2160 - 2184	(+)	0.761	0.803	agcGGCGtgtgcggagggctcgagg
V$HEAT/HSF1.02	Heat shock factor 1	0.75	2170 - 2194	(+)	1.000	0.759	gcggagggctCGAGgccctgccagg
V$ZFIA/ZID.01	Zinc finger with interaction domain	0.85	2175 - 2187	(+)	1.000	0.852	ggGCTCgaggccc
V$MYOD/TAL1_E2A.01	Complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1	0.98	2186 - 2202	(+)	1.000	0.984	cctgcCAGGtggcgtct
V$EBOX/USF.04	Upstream stimulating factor 1/2	0.90	2188 - 2200	(-)	0.829	0.928	acgcCACCtggca
V$NEUR/NEUROD1.01	DNA binding site for NEUROD1 (BETA-2 / E47 dimer)	0.83	2188 - 2200	(-)	0.767	0.855	acgcCACCtggca
V$HAND/HAND2_E12.01	Heterodimers of the bHLH transcription factors HAND2 (Thing2) and E12	0.75	2190 - 2204	(-)	1.000	0.766	tgagacGCCAcctgg
V$WHNF/WHN.01	Winged helix protein, involved in hair keratinization and thymus epithelium differentiation	0.95	2193 - 2203	(-)	1.000	0.954	gagACGCcacc
V$STAF/STAF.01	Se-Cys tRNA gene transcription activating factor	0.77	2208 - 2230	(+)	1.000	0.774	ctatCCCAcactccaagccacgt
V$P53F/P53.01	Tumor suppressor p53	0.73	2212 - 2234	(-)	0.792	0.731	ccagaCGTGgcttggagtgtggg
V$CREB/ATF6.02	Activating transcription factor 6, member of b-zip family, induced by ER stress	0.85	2218 - 2238	(-)	1.000	0.887	cacgccaGACGtggcttggag
V$HIFF/HIF1.02	Hypoxia inducible factor, bHLH / PAS protein family	0.93	2224 - 2236	(-)	1.000	0.971	cgccagaCGTGgc
V$MYBL/CMYB.02	c-Myb, important in hematopoesis, cellular equivalent to avian myoblastosis virus oncogene v-myb	0.96	2238 - 2250	(-)	0.989	0.963	ccCAACcggctcc
V$EVI1/MEL1.02	MEL1 (MDS1/EVI1-like gene 1) DNA-binding domain 2	0.99	2248 - 2264	(-)	1.000	0.994	gatgtggGATGaggccc
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	2250 - 2264	(+)	0.750	0.838	gccTCATcccacatc
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2264 - 2278	(-)	1.000	0.881	cCCCAatccccctcg
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	2277 - 2285	(-)	1.000	0.993	GTCTgggcc
V$MOKF/MOK2.02	Ribonucleoprotein associated zinc finger protein MOK-2 (human)	0.98	2283 - 2303	(-)	1.000	0.991	gcggccgactgtgCCTTtgtc

V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2298 - 2320	(+)	1.000	0.892	ggccgcgCCGCtcctccagagag
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2331 - 2353	(-)	1.000	0.914	gcggcggCCCCcgcctcctagcc
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2334 - 2348	(+)	0.771	0.883	taggAGGCgggggcc
V$PURA/PURALPHA.01	Purine-rich element binding protein A	0.97	2336 - 2348	(+)	1.000	0.991	ggAGGCgggggcc
V$AP4R/AP4.01	Activator protein 4	0.85	2344 - 2360	(-)	1.000	0.854	cccctCAGCggcggccc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2346 - 2368	(-)	1.000	0.929	ggccccgCCCCCtcagcggcggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2349 - 2371	(-)	1.000	0.980	cctggccCCGCcccctcagcggc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2351 - 2367	(+)	1.000	0.985	cgctgaggGGGCggggc
V$GCMF/GCM1.01	Glial cells missing homolog 1, chorion-specific transcription factor GCMa	0.85	2351 - 2361	(-)	1.000	0.857	ccCCCTcagcg
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2355 - 2369	(+)	1.000	1.000	gaggGGGCggggcca
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2357 - 2369	(+)	1.000	0.940	gggggcGGGGcca
V$P53F/P53.05	Tumor suppressor p53	0.78	2358 - 2380	(-)	1.000	0.812	ctaaCAAGacctggccccgcccc
V$INSM/INSM1.01	Zinc finger protein insulinoma-associated 1 (IA-1) functions as a transcriptional repressor	0.90	2375 - 2387	(+)	1.000	0.923	tgttaGGGGcgtg
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2377 - 2391	(+)	1.000	0.868	ttaGGGGcgtggtct
V$TBPF/MTATA.01	Muscle TATA box	0.84	2381 - 2397	(-)	0.777	0.852	ccataTAGAccacgccc
V$SRFF/SRF.01	Serum response factor	0.66	2383 - 2401	(-)	1.000	0.703	ctgaccaTATAgaccacgc
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	2389 - 2399	(-)	1.000	0.963	gaCCATataga
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	2395 - 2415	(+)	0.750	0.721	tggtcaGGACgcgttgcctcg
V$MEF3/MEF3.01	MEF3 binding site, present in skeletal muscle-specific transcriptional enhancers	0.89	2395 - 2407	(+)	1.000	0.927	tggTCAGgacgcg
V$WHNF/WHN.01	Winged helix protein, involved in hair keratinization and thymus epithelium differentiation	0.95	2400 - 2410	(+)	1.000	0.976	aggACGCgttg
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2404 - 2426	(-)	1.000	0.934	ggttccgCCCCCgaggcaacgcg
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	2407 - 2421	(+)	1.000	0.935	gttGCCTcgggggcg
V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2407 - 2429	(-)	1.000	0.946	ccaggttccgCCCCCgaggcaac
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2409 - 2425	(+)	1.000	0.923	tgcctcggGGGCggaac
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2413 - 2427	(+)	1.000	0.912	tcggGGGCggaacct
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2425 - 2439	(-)	1.000	0.808	cCCCAcaagaccagg
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	2431 - 2445	(-)	0.750	0.838	gccACACcccacaag
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2433 - 2447	(+)	1.000	0.942	tgtGGGGtgtggcta
V$EKLF/BKLF.01	Basic krueppel-like factor (KLF3)	0.95	2435 - 2451	(+)	1.000	0.979	tgGGGTgtggctaaatg
V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	2441 - 2455	(+)	0.750	0.822	gtggctAAATgtttg
V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	2446 - 2460	(-)	1.000	0.829	acctccAAACattta
V$SP1F/GC.01	GC box elements	0.88	2453 - 2467	(+)	0.872	0.892	ttggaGGTGgggcct
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2455 - 2467	(+)	1.000	0.900	ggaggtGGGGcct
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2480 - 2502	(-)	1.000	0.934	ggctccgCCCCCgaggcgccaag
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	2483 - 2497	(+)	1.000	0.940	ggcGCCTcgggggcg
V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2483 - 2505	(-)	1.000	0.949	tccggctccgCCCCCgaggcgcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2485 - 2501	(+)	1.000	0.939	cgcctcggGGGCggagc
V$SP1F/GC.01	GC box elements	0.88	2489 - 2503	(+)	1.000	0.957	tcgggGGCGgagccg
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2500 - 2522	(-)	1.000	0.932	cgcccccgCCCCCgggtctccggc

V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2503 - 2525	(-)	1.000	0.948	gcacgcccccgCCCCCcgggtctcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2505 - 2521	(+)	1.000	0.866	agacccggGGGCggggc
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2509 - 2523	(+)	1.000	1.000	ccggGGGCggggcgt
V$AHRR/AHRARNT.01	Aryl hydrocarbon receptor / Arnt heterodimers	0.92	2510 - 2534	(+)	1.000	0.934	cgggggcggggCGTGcacgggaggg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2510 - 2526	(+)	1.000	0.882	cgggggcgGGGCgtgca
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2511 - 2527	(+)	1.000	0.972	gggggcGGGGcgtgcac
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2511 - 2523	(+)	1.000	0.915	ggggggcGGGGcgt
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2514 - 2528	(+)	1.000	0.859	ggcGGGGcgtgcacg
V$HESF/HELT.01	Hey-like bHLH-transcriptional repressor	0.91	2521 - 2535	(+)	1.000	0.926	cgtgCACGggagggc
V$EGRF/CKROX.01	Collagen krox protein (zinc finger protein 67 - zfp67)	0.88	2524 - 2540	(+)	1.000	0.920	gcacGGGAgggcgggga
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2528 - 2542	(+)	1.000	0.934	gggaGGGCggggacg
V$E2FF/E2F1_DP2.01	E2F-1/DP-2 heterodimeric complex	0.78	2529 - 2545	(+)	1.000	0.801	ggagGGCGgggacggga
V$PURA/PURALPHA.01	Purine-rich element binding protein A	0.97	2529 - 2541	(+)	1.000	0.977	ggAGGGcggggac
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2530 - 2542	(+)	1.000	0.896	gagggcGGGGacg
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2534 - 2542	(+)	1.000	0.991	gcGGGGacg
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	2539 - 2561	(-)	1.000	0.753	caccccCCCAaccaactcccgtc
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2542 - 2556	(-)	1.000	0.889	cCCCAaccaactccc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2542 - 2564	(-)	1.000	0.947	ccccaccCCCCcaaccaactccc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2544 - 2566	(-)	1.000	0.935	ccccccaCCCCcccaaccaactc
V$INSM/INSM1.01	Zinc finger protein insulinoma-associated 1 (IA-1) functions as a transcriptional repressor	0.90	2548 - 2560	(+)	1.000	0.922	tggttGGGGgggt
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2549 - 2563	(-)	1.000	0.948	cccacccCCCCaacc
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2550 - 2566	(+)	1.000	0.927	gttgggGGGGtgggggg
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2550 - 2564	(-)	1.000	0.860	cCCCAccccccaac
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2551 - 2565	(+)	1.000	0.858	ttgGGGGggtgggggg

40 matches found in this sequence.

Table A.2 Genomatix Analysis of the Human Perlecan Promoter Region Published By Renato Iozzo (1997)

Individual binding sites in a promoter are NEVER sufficient to indicate transcriptional function. Functional assessment of binding sites can be carried out by our other tools, e.g. ModelInspector, Comparative Genomics, FrameWorker, BiblioSphere

If MatInspector does **not** identify a known site, please send an email to support@genomatix.de citing the corresponding paper!

Search Results (393 matches)

MatInspector Release professional 7.4.8, May 2007 **Wed Jun 27 16:31:53**

Solution parameters:

Sequence file: IozzoPaper.seq (2565 bp)
Family matches: yes
MatInspector library: Matrix Family Library Version 6.3 (March 2007)
Selected groups (core/matrix sim)
- ALL vertebrates.lib (0.75/Optimized)

Inspecting sequence IozzoPaper (1 - 2565):

Family/matrix	Further Information	Opt.	Position from - to	Str.	Core sim.	Matrix sim.	Sequence (red: ci-value > 60 capitals: core sequence)
V$SF1F/FTF.01	Alpha (1)-fetoprotein transcription factor (FTF), liver receptor homologue-1 (LRH-1)	0.94	12 - 24	(-)	1.000	0.960	tttcCAAGgcctt
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	17 - 35	(+)	1.000	0.890	cttGGAAaaatcctgccac
V$CIZF/NMP4.01	NMP4 (nuclear matrix protein 4) / CIZ (Cas-interacting zinc finger protein)	0.97	20 - 30	(+)	1.000	0.972	ggAAAAatcct
V$BTBF/KAISO.01	Transcription factor Kaiso, ZBTB33	0.92	25 - 35	(+)	1.000	0.992	aatcCTGCcac
V$EBOX/ATF6.01	Member of b-zip family, induced by ER damage/stress, binds to the ERSE in association with NF-Y	0.93	29 - 41	(+)	1.000	0.933	ctgCCACtagggc
V$HAND/HAND2_E12.01	Heterodimers of the bHLH transcription factors HAND2 (Thing2) and E12	0.75	38 - 52	(+)	1.000	0.758	gggctgGCCAcctgc
V$NF1F/NF1.01	Nuclear factor 1	0.82	38 - 58	(+)	0.763	0.851	gggCTGGccacctgccagctc
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	38 - 58	(-)	1.000	0.901	gagcTGGCaggtggccagccc
V$MYOD/E47.01	MyoD/E47 and MyoD/E12 dimers	0.92	40 - 56	(-)	1.000	0.953	gctgGCAGgtggccagc
V$HESF/HES1.02	Drosophila hairy and enhancer of split homologue 1 (HES-1)	0.87	41 - 55	(-)	0.750	0.873	ctggCAGGtggccag
V$NEUR/NEUROD1.01	DNA binding site for NEUROD1 (BETA-2 / E47 dimer)	0.83	42 - 54	(+)	0.767	0.905	tggcCACCtgcca
V$CREB/CJUN_ATF2.01	c-Jun/ATF2 heterodimers	0.99	52 - 72	(-)	1.000	0.991	ctccacTGACttcagagctgg
V$CREB/ATF2.01	Activating transcription factor 2	0.87	53 - 73	(+)	0.777	0.890	cagctcTGAAgtcagtggagt
V$PAX5/PAX5.01	B-cell-specific activator protein	0.79	57 - 85	(+)	0.857	0.799	tctgaaGTCAgtggagttttgaagccttt
V$CSEN/DREAM.01	Downstream regulatory element-antagonist modulator, Ca2+-binding protein of the neuronal calcium sensors family that binds DRE (downstream regulatory element) sites as a tetramer	0.95	61 - 71	(+)	1.000	0.963	aaGTCAgtgga
V$EVI1/MEL1.02	MEL1 (MDS1/EVI1-like gene 1) DNA-binding domain 2	0.99	82 - 98	(-)	1.000	0.990	cctgtccGATGagaaag
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	89 - 107	(-)	0.956	0.891	tggaaactccctGTCCgat
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	91 - 109	(-)	1.000	0.871	cttGGAAactccctgtccg
V$SP1F/BTEB3.01	Basic transcription element (BTE) binding protein, BTEB3, FKLF-2	0.93	93 - 107	(+)	1.000	0.958	gacagGGAGtttcca
V$NFKB/NFKAPPAB65.01	NF-kappaB (p65)	0.87	95 - 107	(+)	1.000	0.991	cagggagtTTCCa
V$CHRE/CHREBP_MLX.01	Carbohydrate response element binding protein (CHREBP) and Max-like protein X (Mlx) bind as heterodimers to glucose-responsive promoters	0.83	106 - 122	(+)	0.833	0.892	CAAGtgcaaacctggtg

V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	110 - 128	(+)	0.869	0.894	tgcaaacctggtGTACtct
V$NR2F/TR4.02	TR4 homodimer, DR1 site	0.75	115 - 139	(-)	0.777	0.751	catttgAGGGgagagtacaccaggt
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	126 - 138	(-)	1.000	0.908	atttGAGGggaga
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	126 - 134	(-)	1.000	0.991	gaGGGGaga
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	132 - 142	(-)	1.000	0.984	tcCCATttgag
V$GLIF/GLI1.01	Zinc finger transcription factor GLI1	0.87	134 - 148	(-)	1.000	0.929	gggacctCCCAtttg
V$NFKB/NFKAPPAB.01	NF-kappaB	0.89	137 - 149	(+)	1.000	0.937	atGGGAggtccct
V$NFKB/NFKAPPAB.01	NF-kappaB	0.89	138 - 150	(-)	1.000	0.938	caGGGAcctccca
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	139 - 161	(+)	1.000	0.874	gggaggTCCCtggggtggctgtg
V$EBOX/ATF6.01	Member of b-zip family, induced by ER damage/stress, binds to the ERSE in association with NF-Y	0.93	147 - 159	(-)	1.000	0.936	cagCCACcccagg
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	147 - 169	(-)	0.761	0.800	gcagccTCCAcagccaccccagg
V$GZF1/GZF1.01	GDNF-inducible zinc finger protein 1 (ZNF336)	0.73	167 - 179	(+)	0.750	0.798	TGCTcctctatca
V$GATA/GATA1.03	GATA-binding factor 1	0.95	170 - 182	(-)	1.000	0.955	gtctGATAgagga
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	183 - 205	(+)	1.000	0.844	ctcagcTCCCcagggccaagtc
V$P53F/P53.03	Tumor suppressor p53 (3' half site)	0.92	190 - 212	(+)	1.000	0.932	ccccaagggccaagtCATGtctc
V$ATBF/ATBF1.01	AT-binding transcription factor 1	0.79	235 - 251	(-)	0.782	0.790	tcttattagtATTTgtg
V$SATB/SATB1.01	Special AT-rich sequence-binding protein 1, predominantly expressed in thymocytes, binds to matrix attachment regions (MARs)	0.94	242 - 256	(+)	1.000	0.955	actAATAagagaaat
V$ATBF/ATBF1.01	AT-binding transcription factor 1	0.79	254 - 270	(+)	0.782	0.793	aatggctaccACTTatt
V$NKXH/NKX32.01	Homeodomain protein NKX3.2 (BAPX1, NKX3B, Bagpipe homolog)	0.96	259 - 273	(-)	1.000	0.968	tgaaataAGTGgtag
V$PPAR/PPARG.01	Pal3 motif, bound by a PPAR-gamma homodimer, IR3 sites	0.67	264 - 286	(-)	0.794	0.676	cacTTGGtaagcatgaaataagt
V$EBOX/USF.04	Upstream stimulating factor 1/2	0.90	278 - 290	(-)	0.851	0.942	cagaCACTtggta
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	278 - 298	(-)	0.750	0.804	agccatttcagacACTTggta
V$FKHD/ILF1.01	Winged-helix transcription factor IL-2 enhancer binding factor (ILF), forkhead box K2 (FOXK2)	0.98	295 - 311	(-)	1.000	0.987	ttttaaaaAACAcagcc
V$SATB/SATB1.01	Special AT-rich sequence-binding protein 1, predominantly expressed in thymocytes, binds to matrix attachment regions (MARs)	0.94	310 - 324	(-)	1.000	0.964	attAATAtatttctt
V$BRNF/BRN3.02	Brn-3, POU-IV protein class	0.89	314 - 332	(+)	1.000	0.913	aatatatTAATttatctta
V$OCT1/OCT1.06	Octamer-binding factor 1	0.81	314 - 328	(+)	1.000	0.891	aatatattAATTtat
V$EVI1/EVI1.04	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.73	315 - 331	(-)	0.750	0.733	aagataaattaaTATAt
V$LHXF/LHX3.01	Homeodomain binding site in LIM/Homeodomain factor LHX3	0.81	315 - 329	(+)	1.000	0.867	atataTTAAtttatc
V$HOMF/MSX.01	Homeodomain proteins MSX-1 and MSX-2	0.97	316 - 328	(+)	1.000	0.972	tatatTAATttat
V$RBIT/BRIGHT.01	Bright, B cell regulator of IgH transcription	0.92	317 - 329	(-)	1.000	0.956	gataaATTAatat
V$SORY/HMGA.01	HMGA family of architectural transcription factors (HMGA1, HMGA2)	0.88	319 - 335	(+)	1.000	0.903	attAATTtatcttaatt
V$EVI1/EVI1.03	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.79	320 - 336	(-)	1.000	0.795	gaattAAGAtaaattaa
V$GATA/GATA1.03	GATA-binding factor 1	0.95	321 - 333	(-)	1.000	0.961	ttaaGATAaatta
V$OCT1/OCT1.06	Octamer-binding factor 1	0.81	324 - 338	(+)	1.000	0.888	tttatcttAATTctc
V$SNAP/PSE.02	Proximal sequence element (PSE) of RNA polymerase III-transcribed genes	0.73	324 - 342	(+)	0.857	0.781	tttatCTTAattctcataa
V$NKXH/NKX25.02	Homeo domain factor Nkx-2.5/Csx, tinman homolog low affinity sites	0.88	326 - 340	(+)	1.000	0.971	tatctTAATtctcat

V$OCTB/TST1.01	POU-factor Tst-1/Oct-6	0.90	326 - 338	(-)	1.000	0.902	gagaATTAagata
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	328 - 346	(-)	0.807	0.876	gttgttatgAGAAttaaga
V$OCT1/OCT1.06	Octamer-binding factor 1	0.81	329 - 343	(-)	1.000	0.910	gttatgagAATTaag
V$PARF/DBP.01	Albumin D-box binding protein	0.84	331 - 347	(-)	1.000	0.862	tgttgTTATgagaatta
V$CREB/ATF.02	Activating transcription factor	0.83	357 - 377	(+)	0.750	0.832	acgtctTAACgttattctcat
V$MYBL/VMYB.05	v-Myb, variant of AMV v-myb	0.90	360 - 372	(-)	1.000	0.908	aatAACGttaaga
V$MYBL/VMYB.03	v-Myb, viral myb variant from transformed BM2 cells	0.87	361 - 373	(+)	1.000	0.885	cttAACGttattc
V$IRFF/IRF3.01	Interferon regulatory factor 3 (IRF-3)	0.85	365 - 385	(-)	0.758	0.850	tgtagaaaatGAGAataacgt
V$OCT1/OCT1.04	Octamer-binding factor 1	0.80	366 - 380	(-)	0.846	0.838	aaAATGagaataacg
V$GCNR/RTR.01	Retinoid receptor-related testis-associated receptor (GCNF/RTR), DR0 sites	0.81	400 - 418	(-)	1.000	0.838	cacatgtTCAAgttccatg
V$MITF/MIT.01	MIT (microphthalmia transcription factor) and TFE3	0.81	406 - 424	(+)	1.000	0.862	acttgaaCATGtgctcaac
V$AP4R/PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class B bHLH factors, forms heterodimers with E12	0.86	407 - 423	(-)	0.882	0.882	ttgAGCAcatgttcaag
V$EBOX/MYCMAX.02	c-Myc/Max heterodimer	0.92	410 - 422	(-)	0.860	0.936	tgagcaCATGttc
V$SORY/SOX5.01	Sox-5	0.87	467 - 483	(+)	1.000	0.990	tgagaaCAATacccgga
V$P53F/P53.05	Tumor suppressor p53	0.78	469 - 491	(+)	0.760	0.805	agaaCAATacccggacagggact
V$HEAT/HSF2.02	Heat shock factor 2	0.95	484 - 508	(-)	1.000	0.965	gaggtgtggggaAGAAtagtccctg
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	487 - 507	(-)	1.000	0.961	aggtgtggGGAAgaatagtcc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	495 - 503	(-)	1.000	1.000	gtGGGGaag
V$GATA/GATA1.03	GATA-binding factor 1	0.95	504 - 516	(-)	1.000	0.957	atctGATAgaggt
V$HOXF/CRX.01	Cone-rod homeobox-containing transcription factor / otx-like homeobox gene	0.94	506 - 522	(-)	1.000	0.952	ttctTAATctgatagag
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	529 - 549	(+)	1.000	0.907	GAGGgccaagattgggcgtcc
V$GABF/GAGA.01	GAGA-Box	0.78	551 - 575	(-)	0.750	0.780	cagggAGATaggggtggacagagga
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	556 - 574	(+)	1.000	0.835	tgtCCACccctatctccct
V$GATA/GATA1.01	GATA-binding factor 1	0.96	561 - 573	(-)	1.000	1.000	gggaGATAggggt
V$CP2F/CP2.01	CP2	0.90	616 - 634	(+)	1.000	0.920	acCTGGgttgggccaggc
V$MYBL/CMYB.01	c-Myb, important in hematopoesis, cellular equivalent to avian myoblastosis virus oncogene v-myb	0.90	629 - 641	(-)	1.000	0.997	gcCAACtgcctgg
V$IRFF/IRF4.02	Interferon regulatory factor 4	0.69	648 - 668	(-)	1.000	0.738	aacaGAAAttgcatccacggt
V$OCT1/OCT1.02	Octamer-binding factor 1	0.85	652 - 666	(+)	1.000	0.872	tggATGCaatttctg
V$CHOP/CHOP.01	Heterodimers of CHOP and C/EBPalpha	0.90	653 - 665	(+)	1.000	0.911	ggatGCAAtttct
V$GREF/PRE.01	Progesterone receptor binding site, IR3 sites	0.84	654 - 672	(+)	1.000	0.915	gatgcaatttcTGTTctt
V$MYBL/VMYB.01	v-Myb	0.88	659 - 671	(-)	0.817	0.882	aagAACAgaaatt
V$FKHD/FREAC2.01	Fork head related activator-2 (FOXF2)	0.84	663 - 679	(-)	1.000	0.859	gagttgTAAAgaacaga
V$PAX6/PAX6.02	PAX6 paired domain and homeodomain are required for binding to this site	0.87	678 - 696	(-)	1.000	0.871	tgtgtgggaCCAGctcaga
V$OCTP/OCT1P.01	Octamer-binding factor 1, POU-specific domain	0.86	695 - 707	(+)	1.000	0.914	caaATATgcccca
V$OCTP/OCT1P.01	Octamer-binding factor 1, POU-specific domain	0.86	708 - 720	(-)	1.000	0.914	aaaATATgccgtg
V$AIRE/AIRE.01	Autoimmune regulator	0.86	725 - 751	(+)	0.857	0.878	atatctttggagatagGGGAtctatc
V$GATA/GATA1.01	GATA-binding factor 1	0.96	733 - 745	(+)	1.000	1.000	tggaGATAgggga
V$MZF1/MZF1.02	Myeloid zinc finger protein MZF1	0.99	739 - 747	(+)	1.000	0.994	taGGGGatc
V$CLOX/CDPCR3HD.01	Cut-like homeodomain protein	0.94	740 - 758	(-)	1.000	0.978	catcccagataGATCccct

V$GATA/GATA1.03	GATA-binding factor 1	0.95	743 - 755	(-)	1.000	0.953	cccaGATAgatcc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	747 - 769	(-)	1.000	0.920	atcctgaCCCCCcatcccagatag
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	751 - 771	(-)	1.000	0.723	gcatccTGACccccatcccag
V$RORA/REV-ERBA.01	Orphan nuclear receptor rev-erb alpha (NR1D1)	0.88	752 - 774	(+)	1.000	0.913	tgggatggggGTCAggatgccag
V$GCMF/GCM1.01	Glial cells missing homolog 1, chorion-specific transcription factor GCMa	0.85	754 - 764	(-)	0.789	0.899	gaCCCCCcatcc
V$EREF/ER.01	Estrogen receptor, IR3 sites	0.83	758 - 776	(+)	1.000	0.849	ggggGTCAggatgccagtg
V$ETSF/PDEF.01	Prostate-derived Ets factor	0.93	758 - 778	(+)	1.000	0.942	gggggtcaGGATgccagtgtt
V$MEF3/MEF3.01	MEF3 binding site, present in skeletal muscle-specific transcriptional enhancers	0.89	760 - 772	(+)	1.000	0.946	gggTCAGgatgcc
V$MYOD/MYOD.01	Myogenic regulatory factor MyoD (myf3)	0.88	785 - 801	(-)	1.000	0.937	ccaGGCATctgggggat
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	785 - 803	(+)	0.944	0.835	atcCCCCagatgcctggat
V$NEUR/NEUROD1.01	DNA binding site for NEUROD1 (BETA-2 / E47 dimer)	0.83	788 - 800	(-)	1.000	0.832	caggCATCtgggg
V$DMTF/DMP1.01	Cyclin D-interacting myb-like protein, DMTF1 - cyclin D binding myb-like transcription factor 1	0.82	795 - 807	(+)	1.000	0.835	tgcctGGATgaaa
V$MOKF/MOK2.02	Ribonucleoprotein associated zinc finger protein MOK-2 (human)	0.98	802 - 822	(-)	1.000	1.000	aagcacattgggggCCTTtcat
V$BNCF/BNC.01	Basonuclin, cooperates with USF1 in rDNA PolI transcription)	0.85	806 - 824	(+)	0.789	0.864	aaqqccccaaTGTGcttqq
V$INSM/INSM1.01	Zinc finger protein insulinoma-associated 1 (IA-1) functions as a transcriptional repressor	0.90	832 - 844	(-)	1.000	0.925	tgataGGGGtccg
V$GATA/GATA1.01	GATA-binding factor 1	0.96	835 - 847	(-)	1.000	0.992	ctgtGATAgcggt
V$ETSF/ELK1.02	Elk-1	0.91	849 - 869	(-)	1.000	0.971	ctggctccGGAAgctatgttc
V$HESF/HES1.01	Drosophila hairy and enhancer of split homologue 1 (HES-1)	0.92	868 - 882	(+)	1.000	0.950	aggcctgGTGCcgcc
V$SP1F/SP1.02	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.85	873 - 887	(-)	1.000	0.867	cactGGGCggcacca
V$NR2F/TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	0.76	880 - 904	(-)	0.780	0.762	gaaggaaatgcccaGCTCactgggc
V$NFKB/CREL.01	c-Rel	0.91	890 - 902	(+)	1.000	0.969	ctgggcatTTCCt
V$NR2F/ARP1.01	Apolipoprotein AI regulatory protein 1, NR2F2, DR1 sites	0.82	899 - 923	(+)	0.809	0.861	tccttctgtccacaGCTCacctcac
V$RXRF/VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	0.79	900 - 924	(-)	0.952	0.791	agtGAGGtgagctgtggacagaagg
V$SREB/SREBP.01	Sterol regulatory element binding protein 1 and 2	0.90	912 - 926	(+)	1.000	0.952	agcTCACctcattcc
V$BRAC/BRACH.01	Brachyury	0.66	916 - 936	(-)	0.750	0.698	tttgcagccAGGAgtgaggtg
V$PAX6/PAX4_PD.01	PAX4 paired domain binding site	0.91	918 - 936	(-)	0.965	0.941	tttGCAGccaggagtgagg
V$OAZF/ROAZ.01	Rat C2H2 Zn finger protein involved in olfactory neuronal differentiation	0.73	919 - 935	(-)	0.750	0.794	ttGCAGccaggagtgag
V$HEAT/HSF1.01	Heat shock factor 1	0.84	941 - 965	(+)	0.952	0.878	gccatgagttctGGAAcctagcaac
V$XBBF/RFX1.01	X-box binding protein RFX1	0.89	951 - 969	(+)	1.000	0.942	ctggaacctaGCAActctc
V$MYT1/MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finger factor 1	0.92	958 - 970	(-)	1.000	0.958	tgagAGTTgctag
V$ETSF/CETS1P54.01	c-Ets-1(p54)	0.92	965 - 985	(+)	0.901	0.920	ctctcaCAGGaaacaatggaa
V$CLOX/CDPCR3.01	Cut-like homeodomain protein	0.73	966 - 984	(+)	1.000	0.730	ttcacaggaaacaATGGa
V$FKHD/FKHRL1.01	Fkh-domain factor FKHRL1 (FOXO)	0.83	968 - 984	(+)	1.000	0.846	tcacaggaAACAatgga
V$HEAT/HSF2.01	Heat shock factor 2	0.88	970 - 994	(+)	0.875	0.885	acaggaaacaatgGAAActtcagtt
V$SORY/SOX5.01	Sox-5	0.87	972 - 988	(+)	1.000	0.988	aggaaaCAATggaaact
V$XBBF/RFX1.02	X-box binding protein RFX1	0.90	972 - 990	(+)	0.881	0.919	aggaaacaatgGAAActtc
V$IRFF/ISRE.01	Interferon-stimulated response element	0.81	973 - 993	(+)	1.000	0.849	ggaaacaatgGAAActtcagt
V$HEAT/HSF1.03	Heat shock factor 1	0.76	979 - 1003	(-)	0.868	0.768	ggagaataaaacTGAAgtttccatt
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	979 - 997	(+)	1.000	0.875	aatGGAAAacttcagtttta
V$MYT1/MYT1.01	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.75	982 - 994	(+)	0.750	0.756	ggaAACTtcagtt
V$CDXF/CDX2.01	Cdx-2 mammalian caudal related intestinal transcr. factor	0.84	987 - 1005	(+)	1.000	0.849	cttcagtTTTAttctcctc
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	997 - 1009	(-)	1.000	0.909	agagGAGGagaat

V$MEF2/SL1.01	Member of the RSRF (related to serum response factor) protein family from Xenopus laevis	0.84	1001 - 1023	(+)	1.000	0.865	tcctcctCTATcattactcaaaa
V$GATA/GATA1.01	GATA-binding factor 1	0.96	1004 - 1016	(-)	1.000	0.960	taatGATAgagga
V$HOXF/HOX1-3.01	Hox-1.3, vertebrate homeobox protein	0.82	1004 - 1020	(-)	1.000	0.831	tgagTAATgatagagga
V$CLOX/CUT2.01	Cut repeat II	0.67	1005 - 1023	(-)	0.750	0.687	ttttgagtaATGAtagagg
V$PARF/TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	0.78	1009 - 1025	(+)	1.000	0.780	tatcaTTACtcaaaagg
V$PARF/HLF.01	Hepatic leukemia factor	0.84	1010 - 1026	(-)	1.000	0.858	acctttgaGTAAtgat
V$AP1F/AP1.02	Activator protein 1	0.87	1012 - 1022	(-)	1.000	0.934	tttGAGTaatg
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	1016 - 1034	(-)	1.000	0.976	tgaGGAAAaacctttgagt
V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	1020 - 1034	(-)	1.000	0.835	tgaggaAAACctttt
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	1022 - 1040	(-)	1.000	0.882	tagctttgaGGAAaacctt
V$LEFF/LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.94	1026 - 1042	(+)	1.000	0.949	ttttcctCAAAgctaca
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	1042 - 1060	(-)	1.000	0.964	agaGGAAaactatgtatgt
V$HOXC/HOX_PBX.01	HOX/PBX binding sites	0.81	1058 - 1074	(-)	1.000	0.831	aggcTGATgggtggaga
V$PAX6/PAX6.03	Pax-6 paired domain binding site	0.76	1058 - 1076	(+)	0.806	0.780	tctccACCCatcagcctcg
V$CAAT/ACAAT.01	Avian C-type LTR CCAAT box	0.83	1060 - 1074	(+)	0.750	0.874	tccaCCCCAtcagcct
V$HEAT/HSF2.01	Heat shock factor 2	0.88	1074 - 1098	(+)	0.875	0.902	tcgggctgccctgGAAAtttcaggc
V$HICF/HIC1.01	Hypermethylated in cancer 1, transcriptional repressor containing five Krüppel-like C2H2 zinc fingers, for optimal binding multiple binding sites are required.	0.93	1075 - 1087	(+)	1.000	0.945	cgggcTGCCctgg
V$STAT/STAT6.01	STAT6: signal transducer and activator of transcription 6	0.84	1076 - 1094	(+)	0.758	0.879	gggcTGCCctggaaatttc
V$PAX6/PAX6.02	PAX6 paired domain and homeodomain are required for binding to this site	0.87	1078 - 1096	(-)	1.000	0.949	ctgaaatttCCAGggcagc
V$HEAT/HSF1.01	Heat shock factor 1	0.84	1083 - 1107	(-)	0.857	0.886	ccttcttctgcTGAAatttccagg
V$SORY/HMGIY.01	HMGI(Y) high-mobility-group protein I (Y), architectural transcription factor organizing the framework of a nuclear protein-DNA transcriptional complex	0.92	1085 - 1101	(+)	1.000	0.948	tggaAATTtcaggcaga
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	1115 - 1135	(-)	0.750	0.798	gacatattcagtgCCTAttct
V$CP2F/CP2.02	LBP-1c (leader-binding protein-1c), LSF (late SV40 factor), CP2, SEF (SAA3 enhancer factor)	0.84	1123 - 1141	(+)	1.000	0.902	cACTGaatatgtctggggg
V$OCTP/OCT1P.01	Octamer-binding factor 1, POU-specific domain	0.86	1123 - 1135	(-)	1.000	0.903	gacATATtcagtg
V$INSM/INSM1.01	Zinc finger protein insulinoma-associated 1 (IA-1) functions as a transcriptional repressor	0.90	1132 - 1144	(+)	1.000	0.979	tgttcGGGGgctt
V$MYBL/CMYB.02	c-Myb, important in hematopoesis, cellular equivalent to avian myoblastosis virus oncogene v-myb	0.96	1158 - 1170	(-)	0.989	0.961	ccCAACcgcaggc
V$RXRF/RAR_RXR.03	Retinoic acid receptor / retinoid X receptor heterodimer, DR5 sites	0.81	1164 - 1188	(+)	1.000	0.933	ggttgGGTCagaaacagatcatggg
V$NR2F/TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	0.76	1166 - 1190	(+)	0.780	0.840	ttgggtcagaaaacGATCatgggggc
V$ZFHX/AREB6.04	AREB6 (Atp1a1 regulatory element binding factor 6)	0.98	1171 - 1183	(-)	1.000	1.000	gatctGTTTctga
V$GFI1/GFI1.01	Growth factor independence 1 zinc finger protein acts as transcriptional repressor	0.96	1186 - 1200	(-)	1.000	0.985	taaAATCacagcccc
V$HOXF/HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	0.88	1191 - 1207	(-)	1.000	0.934	tgggtggTAAAatcaca
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	1196 - 1212	(-)	1.000	0.927	tcgggTGGGtggtaaaa
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	1197 - 1211	(+)	0.827	0.914	tttaccaCCCAcccg
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	1198 - 1214	(-)	0.754	0.845	gtcGGGTgggtggtaa
V$AP4R/TAL1ALPHAE47.01	Tal-1alpha/E47 heterodimer	0.87	1208 - 1224	(-)	1.000	0.921	catcaCAGAtgctcggg
V$RXRF/CAR_RXR.01	Constitutive androstane receptor / retinoid X receptor heterodimer, DR4 sites	0.75	1236 - 1260	(-)	1.000	0.782	acttcaGGTCcagacagaccagaccc

V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	1238 - 1246	(+)	1.000	0.993	GTCTggtct
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	1247 - 1255	(+)	1.000	0.996	GTCTggacc
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	1261 - 1277	(+)	0.782	0.821	gtgtGAGTggtgtggt
V$IRFF/IRF4.02	Interferon regulatory factor 4	0.69	1264 - 1284	(-)	1.000	0.706	cccaGAAAccacaccaactca
V$HAML/AML3.01	Runt-related transcription factor 2 / CBFA1 (core-binding factor, runt domain, alpha subunit 1)	0.84	1269 - 1283	(+)	1.000	0.972	tggtGTGGtttctgg
V$GFI1/GFI1.02	Growth factor independence 1	0.90	1291 - 1305	(-)	1.000	0.991	ataAATCacagcccc
V$BRNF/BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS-1)	0.74	1292 - 1310	(-)	1.000	0.756	atcaCATAaatcacagccc
V$TBPF/MTATA.01	Muscle TATA box	0.84	1293 - 1309	(-)	1.000	0.862	tcacaTAAAtcacagcc
V$HOXC/PBX_HOXA9.01	PBX - HOXA9 binding site	0.79	1294 - 1310	(+)	1.000	0.954	gctgTGATTtatgtgat
V$HOXF/HOXA9.01	Member of the vertebrate HOX - cluster of homeobox factors	0.87	1295 - 1311	(-)	1.000	0.968	aatcacataAATCacag
V$PARF/TEF.01	Thyrotrophic embryonic factor	0.85	1297 - 1313	(+)	0.772	0.898	gtgatttatGTGAttca
V$PBXC/PBX1_MEIS1.01	Binding site for a Pbx1/Meis1 heterodimer	0.74	1303 - 1319	(+)	1.000	0.777	tatgTGATTcaaagttg
V$LEFF/LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.94	1305 - 1321	(+)	1.000	0.977	tgtgattCAAAgttggt
V$CHRF/CHR.01	Cell cycle gene homology region (CDE/CHR tandem elements regulate cell cycle dependent repression)	0.92	1306 - 1318	(-)	1.000	0.943	aactTTGAatcac
V$BARB/BARBIE.01	Barbiturate-inducible element	0.88	1309 - 1323	(+)	1.000	0.894	attcAAAGttggtgt
V$MYT1/MYT1.02	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.88	1311 - 1323	(+)	1.000	0.882	tcaAAGTtggtgt
V$HOXF/CRX.01	Cone-rod homeobox-containing transcription factor / otx-like homeobox gene	0.94	1322 - 1338	(-)	1.000	0.947	tgttTAATcattcacac
V$AP1F/AP1.02	Activator protein 1	0.87	1323 - 1333	(+)	1.000	0.897	tgtGAGTgatt
V$FKHD/FREAC2.01	Fork head related activator-2 (FOXF2)	0.84	1327 - 1343	(+)	1.000	0.881	agtgatTAAAcatggga
V$E2FF/E2F.01	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.75	1333 - 1349	(+)	1.000	0.762	taaacatggGAAAatgg
V$RBPF/RBPJK.02	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.94	1335 - 1349	(+)	1.000	0.965	aacaTGGGaaaatgg
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1336 - 1354	(+)	1.000	0.833	acatggGAAAatggtgcag
V$YY1F/YY1.02	Yin and Yang 1 repressor sites	0.94	1336 - 1354	(-)	1.000	0.962	ctgcaCCATttcccatgt
V$PTF1/PTF1.01	PTF1 binding sites are bipartite with an E-box and a TC-box (RBP-J/L) spaced one helical turn apart	0.76	1339 - 1359	(-)	1.000	0.854	cccaCCTGcaccatttccca
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	1341 - 1351	(-)	1.000	0.961	caCCATtttcc
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	1343 - 1365	(-)	1.000	0.749	gccccacCCCAcctgcaccatttt
V$MYOD/E47.01	MyoD/E47 and MyoD/E12 dimers	0.92	1347 - 1363	(+)	1.000	0.946	tggtGCAGgtgggtgg
V$EKLF/EKLF.01	Erythroid krueppel like factor (EKLF)	0.89	1351 - 1367	(+)	1.000	0.930	gcaggtgGGGTgggcag
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	1352 - 1366	(-)	0.750	0.849	tgcCCACcccacctg
V$RXRF/CAR_RXR.01	Constitutive androstane receptor / retinoid X receptor heterodimer, DR4 sites	0.75	1357 - 1381	(+)	0.770	0.805	ggggtGGGCagcttcagttcagtaac
V$CREB/E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	0.80	1367 - 1387	(+)	1.000	0.802	gctcagttcaGTAAcccagtg
V$PARF/HLF.01	Hepatic leukemia factor	0.84	1368 - 1384	(+)	1.000	0.856	ctcagttcaGTAAccca
V$PARF/TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	0.78	1369 - 1385	(-)	1.000	0.805	ctgggTTACtgaactga
V$FXRE/FXRE.01	Farnesoid X - activated receptor (RXR/FXR dimer), IR1 sites	0.80	1371 - 1383	(+)	0.750	0.832	AGTTcagtaaccc
V$FXRE/FXRE.01	Farnesoid X - activated receptor (RXR/FXR dimer), IR1 sites	0.80	1371 - 1383	(-)	0.875	0.881	GGGTtactgaact
V$CLOX/CDP.01	Cut-like homeodomain protein	0.75	1398 - 1416	(-)	1.000	0.793	acccacTAATcacagtgcc
V$GFI1/GFI1.02	Growth factor independence 1	0.90	1398 - 1412	(-)	1.000	0.914	actAATCacagtgcc
V$HOXF/CRX.01	Cone-rod homeobox-containing transcription factor / otx-like homeobox gene	0.94	1398 - 1414	(-)	1.000	0.961	ccacTAATcacagtgcc
V$PDX1/PDX1.01	Pdx1 (IDX1/IPF1) pancreatic and intestinal homeodomain TF	0.74	1399 - 1419	(-)	1.000	0.764	ctcacccacTAATcacagtgc
V$CAAT/ACAAT.01	Avian C-type LTR CCAAT box	0.83	1401 - 1415	(-)	0.750	0.874	cccaCTAAtcacagt

V$NR2F/TR4.02	TR4 homodimer, DR1 site	0.75	1417 - 1441	(+)	1.000	0.778	gagaacAGGTaaaagatacaggctg
V$ZFHX/AREB6.01	AREB6 (Atp1a1 regulatory element binding factor 6)	0.93	1419 - 1431	(-)	1.000	0.940	cttttACCTgttc
V$PLZF/PLZF.01	Promyelocytic leukemia zink finger (TF with nine Krueppel-like zink fingers)	0.86	1430 - 1444	(+)	1.000	0.897	agaTACAggctgagg
V$HOXF/GSC.01	Vertebrate bicoid-type homeodomain protein Goosecoid	0.98	1465 - 1481	(+)	1.000	0.983	cctgTAATcccatcact
V$RXRF/VDR_RXR.02	VDR/RXR Vitamin D receptor RXR heterodimer, DR3 sites	0.86	1484 - 1508	(+)	0.777	0.898	tgggagggcaagGCGGgcagatcac
V$E2FF/E2F1_DP2.01	E2F-1/DP-2 heterodimeric complex	0.78	1491 - 1507	(+)	1.000	0.810	gcaaGGCGggcagatca
V$NR2F/HNF4.02	Hepatic nuclear factor 4, DR2 sites	0.76	1497 - 1521	(+)	0.750	0.805	cgggcagatcaCAAGgtcaggagtt
V$EREF/ERR.01	Estrogen related receptor	0.87	1502 - 1520	(+)	1.000	0.957	agatcaCAAGGtcaggagt
V$RORA/RORA1.01	RAR-related orphan receptor alpha1	0.93	1502 - 1524	(+)	1.000	0.942	agatcacaaGGTCaggagttcga
V$SF1F/SF1.01	SF1 steroidogenic factor 1	0.95	1504 - 1516	(+)	1.000	0.996	atcaCAAGgtcag
V$NBRE/NBRE.01	Monomers of the nur subfamily of nuclear receptors (nur77, nurr1, nor-1)	0.86	1505 - 1519	(+)	1.000	0.932	tcacAAGGtcaggag
V$OCTB/TST1.01	POU-factor Tst-1/Oct-6	0.90	1540 - 1552	(-)	0.900	0.926	gggtTTTAccatg
V$HOXF/BARX2.01	Barx2, homeobox transcription factor that preferentially binds to paired TAAT motifs	0.95	1551 - 1567	(-)	1.000	0.953	ttttTAATagagatggg
V$MEF2/SL1.01	Member of the RSRF (related to serum response factor) protein family from Xenopus laevis	0.84	1551 - 1573	(+)	1.000	0.845	cccatctCTATtaaaatacaaa
V$HOXF/HOXC13.01	Homeodomain transcription factor HOXC13	0.91	1555 - 1571	(+)	1.000	0.933	tctctatTAAAaataca
V$BRNF/BRN2.01	Brn-2, POU-III protein class	0.86	1557 - 1575	(+)	0.966	0.883	tcTATTaaaaatacaaaaa
V$EBOX/ATF6.01	Member of b-zip family, induced by ER damage/stress, binds to the ERSE in association with NF-Y	0.93	1580 - 1592	(-)	1.000	0.938	ccaCCACgcctgg
V$RXRF/VDR_RXR.01	VDR/RXR Vitamin D receptor RXR heterodimer, DR3 sites	0.85	1612 - 1636	(+)	1.000	0.855	attcaggaggctGAGGccggagaat
V$BCL6/BCL6.01	POZ/zinc finger protein, transcriptional repressor, translocations observed in diffuse large cell lymphoma	0.76	1633 - 1649	(+)	0.756	0.769	gaaTTGCttgaacccgg
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	1642 - 1656	(-)	1.000	0.927	tccGCCTccggttc
V$PURA/PURALPHA.01	Purine-rich element binding protein A	0.97	1648 - 1660	(+)	1.000	0.985	ggAGGCggaggtt
V$NF1F/NF1.01	Nuclear factor 1	0.82	1655 - 1675	(-)	1.000	0.834	atcTTGGctcactgcaacctc
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	1655 - 1675	(+)	0.750	0.877	gaggTTGCagtgagccaagat
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	1674 - 1690	(-)	0.785	0.823	gagtGCGGtggtgggat
V$AHRR/AHR.01	Aryl hydrocarbon / dioxin receptor	0.78	1676 - 1700	(-)	0.750	0.801	ccccaggctgGAGTgcggtggtggg
V$CHRE/CHREBP_MLX.01	Carbohydrate response element binding protein (CHREBP) and Max-like protein X (Mlx) bind as heterodimers to glucose-responsive promoters	0.83	1681 - 1697	(-)	0.833	0.836	CAGGctggagtgcggtg
V$AP2F/AP2.01	Activator protein 2	0.90	1690 - 1704	(+)	1.000	0.901	ccaGCCTgggggacag
V$GATA/GATA1.06	Complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 2	0.96	1712 - 1724	(-)	1.000	0.970	ttttGATAaggag
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	1758 - 1778	(-)	0.750	0.744	gcccacatcattgCCTGcatg
V$ETSF/PU1.01	Pu.1 (Pu120) Ets-like transcription factor identified in lymphoid B-cells	0.89	1797 - 1817	(+)	1.000	0.899	cctgcagaGGAAtctatgtga
V$CLOX/CDP.02	Transcriptional repressor CDP	0.81	1800 - 1818	(+)	0.806	0.816	gcagaggaATCTatgtgaa
V$TEAF/TEF1.01	TEF-1 related muscle factor	0.84	1801 - 1813	(-)	0.750	0.855	ataGATTcctctg
V$CLOX/CDPCR3HD.01	Cut-like homeodomain protein	0.94	1803 - 1821	(-)	0.885	0.943	cttttcacataGATTcctc
V$WHNF/WHN.01	Winged helix protein, involved in hair keratinization and thymus epithelium differentiation	0.95	1818 - 1828	(-)	1.000	0.977	aggACGCcttt
V$EGRF/CKROX.01	Collagen krox protein (zinc finger protein 67 - zfp67)	0.88	1819 - 1835	(-)	1.000	0.920	gagcGGGAggacgcctt

V$CREB/CREB.02	cAMP-responsive element binding protein	0.89	1829 - 1849	(+)	1.000	0.920	cccgctccgTGACgttgcttg
V$CREB/ATF.01	Activating transcription factor	0.90	1832 - 1852	(+)	1.000	0.965	gctccgTGACgttgcttggga
V$E4FF/E4F.01	GLI-Krueppel-related transcription factor, regulator of adenovirus E4 promoter	0.82	1837 - 1849	(+)	1.000	0.887	gtgACGTtgcttg
V$PAX6/PAX6.01	Pax-6 paired domain binding site	0.75	1848 - 1866	(-)	1.000	0.768	cgatcACGCatacgtccca
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	1849 - 1869	(-)	0.750	0.747	cctcgaTCACgcatacgtccc
V$HIFF/HIF1.01	Hypoxia induced factor-1 (HIF-1)	0.87	1849 - 1861	(-)	1.000	0.895	acgcatACGTccc
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	1866 - 1886	(+)	1.000	0.885	GAGGggctgagtgtggtgtga
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	1875 - 1889	(-)	1.000	0.838	cccTCACaccacact
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	1907 - 1919	(+)	1.000	0.919	ggtgGAGGtgagc
V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	1915 - 1929	(-)	1.000	0.856	gcttccAAACgctca
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1928 - 1946	(+)	0.787	0.839	gcgagtTAAAgtgggcatg
V$HOMF/EN1.01	Homeobox protein engrailed (en-1)	0.77	1930 - 1942	(+)	0.826	0.801	gagTTAAagtggg
V$NKXH/HMX3.01	H6 homeodomain HMX3/Nkx5.1 transcription factor	0.89	1930 - 1944	(+)	1.000	0.894	gagttaAAGTgggca
V$PLZF/PLZF.01	Promyelocytic leukemia zink finger (TF with nine Krueppel-like zink fingers)	0.86	1931 - 1945	(+)	0.958	0.866	agtTAAAgtgggcat
V$P53F/P53.02	Tumor suppressor p53 (5' half site)	0.91	1939 - 1961	(-)	1.000	0.913	atcctcaccggctcaCATGccca
V$CAAT/NFY.01	Nuclear factor Y (Y-box binding factor)	0.90	1954 - 1968	(-)	1.000	0.927	ccaaCCAAtcctcac
V$ATBF/ATBF1.01	AT-binding transcription factor 1	0.79	1960 - 1976	(+)	0.782	0.793	attggttggtACTTcag
V$RU49/RU49.01	Zinc finger transcription factor RU49 (zinc finger proliferation 1 - Zipro 1). RU49 exhibits a strong preference for binding to tandem repeats of the minimal RU49 consensus binding site.	0.98	1967 - 1973	(-)	1.000	1.000	aAGTAcc
V$RBPF/RBPJK.01	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.84	1987 - 2001	(+)	0.789	0.871	agagTGTGaaagtgt
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1988 - 2006	(+)	1.000	0.858	gagtgtGAAAgtgttcccg
V$E2FF/E2F.01	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.75	1996 - 2012	(-)	0.750	0.769	gctacccggGAACactt
V$STAT/STAT6.01	STAT6: signal transducer and activator of transcription 6	0.84	1996 - 2014	(-)	0.793	0.876	gcgcTACCcgggaacactt
V$XBBF/RFX1.01	X-box binding protein RFX1	0.89	1996 - 2014	(-)	0.881	0.917	gcgctacccgGGAAcactt
V$IKRS/IK3.01	Ikaros 3, potential regulator of lymphocyte differentiation	0.84	1997 - 2009	(-)	1.000	0.876	acccgGGAAcact
V$OAZF/ROAZ.01	Rat C2H2 Zn finger protein involved in olfactory neuronal differentiation	0.73	2009 - 2025	(+)	0.750	0.735	taGCGCacaagtgtgtt
V$NKXH/HMX3.01	H6 homeodomain HMX3/Nkx5.1 transcription factor	0.89	2011 - 2025	(+)	1.000	0.906	gcgcacAAGTgtgtt
V$RUSH/SMARCA3.02	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.98	2014 - 2024	(-)	1.000	0.985	acacACTTgtg
V$E2FF/E2F.02	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.84	2024 - 2040	(+)	0.857	0.884	ttcgtgcggTAAAagtt
V$CLOX/CDPCR3.01	Cut-like homeodomain protein	0.73	2027 - 2045	(+)	1.000	0.747	gtgcggtaaaagttATGGt
V$BRNF/BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS-1)	0.74	2029 - 2047	(-)	1.000	0.778	acacCATAactttttaccgc
V$MYT1/MYT1.02	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.88	2033 - 2045	(+)	1.000	0.891	taaAAGTtatggt
V$GREF/GRE.01	Glucocorticoid receptor, C2C2 zinc finger protein binds glucocorticoid dependent to GREs, IR3 sites	0.85	2043 - 2061	(+)	1.000	0.910	ggtgtggaaggtGTTCttg
V$EKLF/BKLF.01	Basic krueppel-like factor (KLF3)	0.95	2059 - 2075	(+)	1.000	0.960	ttGGGTgtggaagttgg
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	2059 - 2079	(+)	1.000	0.974	ttgggtgtGGAAgttgggcgt
V$PAX6/PAX6.01	Pax-6 paired domain binding site	0.75	2066 - 2084	(-)	1.000	0.842	gtttcACGCccaacttcca
V$E2FF/RB_E2F1_DP1.01	RB/E2F-1/DP-1 heterotrimeric complex	0.71	2068 - 2084	(-)	0.765	0.809	gtttcACGCccaacttc
V$E2FF/E2F.02	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.84	2071 - 2087	(+)	1.000	0.909	gttggcgtGAAAcgtg
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	2074 - 2092	(+)	1.000	0.824	gggcgtGAAAcgtgtgagc

V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	2075 - 2089	(+)	1.000	0.887	ggcgtgAAACgtgtg
V$HIFF/ARNT.01	AhR nuclear translocator homodimers	0.89	2077 - 2089	(+)	1.000	0.892	cgtgaaaCGTGtg
V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	2080 - 2094	(-)	0.750	0.837	cggctcACACgtttc
V$NRSF/NRSE.01	Neural-restrictive-silencer-element	0.67	2085 - 2105	(+)	1.000	0.687	gtgtgagccgCGGAcgacagc
V$AP4R/AP4.01	Activator protein 4	0.85	2096 - 2112	(-)	1.000	0.882	gcacgCAGCtgtcgtcc
V$MYOD/E47.01	MyoD/E47 and MyoD/E12 dimers	0.92	2096 - 2112	(-)	1.000	0.925	gcacGCAGctgtcgtcc
V$AP4R/AP4.02	Activator protein 4	0.92	2097 - 2113	(+)	1.000	0.935	gacgacAGCTgcgtgcg
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	2103 - 2119	(+)	1.000	0.815	agctGCGTgcgtgtgag
V$EGRF/EGR3.01	Early growth response gene 3 product	0.77	2107 - 2123	(+)	1.000	0.772	gcgtGCGTgtgagcgtg
V$EGRF/EGR3.01	Early growth response gene 3 product	0.77	2115 - 2131	(+)	1.000	0.772	gtgaGCGTgggaaggag
V$RBPF/RBPJK.02	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.94	2118 - 2132	(+)	1.000	0.962	agcgTGGGaaggaga
V$HESF/HELT.01	Hey-like bHLH-transcriptional repressor	0.91	2163 - 2177	(-)	1.000	0.931	cccgCACGggcgact
V$AHRR/AHRARNT.01	Aryl hydrocarbon receptor / Arnt heterodimers	0.92	2168 - 2192	(+)	1.000	0.934	cccgtgcgggggCGTGcagggacgtg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2168 - 2184	(+)	1.000	0.865	cccgtgcgGGGGCgtgca
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2172 - 2186	(+)	1.000	0.859	tgcGGGGcgtgcagg
V$CREB/ATF6.02	Activating transcription factor 6, member of b-zip family, induced by ER stress	0.85	2180 - 2200	(+)	1.000	0.883	gtgcaggGACGtggaagtcgc
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	2184 - 2204	(+)	1.000	0.966	agggacgtGGAAgtcgccggc
V$DEAF/NUDR.01	NUDR (nuclear DEAF-1 related transcriptional regulator protein)	0.73	2188 - 2206	(-)	0.777	0.735	gcgCCGGcgacttccacgt
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2193 - 2209	(-)	1.000	0.819	cgcGCGCcggcgacttc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2194 - 2210	(+)	0.750	0.786	aagTCGCcggcgcgcgc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2199 - 2215	(-)	0.750	0.826	tccCCGCgcgcgccggc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2200 - 2216	(+)	1.000	0.788	ccgGCGCgcgcgggaa
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	2200 - 2210	(-)	1.000	0.963	gcgcGCGCcgg
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	2203 - 2213	(+)	1.000	0.966	gcgcGCGCggg
V$ETSF/ETS1.01	c-Ets-1 binding site	0.92	2205 - 2225	(+)	1.000	0.920	gcgcgcggGGAAgcgggggag
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2208 - 2230	(-)	1.000	0.936	cccggctCCCCcgcttccccgcg
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2209 - 2217	(+)	1.000	0.991	gcGGGGaag
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	2213 - 2229	(+)	0.785	0.809	ggaaGCGGgggagccgg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2234 - 2246	(+)	1.000	0.959	cgggGAGGcgaga
V$EBOX/MYCMAX.03	MYC-MAX binding sites	0.91	2245 - 2257	(-)	0.789	0.914	gggccaGGCGctc
V$P53F/P53.01	Tumor suppressor p53	0.73	2266 - 2288	(+)	1.000	0.759	catccCATGcccgggcccgggcc
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2270 - 2290	(-)	0.958	0.889	GGGGcccgggcccgggcatgg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2284 - 2304	(-)	0.958	0.907	GGGGcgggggaccgggggccc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2288 - 2310	(+)	1.000	0.932	ccccggtCCCCCgccccgtccca
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2289 - 2305	(-)	0.953	0.971	cggggCGGGggaccggg
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2291 - 2313	(+)	1.000	0.874	cggtcccCCGCcccgtcccatcc
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2293 - 2305	(-)	1.000	0.892	cggggcGGGGgac
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2293 - 2307	(-)	1.000	0.997	gacgGGGCgggggac
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2294 - 2310	(-)	1.000	0.936	tgggacGGGGcgggga

V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2289 - 2305	(-)	0.953	0.971	cggggCGGGggaccggg
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2291 - 2313	(+)	1.000	0.874	cggtcccCCGCcccgtcccatcc
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2293 - 2305	(-)	1.000	0.892	cggggcGGGGgac
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2293 - 2307	(-)	1.000	0.997	gacgGGGCgggggac
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2294 - 2310	(-)	1.000	0.936	tgggacGGGGcgggggga
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2295 - 2311	(-)	1.000	0.888	atgggacgGGGCggggg
V$E2FF/E2F.02	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.84	2327 - 2343	(-)	1.000	0.896	gctccccgcCAAAcccg
V$NF1F/NF1.01	Nuclear factor 1	0.82	2329 - 2349	(+)	1.000	0.838	ggtTTGGcggggagccgggcc
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	2329 - 2349	(-)	0.750	0.810	ggccCGGCtccccgccaaacc
V$E2FF/RB_E2F1_DP1.01	RB/E2F-1/DP-1 heterotrimeric complex	0.71	2330 - 2346	(+)	0.795	0.759	gtttgGCGGggagccgg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2331 - 2343	(+)	0.866	0.901	tttgGCGGggagc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2335 - 2343	(+)	1.000	0.991	gcGGGGagc
V$NRSF/NRSE.01	Neural-restrictive-silencer-element	0.67	2346 - 2366	(+)	0.782	0.681	ggccgggccgCGGCccgcgcg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2355 - 2375	(+)	0.833	0.887	GCGGcccgcgcgggggggctg
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	2358 - 2374	(+)	0.762	0.818	gcccGCGCgggggggct
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2360 - 2376	(+)	0.953	0.984	ccgcgCGGGgggctgg
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	2361 - 2383	(-)	1.000	0.817	tgggccCCCAgccccccgcgcg
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2362 - 2378	(+)	0.837	0.920	gcgcgGGGGggctgggg
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2363 - 2375	(+)	1.000	0.929	cgcgggGGGGctg
V$RXRF/VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	0.79	2363 - 2387	(+)	0.904	0.812	cgcGGGGgggctgggggcccagaca
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2364 - 2378	(-)	1.000	0.869	cCCCAgccccccgc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2364 - 2386	(-)	1.000	0.917	gtctgggCCCCcagccccccgc
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2366 - 2380	(+)	1.000	0.895	ggggGGGCtgggggc
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	2378 - 2386	(-)	1.000	0.993	GTCTgggcc
V$NRSF/NRSE.01	Neural-restrictive-silencer-element	0.67	2395 - 2415	(+)	0.782	0.673	agtagctgcgCGGCcggctgg
V$STAF/ZNF76_143.01	ZNF143 is the human ortholog of Xenopus Staf, ZNF76 is a DNA binding protein related to ZNF143 and Staf	0.76	2398 - 2420	(-)	1.000	0.783	tcgcCCCAgccggccgcgcagct
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2407 - 2423	(+)	1.000	0.892	gccggctgGGGCgagca
V$CP2F/CP2.01	CP2	0.90	2410 - 2428	(+)	1.000	0.920	ggCTGGggcgagcagagcc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2426 - 2448	(-)	1.000	0.949	cggaccgCCCCcgggccgcgggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2429 - 2451	(-)	1.000	0.885	ccacggaCCGCccccgggccgcg
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	2431 - 2445	(-)	0.905	0.922	accGCCCccgggccg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2431 - 2447	(+)	1.000	0.868	cggcccggGGGCggtcc
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2434 - 2448	(-)	1.000	0.956	cggaccgCCCCcggg
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2435 - 2449	(+)	1.000	0.894	ccggGGGCggtccgt
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2440 - 2462	(-)	1.000	0.900	ccaggccCCGCccacggaccgcc
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	2442 - 2458	(+)	0.751	0.887	cggtCCGTgggcggggc
V$SP1F/SP1.02	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.85	2446 - 2460	(+)	1.000	0.966	ccgtGGGCggggcct
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2448 - 2460	(+)	1.000	0.899	gtgggcGGGGcct
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	2457 - 2479	(-)	1.000	0.834	cgccccTCCCcggagcgccaggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2465 - 2487	(-)	1.000	0.882	ccccgaaCCGCcccctccccggag
V$SP1F/GC.01	GC box elements	0.88	2466 - 2480	(+)	0.876	0.933	tccggGGAGggggcgg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2467 - 2483	(+)	1.000	0.903	ccgggagGGGCggttc
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2468 - 2484	(+)	1.000	0.963	cgggaGGGGcggttcg

V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2468 - 2480	(+)	1.000	0.969	cgggGAGGggcgg
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2470 - 2484	(-)	1.000	0.944	cgaaccgCCCCtccc
V$SP1F/GC.01	GC box elements	0.88	2471 - 2485	(+)	1.000	0.887	ggaggGGCGgttcgg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2472 - 2492	(+)	1.000	0.907	GAGGggcggttcgggggcccgg
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2473 - 2487	(-)	0.750	0.837	cCCCGaaccgcccct
V$PAX9/PAX9.01	Zebrafish PAX9 binding sites	0.78	2485 - 2505	(-)	0.882	0.794	cgCAGCgccgggggccgggccc
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2485 - 2499	(-)	1.000	0.898	gccgGGGCcgggccc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2488 - 2504	(-)	1.000	0.788	gcaGCGCcggggccggg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2489 - 2505	(+)	0.750	0.784	ccgGCCCCcggcgctgcg
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2494 - 2516	(-)	1.000	0.935	cgccccgCCCCcgcagcgccggg
V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2497 - 2519	(-)	1.000	0.956	gcccgccccgCCCCcgcagcgcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2499 - 2515	(+)	1.000	0.991	cgctgcggGGGCggggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2502 - 2524	(-)	1.000	0.885	tggccgcCCGCcccgcccccgca
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2503 - 2517	(+)	1.000	1.000	gcggGGGCggggcgg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2504 - 2520	(+)	1.000	0.892	cgggggcgGGGCggcg
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2505 - 2521	(+)	1.000	0.961	gggggcGGGGcgggcgg
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2505 - 2517	(+)	1.000	0.916	gggggcGGGGcgg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2508 - 2524	(+)	1.000	0.862	ggcgggcGGGCggcca
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2508 - 2522	(+)	1.000	0.976	ggcgGGGCgggcggc
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2510 - 2526	(+)	0.953	0.922	cggggCGGGcggccagg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2518 - 2538	(+)	0.833	0.880	GCGGccaggaaaggggcggt
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2519 - 2541	(-)	1.000	0.937	cccaccgCCCCctttcctggccg
V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2522 - 2544	(-)	1.000	0.946	cggcccaccgCCCCctttcctgg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2524 - 2540	(+)	1.000	0.865	aggaaaggGGGCggtgg
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2527 - 2541	(-)	1.000	0.937	cccaccgCCCCcttt
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2528 - 2542	(+)	1.000	0.911	aaggGGGCggtgggc
V$BNCF/BNC.01	Basonuclin, cooperates with USF1 in rDNA PolI transcription)	0.85	2545 - 2563	(+)	1.000	0.887	agggccgcgcTGTCccgag
V$CDEF/CDE.01	Cell cycle-dependent element, CDF-1 binding site (CDE/CHR tandem elements regulate cell cycle dependent repression)	0.87	2546 - 2558	(+)	1.000	0.886	gggcCGCGctgtc

93 matches found in this sequence.

Table A.3 Genomatix Analysis of the Human Perlecan Promoter Region from online Databases

Search Results (424 matches)

latInspector Release professional 7.4.8.1, May 2007 **Wed Jul 11 19:12:41 200**

olution parameters:

equence file: CorrectEnsembl.seq (2565 bp)
amily matches: yes
latInspector library: Matrix Family Library Version 6.3 (March 2007)
elected groups (core/matrix sim)
- ALL vertebrates.lib (0.75/Optimized)

nspecting sequence Ensembl_HUMAN_perlecan_CORRECT [Ensembl_HUMAN] (1 - 2565):

nsembl_HUMAN_perlecan_CORRECT_SEQUENCE_plus_strand, Reverse-Complement]

Family/matrix	Further Information	Opt.	Position from - to	Str.	Core sim.	Matrix sim.	Sequence (red: ci-value > 60 capitals: core sequence)
V$CLOX/CLOX.01	Cut-like homeo box	0.81	7 - 25	(+)	0.804	0.824	gctgacaaATCCatggaca
V$HNF6/HNF6.01	Liver enriched Cut - Homeodomain transcription factor HNF6 (ONECUT)	0.82	8 - 24	(+)	0.833	0.857	ctgacaaaTCCAtggac
V$HOXH/MEIS1B_HOXA9.01	Meis1b and Hoxa9 form heterodimeric binding complexes on target DNA	0.78	9 - 23	(+)	1.000	0.817	TGACaaatccatgga
V$P53F/P53.04	Tumor suppressor p53	0.78	13 - 35	(+)	1.000	0.799	aaatcCATGgacaggcaaggcct
V$P53F/P53.01	Tumor suppressor p53	0.73	14 - 36	(-)	0.844	0.737	aaggcCTTGcctgtccatggatt
V$SF1F/FTF.01	Alpha (1)-fetoprotein transcription factor (FTF), liver receptor homologue-1 (LRH-1)	0.94	29 - 41	(-)	1.000	0.960	tttcCAAGgcctt
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	34 - 52	(+)	1.000	0.890	cttGGAAaaatcctgccac
V$CIZF/NMP4.01	NMP4 (nuclear matrix protein 4) / CIZ (Cas-interacting zinc finger protein)	0.97	37 - 47	(+)	1.000	0.972	ggAAAAatcct
V$BTBF/KAISO.01	Transcription factor Kaiso, ZBTB33	0.92	42 - 52	(+)	1.000	0.992	aatcCTGCcac
V$EBOX/ATF6.01	Member of b-zip family, induced by ER damage/stress, binds to the ERSE in association with NF-Y	0.93	46 - 58	(+)	1.000	0.933	ctgCCACtagggc
V$HAND/HAND2_E12.01	Heterodimers of the bHLH transcription factors HAND2 (Thing2) and E12	0.75	55 - 69	(+)	1.000	0.758	gggctgGCCAcctgc
V$NF1F/NF1.01	Nuclear factor 1	0.82	55 - 75	(+)	0.763	0.851	gggCTGGccacctgccagctc
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	55 - 75	(-)	1.000	0.901	gagcTGGCaggtggccagccc
V$MYOD/E47.01	MyoD/E47 and MyoD/E12 dimers	0.92	57 - 73	(-)	1.000	0.953	gctgGCAGgtggccagc
V$HESF/HES1.02	Drosophila hairy and enhancer of split homologue 1 (HES-1)	0.87	58 - 72	(-)	0.750	0.873	ctggCAGGtggccag
V$NEUR/NEUROD1.01	DNA binding site for NEUROD1 (BETA-2 / E47 dimer)	0.83	59 - 71	(+)	0.767	0.905	tggcCACCtgcca
V$CREB/CJUN_ATF2.01	c-Jun/ATF2 heterodimers	0.99	69 - 89	(-)	1.000	0.991	ctccacTGACttcagagctgg
V$CREB/ATF2.01	Activating transcription factor 2	0.87	70 - 90	(+)	0.777	0.890	cagctcTGAAgtcagtggagt
V$PAX5/PAX5.01	B-cell-specific activator protein	0.79	74 - 102	(+)	0.857	0.799	tctgaaGTCAgtggagttttgaagccttt
V$CSEN/DREAM.01	Downstream regulatory element-antagonist modulator, Ca2+-binding protein of the neuronal calcium sensors family that binds DRE (downstream regulatory element) sites as a tetramer	0.95	78 - 88	(+)	1.000	0.963	aaGTCAgtgga
V$EVI1/MEL1.02	MEL1 (MDS1/EVI1-like gene 1) DNA-binding domain 2	0.99	99 - 115	(-)	1.000	0.990	cctgtccGATGagaaag
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	106 - 124	(-)	0.956	0.891	tggaaactccctGTCCgat
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	108 - 126	(-)	1.000	0.871	cttGGAAactccctgtccg

V$SP1F/BTEB3.01	Basic transcription element (BTE) binding protein, BTEB3, FKLF-2	0.93	110 - 124	(+)	1.000	0.958	gacagGGAGttcca
V$NFKB/NFKAPPAB65.01	NF-kappaB (p65)	0.87	112 - 124	(+)	1.000	0.991	cagggagtTTCCa
V$CHRE/CHREBP_MLX.01	Carbohydrate response element binding protein (CHREBP) and Max-like protein X (Mlx) bind as heterodimers to glucose-responsive promoters	0.83	123 - 139	(+)	0.833	0.892	CAAGtgcaaacctggtg
V$GREF/ARE.02	Androgene receptor binding site, IR3 sites	0.89	127 - 145	(+)	0.869	0.894	tgcaaacctggtGTACtct
V$NR2F/TR4.02	TR4 homodimer, DR1 site	0.75	132 - 156	(-)	0.777	0.751	catttgAGGGgagagtacaccaggt
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	143 - 155	(-)	1.000	0.908	atttGAGGggaga
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	143 - 151	(-)	1.000	0.991	gaGGGGaga
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	149 - 159	(-)	1.000	0.984	tcCCATttgag
V$GLIF/GLI1.01	Zinc finger transcription factor GLI1	0.87	151 - 165	(-)	1.000	0.929	gggacctCCCAtttg
V$NFKB/NFKAPPAB.01	NF-kappaB	0.89	154 - 166	(+)	1.000	0.937	atGGGAggtccct
V$NFKB/NFKAPPAB.01	NF-kappaB	0.89	155 - 167	(-)	1.000	0.938	caGGGAcctccca
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	156 - 178	(+)	1.000	0.874	gggaggTCCCtggggtggctgtg
V$EBOX/ATF6.01	Member of b-zip family, induced by ER damage/stress, binds to the ERSE in association with NF-Y	0.93	164 - 176	(-)	1.000	0.936	cagCCACcccagg
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	164 - 186	(-)	0.761	0.800	gcagccTCCAcagccaccccagg
V$GZF1/GZF1.01	GDNF-inducible zinc finger protein 1 (ZNF336)	0.73	184 - 196	(+)	0.750	0.798	TGCTcctctatca
V$GATA/GATA1.03	GATA-binding factor 1	0.95	187 - 199	(-)	1.000	0.955	gtctGATAgagga
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	200 - 222	(+)	1.000	0.844	ctcagcTCCCcaagggccaagtc
V$P53F/P53.03	Tumor suppressor p53 (3' half site)	0.92	207 - 229	(+)	1.000	0.932	ccccaagggccaagtCATGtctc
V$ETSF/FLI.01	ETS family member FLI	0.81	245 - 265	(+)	0.750	0.815	agcacaCCAGaaatagtaata
V$SATB/SATB1.01	Special AT-rich sequence-binding protein 1, predominantly expressed in thymocytes, binds to matrix attachment regions (MARs)	0.94	259 - 273	(+)	1.000	0.944	agtAATAagagaaat
V$ATBF/ATBF1.01	AT-binding transcription factor 1	0.79	271 - 287	(+)	0.782	0.793	aatggctaccACTTatt
V$NKXH/NKX32.01	Homeodomain protein NKX3.2 (BAPX1, NKX3B, Bagpipe homolog)	0.96	276 - 290	(-)	1.000	0.968	tgaaataAGTGgtag
V$PPAR/PPARG.01	Pal3 motif, bound by a PPAR-gamma homodimer, IR3 sites	0.67	281 - 303	(-)	0.794	0.676	cacTTGGtaagcatgaaataagt
V$EBOX/USF.04	Upstream stimulating factor 1/2	0.90	295 - 307	(-)	0.851	0.942	cagaCACTtggta
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	295 - 315	(-)	0.750	0.804	agccatttcagacACTTggta
V$FKHD/ILF1.01	Winged-helix transcription factor IL-2 enhancer binding factor (ILF), forkhead box K2 (FOXK2)	0.98	312 - 328	(-)	1.000	0.987	tttttaaaaAACAcagcc
V$SATB/SATB1.01	Special AT-rich sequence-binding protein 1, predominantly expressed in thymocytes, binds to matrix attachment regions (MARs)	0.94	327 - 341	(-)	1.000	0.964	attAATAtatttctt
V$BRNF/BRN3.02	Brn-3, POU-IV protein class	0.89	331 - 349	(+)	1.000	0.913	aatatatTAATttatctta
V$OCT1/OCT1.06	Octamer-binding factor 1	0.81	331 - 345	(+)	1.000	0.891	aatatattAATTtat
V$EVI1/EVI1.04	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.73	332 - 348	(-)	0.750	0.733	aagataaattaaTATAt
V$LHXF/LHX3.01	Homeodomain binding site in LIM/Homeodomain factor LHX3	0.81	332 - 346	(+)	1.000	0.867	atataTTAAtttatc
V$HOMF/MSX.01	Homeodomain proteins MSX-1 and MSX-2	0.97	333 - 345	(+)	1.000	0.972	tatatTAATttat
V$RBIT/BRIGHT.01	Bright, B cell regulator of IgH transcription	0.92	334 - 346	(-)	1.000	0.956	gataaATTAatat
V$SORY/HMGA.01	HMGA family of architectural transcription factors (HMGA1, HMGA2)	0.88	336 - 352	(+)	1.000	0.903	attAATTtatcttaatt
V$EVI1/EVI1.03	Ecotropic viral integration site 1 encoded factor, amino-terminal zinc finger domain	0.79	337 - 353	(-)	1.000	0.795	gaattAAGAtaaattaa
V$GATA/GATA1.03	GATA-binding factor 1	0.95	338 - 350	(-)	1.000	0.961	ttaaGATAaatta

V$OCT1/OCT1.06	Octamer-binding factor 1	0.81	341 - 355	(+)	1.000	0.888	tttatcttAATTctc
V$SNAP/PSE.02	Proximal sequence element (PSE) of RNA polymerase III-transcribed genes	0.73	341 - 359	(+)	0.857	0.781	tttatCTTAattctcataa
V$NKXH/NKX25.02	Homeo domain factor Nkx-2.5/Csx, tinman homolog low affinity sites	0.88	343 - 357	(+)	1.000	0.971	tatctTAATtctcat
V$OCTB/TST1.01	POU-factor Tst-1/Oct-6	0.90	343 - 355	(-)	1.000	0.902	gagaATTAagata
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	345 - 363	(-)	0.807	0.876	gttgttatgAGAAttaaga
V$OCT1/OCT1.06	Octamer-binding factor 1	0.81	346 - 360	(-)	1.000	0.910	gttatgagAATTaag
V$PARF/DBP.01	Albumin D-box binding protein	0.84	348 - 364	(-)	1.000	0.862	tgttgTTATgagaatta
V$CREB/ATF.02	Activating transcription factor	0.83	374 - 394	(+)	0.750	0.832	acgtctTAACgttattctcat
V$MYBL/VMYB.05	v-Myb, variant of AMV v-myb	0.90	377 - 389	(-)	1.000	0.908	aatAACGttaaga
V$MYBL/VMYB.03	v-Myb, viral myb variant from transformed BM2 cells	0.87	378 - 390	(+)	1.000	0.885	cttAACGttattc
V$IRFF/IRF3.01	Interferon regulatory factor 3 (IRF-3)	0.85	382 - 402	(-)	0.758	0.850	tgtagaaaatGAGAataacgt
V$OCT1/OCT1.04	Octamer-binding factor 1	0.80	383 - 397	(-)	0.846	0.838	aaAATGagaataacg
V$AP1F/AP1.01	Activator protein 1	0.94	424 - 434	(-)	0.833	0.945	catgATTCaac
V$AP1F/AP1.03	Activator protein 1	0.94	424 - 434	(+)	0.857	0.947	gtTGAAtcatg
V$MITF/MIT.01	MIT (microphthalmia transcription factor) and TFE3	0.81	424 - 442	(+)	1.000	0.890	gttgaatCATGtgctcaag
V$AP4R/PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class B bHLH factors, forms heterodimers with E12	0.86	425 - 441	(-)	0.882	0.914	ttgAGCAcatgattcaa
V$EBOX/MYCMAX.02	c-Myc/Max heterodimer	0.92	428 - 440	(-)	0.860	0.934	tgagcaCATGatt
V$GATA/GATA1.03	GATA-binding factor 1	0.95	471 - 483	(-)	1.000	0.955	gtctGATAgagaa
V$SORY/SOX5.01	Sox-5	0.87	484 - 500	(+)	1.000	0.990	tgagaaCAATacccgga
V$P53F/P53.05	Tumor suppressor p53	0.78	486 - 508	(+)	0.760	0.805	agaaCAATacccggacagggact
V$HEAT/HSF2.02	Heat shock factor 2	0.95	501 - 525	(-)	1.000	0.965	gaggtgtggggaAGAAtagtccctg
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	504 - 524	(-)	1.000	0.961	aggtgtggGGAAgaatagtcc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	512 - 520	(-)	1.000	1.000	gtGGGGaag
V$GATA/GATA1.03	GATA-binding factor 1	0.95	521 - 533	(-)	1.000	0.957	atctGATAgaggt
V$HOXF/CRX.01	Cone-rod homeobox-containing transcription factor / otx-like homeobox gene	0.94	523 - 539	(-)	1.000	0.944	ctctTAATctgatagag
V$FKHD/FREAC4.01	Fork head related activator-4 (FOXD1)	0.78	533 - 549	(-)	0.750	0.788	cctcagtaAACTcttaa
V$MYT1/MYT1.01	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.75	534 - 546	(+)	0.750	0.798	taaGAGTttactg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	546 - 566	(+)	1.000	0.907	GAGGgccaagattgggcgtcc
V$GABF/GAGA.01	GAGA-Box	0.78	568 - 592	(-)	0.750	0.780	cagggAGATaggggtggacagagga
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	573 - 591	(+)	1.000	0.835	tgtCCACccctatctccct
V$GATA/GATA1.01	GATA-binding factor 1	0.96	578 - 590	(-)	1.000	1.000	gggaGATAggggt
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	631 - 645	(-)	1.000	0.831	cCCCAacccaggctc
V$CP2F/CP2.01	CP2	0.90	633 - 651	(+)	1.000	0.920	gcCTGGgttggggccaggc
V$MYBL/CMYB.01	c-Myb, important in hematopoesis, cellular equivalent to avian myoblastosis virus oncogene v-myb	0.90	646 - 658	(-)	1.000	0.997	gcCAACtgcctgg
V$NEUR/NEUROD1.01	DNA binding site for NEUROD1 (BETA-2 / E47 dimer)	0.83	648 - 660	(-)	0.767	0.893	aggcCAACtgcct
V$IRFF/IRF4.02	Interferon regulatory factor 4	0.69	665 - 685	(-)	1.000	0.738	aacaGAAAttgcatccacggt
V$OCT1/OCT1.02	Octamer-binding factor 1	0.85	669 - 683	(+)	1.000	0.872	tggATGCaatttctg
V$CHOP/CHOP.01	Heterodimers of CHOP and C/EBPalpha	0.90	670 - 682	(+)	1.000	0.911	ggatGCAAtttct
V$GREF/PRE.01	Progesterone receptor binding site, IR3 sites	0.84	671 - 689	(+)	1.000	0.915	gatgcaatttcTGTTcttt
V$MYBL/VMYB.01	v-Myb	0.88	676 - 688	(-)	0.817	0.882	aagAACAgaaatt

V$FKHD/FREAC2.01	Fork head related activator-2 (FOXF2)	0.84	680 - 696	(-)	1.000	0.859	gagttgTAAAgaacaga
V$PAX6/PAX6.02	PAX6 paired domain and homeodomain are required for binding to this site	0.87	695 - 713	(-)	1.000	0.871	tctgtgggaCCAGctcaga
V$OCTP/OCT1P.01	Octamer-binding factor 1, POU-specific domain	0.86	712 - 724	(+)	1.000	0.914	gaaATATgcccca
V$OCTP/OCT1P.01	Octamer-binding factor 1, POU-specific domain	0.86	725 - 737	(-)	1.000	0.915	aaaATATgccctg
V$AIRE/AIRE.01	Autoimmune regulator	0.86	742 - 768	(+)	0.857	0.878	atatcttttggagatagGGGAtctatc
V$GATA/GATA1.01	GATA-binding factor 1	0.96	750 - 762	(+)	1.000	1.000	tggaGATAgggga
V$MZF1/MZF1.02	Myeloid zinc finger protein MZF1	0.99	756 - 764	(+)	1.000	0.994	taGGGGatc
V$CLOX/CDPCR3HD.01	Cut-like homeodomain protein	0.94	757 - 775	(-)	1.000	0.978	catcccagataGATCccct
V$GATA/GATA1.03	GATA-binding factor 1	0.95	760 - 772	(-)	1.000	0.953	cccaGATAgatcc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	764 - 786	(-)	1.000	0.920	atcctgaCCCCcatcccagatag
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	768 - 788	(-)	1.000	0.723	gcatccTGACccccatcccag
V$RORA/REV-ERBA.01	Orphan nuclear receptor rev-erb alpha (NR1D1)	0.88	769 - 791	(+)	1.000	0.913	tgggatggggGTCAggatgccag
V$GCMF/GCM1.01	Glial cells missing homolog 1, chorion-specific transcription factor GCMa	0.85	771 - 781	(-)	0.789	0.899	gaCCCCcatcc
V$EREF/ER.01	Estrogen receptor, IR3 sites	0.83	775 - 793	(+)	1.000	0.849	ggggGTCAggatgccagtg
V$ETSF/PDEF.01	Prostate-derived Ets factor	0.93	775 - 795	(+)	1.000	0.942	gggggtcaGGATgccagtgtt
V$MEF3/MEF3.01	MEF3 binding site, present in skeletal muscle-specific transcriptional enhancers	0.89	777 - 789	(+)	1.000	0.946	gggTCAGgatgcc
V$MYOD/MYOD.01	Myogenic regulatory factor MyoD (myf3)	0.88	802 - 818	(-)	1.000	0.937	ccaGGCAtctgggggat
V$PAX6/PAX6.04	PAX6 paired domain binding site	0.83	802 - 820	(+)	0.944	0.835	atcCCCCagatgcctggat
V$NEUR/NEUROD1.01	DNA binding site for NEUROD1 (BETA-2 / E47 dimer)	0.83	805 - 817	(-)	1.000	0.832	caggCATCtgggg
V$EVI1/MEL1.02	MEL1 (MDS1/EVI1-like gene 1) DNA-binding domain 2	0.99	811 - 827	(+)	1.000	0.993	atgcctgGATGagaggc
V$DMTF/DMP1.01	Cyclin D-interacting myb-like protein, DMTF1 - cyclin D binding myb-like transcription factor 1	0.82	812 - 824	(+)	1.000	0.831	tgcctGGATgaga
V$BNCF/BNC.01	Basonuclin, cooperates with USF1 in rDNA PolI transcription)	0.85	823 - 841	(+)	0.789	0.881	gaggccccaaTGTGcttgg
V$INSM/INSM1.01	Zinc finger protein insulinoma-associated 1 (IA-1) functions as a transcriptional repressor	0.90	849 - 861	(-)	1.000	0.925	tgataGGGGtccg
V$GATA/GATA1.01	GATA-binding factor 1	0.96	852 - 864	(-)	1.000	0.992	ctgtGATAggggt
V$ETSF/ELK1.02	Elk-1	0.91	866 - 886	(-)	1.000	0.971	ctggctccGGAAgctatgttc
V$HESF/HES1.01	Drosophila hairy and enhancer of split homologue 1 (HES-1)	0.92	885 - 899	(+)	1.000	0.950	aggcctgGTGCcgcc
V$SP1F/SP1.02	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.85	890 - 904	(-)	1.000	0.867	cactGGGCggcacca
V$NR2F/TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	0.76	897 - 921	(-)	0.780	0.762	gaaggaaatgcccaGCTCactgggc
V$NFKB/CREL.01	c-Rel	0.91	907 - 919	(+)	1.000	0.969	ctgggcatTTCCt
V$NR2F/ARP1.01	Apolipoprotein AI regulatory protein 1, NR2F2, DR1 sites	0.82	916 - 940	(+)	0.809	0.861	tccttctgtccacaGCTCacctcac
V$RXRF/VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	0.79	917 - 941	(-)	0.952	0.791	agtGAGGtgagctgtggacagaagg
V$SREB/SREBP.01	Sterol regulatory element binding protein 1 and 2	0.90	929 - 943	(+)	1.000	0.952	agcTCACctcactcc
V$BRAC/BRACH.01	Brachyury	0.66	933 - 953	(-)	0.750	0.698	tttgcagccAGGAgtgaggtg
V$PAX6/PAX4_PD.01	PAX4 paired domain binding site	0.91	935 - 953	(-)	0.965	0.941	tttGCAGccaggagtgagg
V$OAZF/ROAZ.01	Rat C2H2 Zn finger protein involved in olfactory neuronal differentiation	0.73	936 - 952	(-)	0.750	0.794	ttGCAGccaggagtgag
V$HEAT/HSF1.01	Heat shock factor 1	0.84	959 - 983	(+)	0.952	0.878	ccatgagtttctGGAAcctagcaac
V$STAT/STAT1.01	Signal transducer and activator of transcription 1	0.77	960 - 978	(-)	0.767	0.790	taggttccaGAAActcatg
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	962 - 980	(+)	1.000	0.895	tgagtttctGGAAcctagc
V$XBBF/RFX1.01	X-box binding protein RFX1	0.89	969 - 987	(+)	1.000	0.942	ctggaacctaGCAActctc
V$MYT1/MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finger factor 1	0.92	976 - 988	(-)	1.000	0.958	tgagAGTTgctag
V$ETSF/CETS1P54.01	c-Ets-1(p54)	0.92	983 - 1003	(+)	0.901	0.920	ctctcaCAGGaaacaatggaa

V$CLOX/CDPCR3.01	Cut-like homeodomain protein	0.73	984 - 1002	(+)	1.000	0.730	tctcacaggaaacaATGGa
V$FKHD/FKHRL1.01	Fkh-domain factor FKHRL1 (FOXO)	0.83	986 - 1002	(+)	1.000	0.846	tcacaggaAACAatgga
V$HEAT/HSF2.01	Heat shock factor 2	0.88	988 - 1012	(+)	0.875	0.885	acaggaaacaatgGAAActtcagtt
V$SORY/SOX5.01	Sox-5	0.87	990 - 1006	(+)	1.000	0.988	aggaaaCAATggaaact
V$XBBF/RFX1.02	X-box binding protein RFX1	0.90	990 - 1008	(+)	0.881	0.919	aggaaacaatgGAAActtc
V$IRFF/ISRE.01	Interferon-stimulated response element	0.81	991 - 1011	(+)	1.000	0.849	ggaaacaatgGAAActtcagt
V$HEAT/HSF1.03	Heat shock factor 1	0.76	997 - 1021	(-)	0.868	0.768	ggagataaaacTGAAgtttccatt
V$NFAT/NFAT5.01	Nuclear factor of activated T-cells 5	0.83	997 - 1015	(+)	1.000	0.875	aatGGAAAacttcagtttta
V$MYT1/MYT1.01	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.75	1000 - 1012	(+)	0.750	0.756	ggaAACTtcagtt
V$CDXF/CDX2.01	Cdx-2 mammalian caudal related intestinal transcr. factor	0.84	1005 - 1023	(+)	1.000	0.849	cttcagtTTTAttctcctc
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	1015 - 1027	(-)	1.000	0.909	agagGAGGagaat
V$MEF2/SL1.01	Member of the RSRF (related to serum response factor) protein family from Xenopus laevis	0.84	1019 - 1041	(+)	1.000	0.865	tcctcctCTATcattactcaaaa
V$GATA/GATA1.01	GATA-binding factor 1	0.96	1022 - 1034	(-)	1.000	0.960	taatGATAgagga
V$HOXF/HOX1-3.01	Hox-1.3, vertebrate homeobox protein	0.82	1022 - 1038	(-)	1.000	0.831	tgagTAATgatagagga
V$CLOX/CUT2.01	Cut repeat II	0.67	1023 - 1041	(-)	0.750	0.687	ttttgagtaATGAtagagg
V$PARF/TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	0.78	1027 - 1043	(+)	1.000	0.780	tatcaTTACtcaaaagg
V$PARF/HLF.01	Hepatic leukemia factor	0.84	1028 - 1044	(-)	1.000	0.858	acctttgaGTAAtgat
V$AP1F/AP1.02	Activator protein 1	0.87	1030 - 1040	(-)	1.000	0.934	tttGAGTaatg
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	1034 - 1052	(-)	1.000	0.976	tgaGGAAaacctttgagt
V$NKXH/HMX2.02	Hmx2/Nkx5-2 homeodomain transcription factor	0.82	1038 - 1052	(-)	1.000	0.835	tgaggaAAACctttt
V$STAT/STAT.01	Signal transducers and activators of transcription	0.87	1040 - 1058	(-)	1.000	0.882	tagctttgaGGAAaacctt
V$LEFF/LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.94	1044 - 1060	(+)	1.000	0.949	ttttcctCAAAgctaca
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	1060 - 1078	(-)	1.000	0.964	agaGGAAaactatgtgtgt
V$HOXC/HOX_PBX.01	HOX/PBX binding sites	0.81	1076 - 1092	(-)	1.000	0.831	aggcTGATgggtggaga
V$PAX6/PAX6.03	Pax-6 paired domain binding site	0.76	1076 - 1094	(+)	0.806	0.780	tctccACCCatcagcctcg
V$CAAT/ACAAT.01	Avian C-type LTR CCAAT box	0.83	1078 - 1092	(+)	0.750	0.874	tccaCCCAtcagcct
V$HEAT/HSF2.01	Heat shock factor 2	0.88	1092 - 1116	(+)	0.875	0.902	tcgggctgccctgGAAAtttcaggc
V$HICF/HIC1.01	Hypermethylated in cancer 1, transcriptional repressor containing five Krüppel-like C2H2 zinc fingers, for optimal binding multiple binding sites are required.	0.93	1093 - 1105	(+)	1.000	0.945	cgggcTGCCctgg
V$STAT/STAT6.01	STAT6: signal transducer and activator of transcription 6	0.84	1094 - 1112	(+)	0.758	0.879	gggcTGCCctggaaatttc
V$PAX6/PAX6.02	PAX6 paired domain and homeodomain are required for binding to this site	0.87	1096 - 1114	(-)	1.000	0.949	ctgaaatttCCAGggcagc
V$HEAT/HSF1.01	Heat shock factor 1	0.84	1101 - 1125	(-)	0.857	0.886	ccctcttctgccTGAAatttccagg
V$SORY/HMGIY.01	HMGI(Y) high-mobility-group protein I (Y), architectural transcription factor organizing the framework of a nuclear protein-DNA transcriptional complex	0.92	1103 - 1119	(+)	1.000	0.948	tggaAATTtcaggcaga
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	1117 - 1133	(+)	1.000	0.918	agaagaGGGGagctgaa
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	1117 - 1129	(+)	1.000	0.917	agaaGAGGggagc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	1121 - 1129	(+)	1.000	0.991	gaGGGGagc
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	1133 - 1153	(-)	0.750	0.744	gacctattcactgCCTActct
V$NR2F/COUP.01	Chicken ovalbumin upstream promoter 1 (COUP-TFI) and chicken ovalbumin upstream promoter 2 (COUP-TFII), DR1 sites	0.82	1136 - 1160	(+)	1.000	0.839	gtaggcagtgaatAGGTctgggggc
V$MYBL/CMYB.02	c-Myb, important in hematopoesis, cellular equivalent to avian myoblastosis virus oncogene v-myb	0.96	1176 - 1188	(-)	0.989	0.961	ccCAACcgcaggc

V$RXRF/RAR_RXR.03	Retinoic acid receptor / retinoid X receptor heterodimer, DR5 sites	0.81	1182 - 1206	(+)	1.000	0.946	ggttgGGTCagagacagatcatggg
V$NR2F/TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	0.76	1184 - 1208	(+)	0.780	0.840	ttgggtcagagacaGATCatggggc
V$GFI1/GFI1.01	Growth factor independence 1 zinc finger protein acts as transcriptional repressor	0.96	1204 - 1218	(-)	1.000	0.985	taaAATCacagcccc
V$HOXF/HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	0.88	1209 - 1225	(-)	1.000	0.934	tgggtggTAAAatcaca
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	1214 - 1230	(-)	1.000	0.927	tcgggTGGGtggtaaaa
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	1215 - 1229	(+)	0.827	0.914	tttaccaCCCAcccg
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	1216 - 1232	(-)	0.754	0.845	gctcGGGTgggtggtaa
V$AP4R/TAL1ALPHAE47.01	Tal-1alpha/E47 heterodimer	0.87	1226 - 1242	(-)	1.000	0.921	catcaCAGAtgctcggg
V$PAX5/PAX5.03	PAX5 paired domain protein	0.80	1248 - 1276	(-)	0.789	0.812	ctcagGCCCagacagacagaccctgccaa
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	1264 - 1272	(+)	1.000	0.993	GTCTgggcc
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	1278 - 1294	(+)	0.782	0.821	gtgtGAGTtggtgtggt
V$HAML/AML3.01	Runt-related transcription factor 2 / CBFA1 (core-binding factor, runt domain, alpha subunit 1)	0.84	1286 - 1300	(+)	1.000	0.914	tggtGTGGttctggc
V$GFI1/GFI1.02	Growth factor independence 1	0.90	1304 - 1318	(-)	1.000	0.991	ataAATCacagcccc
V$BRNF/BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS-1)	0.74	1305 - 1323	(-)	1.000	0.756	gtcaCATAaatcacagccc
V$TBPF/MTATA.01	Muscle TATA box	0.84	1306 - 1322	(-)	1.000	0.862	tcacaTAAAtcacagcc
V$HOXC/PBX_HOXA9.01	PBX - HOXA9 binding site	0.79	1307 - 1323	(+)	1.000	0.954	gctgTGATttatgtgac
V$HOXF/HOXA9.01	Member of the vertebrate HOX - cluster of homeobox factors	0.87	1308 - 1324	(-)	1.000	0.968	agtcacataAATCacag
V$PARF/TEF.01	Thyrotrophic embryonic factor	0.85	1310 - 1326	(+)	0.772	0.877	gtgatttatGTGActca
V$AP1R/BACH2.01	Bach2 bound TRE	0.89	1311 - 1335	(-)	1.000	0.946	caccaacttTGAGtcacataaatca
V$AP1F/AP1.01	Activator protein 1	0.94	1318 - 1328	(+)	0.904	0.954	tgtgACTCaaa
V$AP1F/AP1.01	Activator protein 1	0.94	1318 - 1328	(-)	1.000	0.968	tttgAGTCaca
V$LEFF/LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathway	0.94	1318 - 1334	(+)	1.000	0.944	tgtgactCAAAgttggt
V$MYT1/MYT1.02	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.88	1324 - 1336	(+)	1.000	0.882	tcaAAGTtggtgt
V$GFI1/GFI1B.01	Growth factor independence 1 zinc finger protein Gfi-1B	0.86	1335 - 1349	(-)	1.000	0.904	gtaAATCactcacac
V$AP1F/AP1.02	Activator protein 1	0.87	1336 - 1346	(+)	1.000	0.897	tgtGAGTgatt
V$TBPF/MTATA.01	Muscle TATA box	0.84	1337 - 1353	(-)	1.000	0.852	ccatgTAAAtcactcac
V$HOXC/PBX_HOXA9.01	PBX - HOXA9 binding site	0.79	1338 - 1354	(+)	1.000	0.839	tgagTGATttacatgga
V$PBXC/PBX1_MEIS1.02	Binding site for a Pbx1/Meis1 heterodimer	0.77	1338 - 1354	(+)	1.000	0.861	tgagTGATttacatgga
V$COMP/COMP1.01	COMP1, cooperates with myogenic proteins in multicomponent complex	0.77	1339 - 1361	(+)	0.782	0.804	gagtgATTTacatggaaaatggt
V$HOXF/HOXA9.01	Member of the vertebrate HOX - cluster of homeobox factors	0.87	1339 - 1355	(-)	1.000	0.882	ttccatgtaAATCactc
V$OCT1/OCT1.05	Octamer-binding factor 1	0.89	1340 - 1354	(-)	1.000	0.905	tcCATGtaaatcact
V$SORY/HMGA.01	HMGA family of architectural transcription factors (HMGA1, HMGA2)	0.88	1340 - 1356	(+)	0.916	0.914	agtGATTtacatggaaa
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	1345 - 1355	(-)	1.000	0.967	ttCCATgtaaa
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1347 - 1365	(+)	1.000	0.816	tacatgGAAAatggtgcag
V$YY1F/YY1.02	Yin and Yang 1 repressor sites	0.94	1347 - 1365	(-)	1.000	0.968	ctgcaCCATtttccatgta
V$PTF1/PTF1.01	PTF1 binding sites are bipartite with an E-box and a TC-box (RBP-J/L) spaced one helical turn apart	0.76	1350 - 1370	(-)	1.000	0.901	cccaCCTGcaccatttttccat
V$RUSH/SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.96	1352 - 1362	(-)	1.000	0.961	caCCATtttcc

V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	1354 - 1376	(-)	1.000	0.749	gcccacCCCAcctgcaccatttt
V$MYOD/E47.01	MyoD/E47 and MyoD/E12 dimers	0.92	1358 - 1374	(+)	1.000	0.946	tggtGCAGgtggggtgg
V$EKLF/EKLF.01	Erythroid krueppel like factor (EKLF)	0.89	1362 - 1378	(+)	1.000	0.930	gcaggtgGGGTgggcag
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	1363 - 1377	(-)	0.750	0.849	tgcCCACcccacctg
V$RXRF/CAR_RXR.01	Constitutive androstane receptor / retinoid X receptor heterodimer, DR4 sites	0.75	1368 - 1392	(+)	0.770	0.805	ggggtGGGCagctcagttcagtacc
V$RXRF/PXR_RXR.01	Pregnane X receptor / retinoid X receptor heterodimer, DR4 sites	0.80	1373 - 1397	(+)	0.790	0.824	gggcaGCTCagttcagtacccagtg
V$RU49/RU49.01	Zinc finger transcription factor RU49 (zinc finger proliferation 1 - Zipro 1). RU49 exhibits a strong preference for binding to tandem repeats of the minimal RU49 consensus binding site.	0.98	1386 - 1392	(+)	1.000	0.994	cAGTAcc
V$CLOX/CDP.01	Cut-like homeodomain protein	0.75	1408 - 1426	(-)	1.000	0.793	acccacTAATcacagtgcc
V$GFI1/GFI1.02	Growth factor independence 1	0.90	1408 - 1422	(-)	1.000	0.914	actAATCacagtgcc
V$HOXF/CRX.01	Cone-rod homeobox-containing transcription factor / otx-like homeobox gene	0.94	1408 - 1424	(-)	1.000	0.961	ccacTAATcacagtgcc
V$PDX1/PDX1.01	Pdx1 (IDX1/IPF1) pancreatic and intestinal homeodomain TF	0.74	1409 - 1429	(-)	1.000	0.764	ctcacccacTAATcacagtgc
V$CAAT/ACAAT.01	Avian C-type LTR CCAAT box	0.83	1411 - 1425	(-)	0.750	0.874	cccaCTAAtcacagt
V$NR2F/TR4.02	TR4 homodimer, DR1 site	0.75	1427 - 1451	(+)	1.000	0.778	gagaacAGGTaaaagatacaggctg
V$ZFHX/AREB6.01	AREB6 (Atp1a1 regulatory element binding factor 6)	0.93	1429 - 1441	(-)	1.000	0.940	cttttACCTgttc
V$PLZF/PLZF.01	Promyelocytic leukemia zink finger (TF with nine Krueppel-like zink fingers)	0.86	1440 - 1454	(+)	1.000	0.897	agaTACAggctgagg
V$HOXF/GSC.01	Vertebrate bicoid-type homeodomain protein Goosecoid	0.98	1475 - 1491	(+)	1.000	0.983	cctgTAATcccatcact
V$CLOX/CDPCR3.01	Cut-like homeodomain protein	0.73	1483 - 1501	(-)	1.000	0.731	gccctcccaaagtgATGGg
V$RXRF/VDR_RXR.02	VDR/RXR Vitamin D receptor RXR heterodimer, DR3 sites	0.86	1493 - 1517	(+)	0.777	0.898	tgggagggcaagGCGGgcagatcac
V$E2FF/E2F1_DP2.01	E2F-1/DP-2 heterodimeric complex	0.78	1500 - 1516	(+)	1.000	0.810	gcaaGGCGggcagatca
V$NR2F/HNF4.02	Hepatic nuclear factor 4, DR2 sites	0.76	1506 - 1530	(+)	0.750	0.805	cgggcagatcaCAAGgtcaggagtt
V$EREF/ERR.01	Estrogen related receptor	0.87	1511 - 1529	(+)	1.000	0.957	agatcacAAGGtcaggagt
V$RORA/RORA1.01	RAR-related orphan receptor alpha1	0.93	1511 - 1533	(+)	1.000	0.942	agatcacaaGGTCaggagttcga
V$SF1F/SF1.01	SF1 steroidogenic factor 1	0.95	1513 - 1525	(+)	1.000	0.996	atcaCAAGgtcag
V$NBRE/NBRE.01	Monomers of the nur subfamily of nuclear receptors (nur77, nurr1, nor-1)	0.86	1514 - 1528	(+)	1.000	0.932	tcacAAGGtcaggag
V$FKHD/FREAC2.01	Fork head related activator-2 (FOXF2)	0.84	1548 - 1564	(+)	1.000	0.846	acatggTAAAaacccca
V$HOXF/BARX2.01	Barx2, homeobox transcription factor that preferentially binds to paired TAAT motifs	0.95	1561 - 1577	(-)	1.000	0.953	ttttTAATagagatggg
V$MEF2/SL1.01	Member of the RSRF (related to serum response factor) protein family from Xenopus laevis	0.84	1561 - 1583	(+)	1.000	0.845	cccatctCTATtaaaaatacaaa
V$HOXF/HOXC13.01	Homeodomain transcription factor HOXC13	0.91	1565 - 1581	(+)	1.000	0.933	tctctatTAAAaataca
V$BRNF/BRN2.01	Brn-2, POU-III protein class	0.86	1567 - 1585	(+)	0.966	0.883	tcTATTaaaaatacaaaaa
V$EBOX/ATF6.01	Member of b-zip family, induced by ER damage/stress, binds to the ERSE in association with NF-Y	0.93	1590 - 1602	(-)	1.000	0.938	ccaCCACgcctgg
V$RXRF/VDR_RXR.01	VDR/RXR Vitamin D receptor RXR heterodimer, DR3 sites	0.85	1622 - 1646	(+)	1.000	0.855	attcaggaggctGAGGccggagaat
V$BCL6/BCL6.01	POZ/zinc finger protein, transcriptional repressor, translocations observed in diffuse large cell lymphoma	0.76	1643 - 1659	(+)	0.756	0.769	gaaTTGCttgaacccgg
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	1652 - 1666	(-)	1.000	0.927	tccGCCTccggttc
V$PURA/PURALPHA.01	Purine-rich element binding protein A	0.97	1658 - 1670	(+)	1.000	0.985	ggAGGCggaggtt
V$NF1F/NF1.01	Nuclear factor 1	0.82	1665 - 1685	(-)	1.000	0.834	atcTTGGctcactgcaacctc
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	1665 - 1685	(+)	0.750	0.877	gaggTTGCagtgagccaagat
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	1684 - 1700	(-)	0.785	0.823	gagtGCGGtggtgggat

V$AHRR/AHR.01	Aryl hydrocarbon / dioxin receptor	0.78	1686 - 1710	(-)	0.750	0.801	ccccaggctgGAGTgcggtggtggg
V$CHRE/CHREBP_MLX.01	Carbohydrate response element binding protein (CHREBP) and Max-like protein X (Mlx) bind as heterodimers to glucose-responsive promoters	0.83	1691 - 1707	(-)	0.833	0.836	CAGGctggagtgcggtg
V$AP2F/AP2.01	Activator protein 2	0.90	1700 - 1714	(+)	1.000	0.901	ccaGCCTgggggacag
V$SP1F/BTEB3.01	Basic transcription element (BTE) binding protein, BTEB3, FKLF-2	0.93	1716 - 1730	(-)	1.000	0.934	gagaaGGAGtctcgc
V$MOKF/MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (mouse)	0.74	1766 - 1786	(-)	0.750	0.744	gcccacatcattgCCTAcatg
V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1789 - 1807	(+)	1.000	0.819	gtgtgtGAAAtgtgcgtgc
V$AHRR/AHRARNT.01	Aryl hydrocarbon receptor / Arnt heterodimers	0.92	1792 - 1816	(+)	1.000	0.944	tgtgaaatgtgCGTGcctgcgagga
V$BCL6/BCL6.01	POZ/zinc finger protein, transcriptional repressor, translocations observed in diffuse large cell lymphoma	0.76	1804 - 1820	(-)	1.000	0.813	agaTTCCtcgcaggcac
V$BTBF/KAISO.01	Transcription factor Kaiso, ZBTB33	0.92	1804 - 1814	(+)	1.000	0.920	gtgcCTGCgag
V$CLOX/CDP.02	Transcriptional repressor CDP	0.81	1809 - 1827	(+)	0.806	0.816	tgcgaggaATCTatgtgaa
V$CLOX/CDPCR3HD.01	Cut-like homeodomain protein	0.94	1812 - 1830	(-)	0.885	0.943	cttttcacataGATTcctc
V$WHNF/WHN.01	Winged helix protein, involved in hair keratinization and thymus epithelium differentiation	0.95	1827 - 1837	(-)	1.000	0.977	aggACGCcttt
V$EGRF/CKROX.01	Collagen krox protein (zinc finger protein 67 - zfp67)	0.88	1828 - 1844	(-)	1.000	0.920	gagcGGGAggacgcctt
V$CREB/ATF6.02	Activating transcription factor 6, member of b-zip family, induced by ER stress	0.85	1841 - 1861	(+)	0.750	0.850	gctccgtGACTtgttgggatg
V$HOXC/HOX_PBX.01	HOX/PBX binding sites	0.81	1853 - 1869	(+)	0.944	0.823	gttgGGATgtatgcgtg
V$AHRR/NXF_ARNT.01	bHLH-PAS type transcription factors NXF/ARNT heterodimer	0.90	1855 - 1879	(+)	1.000	0.911	tgggatgtatgCGTGagtgaggggc
V$PAX6/PAX6.03	Pax-6 paired domain binding site	0.76	1855 - 1873	(-)	1.000	0.765	cactcACGCatacatccca
V$CREB/TAXCREB.02	Tax/CREB complex	0.71	1856 - 1876	(-)	0.750	0.718	cctcacTCACgcatacatccc
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	1861 - 1877	(+)	1.000	0.818	gtatGCGTgagtgaggg
V$PAX8/PAX8.01	PAX 2/5/8 binding site	0.88	1861 - 1873	(-)	0.800	0.922	cacTCACgcatac
V$AP1F/AP1.02	Activator protein 1	0.87	1866 - 1876	(+)	1.000	0.892	cgtGAGTgagg
V$GCMF/GCM1.01	Glial cells missing homolog 1, chorion-specific transcription factor GCMa	0.85	1869 - 1879	(-)	1.000	0.864	gcCCCTcactc
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	1873 - 1893	(+)	1.000	0.885	GAGGggctgagtgtggtgtga
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	1882 - 1896	(-)	1.000	0.838	cccTCACaccacact
V$ZNFP/SZF1.01	SZF1, hematopoietic progenitor-restricted KRAB-zinc finger protein	0.82	1891 - 1915	(-)	0.875	0.822	ccaGGGAcacaggagacagccctca
V$NR2F/TR4.02	TR4 homodimer, DR1 site	0.75	1913 - 1937	(+)	1.000	0.750	tggtggAGGTgagagtttggaagcg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	1914 - 1926	(+)	1.000	0.919	ggtgGAGGtgaga
V$GABF/GAGA.01	GAGA-Box	0.78	1919 - 1943	(+)	1.000	0.787	aggtgAGAGtttggaagcgagttaa
V$MYT1/MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finger factor 1	0.92	1922 - 1934	(+)	1.000	0.958	tgagAGTTtggaa
V$PAX6/PAX6.03	Pax-6 paired domain binding site	0.76	1934 - 1952	(-)	0.870	0.824	catgcACACttaactcgct
V$NKXH/NKX32.01	Homeodomain protein NKX3.2 (BAPX1, NKX3B, Bagpipe homolog)	0.96	1936 - 1950	(+)	1.000	0.968	cgagttaAGTGtgca
V$CLOX/CDP.01	Cut-like homeodomain protein	0.75	1957 - 1975	(-)	0.750	0.757	taccaaCAATcctcaccgg
V$SORY/SOX5.01	Sox-5	0.87	1959 - 1975	(-)	1.000	0.984	taccaaCAATcctcacc
V$CAAT/ACAAT.01	Avian C-type LTR CCAAT box	0.83	1960 - 1974	(-)	0.750	0.874	accaACAAtcctcac
V$RU49/RU49.01	Zinc finger transcription factor RU49 (zinc finger proliferation 1 - Zipro 1). RU49 exhibits a strong preference for binding to tandem repeats of the minimal RU49 consensus binding site.	0.98	1972 - 1978	(-)	1.000	1.000	aAGTAcc
V$RBPF/RBPJK.01	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.84	1992 - 2006	(+)	0.789	0.871	agagTGTGaaagtgt

V$PRDF/BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturation protein-1 (Blimp-1, prdm1)	0.81	1993 - 2011	(+)	1.000	0.858	gagtgtGAAAgtgttcccg
V$E2FF/E2F.01	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.75	2001 - 2017	(-)	0.750	0.769	gctacccggGAACactt
V$STAT/STAT6.01	STAT6: signal transducer and activator of transcription 6	0.84	2001 - 2019	(-)	0.793	0.876	gcgcTACCcgggaacactt
V$XBBF/RFX1.01	X-box binding protein RFX1	0.89	2001 - 2019	(-)	0.881	0.917	gcgctacccgGGAAcactt
V$IKRS/IK3.01	Ikaros 3, potential regulator of lymphocyte differentiation	0.84	2002 - 2014	(-)	1.000	0.876	acccgGGAAcact
V$OAZF/ROAZ.01	Rat C2H2 Zn finger protein involved in olfactory neuronal differentiation	0.73	2014 - 2030	(+)	0.750	0.735	taGCGCacaagtgtgtt
V$NKXH/HMX3.01	H6 homeodomain HMX3/Nkx5.1 transcription factor	0.89	2016 - 2030	(+)	1.000	0.906	gcgcacAAGTgtgtt
V$RUSH/SMARCA3.02	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	0.98	2019 - 2029	(-)	1.000	0.985	acacACTTgtg
V$SNAP/PSE.02	Proximal sequence element (PSE) of RNA polymerase III-transcribed genes	0.73	2034 - 2052	(-)	0.892	0.732	cacacCATAactttactgc
V$MYT1/MYT1.02	MyT1 zinc finger transcription factor involved in primary neurogenesis	0.88	2037 - 2049	(+)	1.000	0.886	gtaAAGTtatggt
V$GREF/PRE.01	Progesterone receptor binding site, IR3 sites	0.84	2046 - 2064	(+)	1.000	0.874	tggtgtgaaggTGTTcttg
V$EKLF/BKLF.01	Basic krueppel-like factor (KLF3)	0.95	2062 - 2078	(+)	1.000	0.960	ttGGGTgtggaagttgg
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	2062 - 2082	(+)	1.000	0.974	ttgggtgtGGAAgttggcgtg
V$AHRR/AHRARNT.01	Aryl hydrocarbon receptor / Arnt heterodimers	0.92	2068 - 2092	(+)	1.000	0.968	gtggaagttggCGTGcacgtgtggc
V$CREB/XBP1.01	X-box-binding protein 1	0.88	2076 - 2096	(+)	1.000	0.881	tggcgtgcACGTgtggcgcgg
V$HESF/DEC2.01	Basic helix-loop-helix protein known as Dec2 or Sharp2	0.96	2078 - 2092	(-)	1.000	0.966	gccacaCGTGcacgc
V$HIFF/ARNT.01	AhR nuclear translocator homodimers	0.89	2078 - 2090	(+)	1.000	0.945	gcgtgcaCGTGtg
V$EBOX/NMYC.01	N-Myc	0.92	2079 - 2091	(+)	1.000	0.971	cgtgcaCGTGtgg
V$HESF/DEC2.01	Basic helix-loop-helix protein known as Dec2 or Sharp2	0.96	2079 - 2093	(+)	1.000	0.984	cgtgcaCGTGtggcg
V$EBOX/NMYC.01	N-Myc	0.92	2080 - 2092	(-)	1.000	0.985	gccacaCGTGcac
V$HIFF/HIF1.02	Hypoxia inducible factor, bHLH / PAS protein family	0.93	2081 - 2093	(-)	1.000	0.979	cgccacaCGTGca
V$E2FF/RB_E2F1_DP1.01	RB/E2F-1/DP-1 heterotrimeric complex	0.71	2083 - 2099	(-)	1.000	0.722	gctccGCGCcacacgtg
V$PAX1/PAX1.01	Pax1 paired domain protein, expressed in the developing vertebral column of mouse embryos	0.62	2083 - 2101	(-)	0.750	0.643	cCGCTccgcgccacacgtg
V$E2FF/E2F.03	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.85	2086 - 2102	(+)	1.000	0.912	gtgtgGCGCggagcggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2086 - 2108	(-)	1.000	0.873	gcagctgCCGCtccgcgccacac
V$HEN1/HEN1.02	HEN1	0.81	2094 - 2114	(-)	1.000	0.849	acgcacgcaGCTGccgctccg
V$HEN1/HEN1.02	HEN1	0.81	2095 - 2115	(+)	1.000	0.844	ggagcggcaGCTGcgtgcgtg
V$AP4R/AP4.02	Activator protein 4	0.92	2097 - 2113	(+)	1.000	0.922	agcggcAGCTgcgtgcg
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	2103 - 2119	(+)	1.000	0.815	agctGCGTgcgtgtgag
V$EGRF/EGR3.01	Early growth response gene 3 product	0.77	2107 - 2123	(+)	1.000	0.772	gcgtGCGTgtgagcgtg
V$EGRF/EGR3.01	Early growth response gene 3 product	0.77	2115 - 2131	(+)	1.000	0.772	gtgaGCGTgggaaggag
V$RBPF/RBPJK.02	Mammalian transcriptional repressor RBP-Jkappa/CBF1	0.94	2118 - 2132	(+)	1.000	0.962	agcgTGGGaaggaga
V$BARB/BARBIE.01	Barbiturate-inducible element	0.88	2143 - 2157	(+)	1.000	0.899	ttcaAAAGctgcgcg
V$AHRR/AHRARNT.01	Aryl hydrocarbon receptor / Arnt heterodimers	0.92	2168 - 2192	(+)	1.000	0.934	gccgtgcggggCGTGcaggggcgtg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2168 - 2184	(+)	1.000	0.865	gccgtgcgGGGGCgtgca
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2172 - 2186	(+)	1.000	0.859	tgcGGGGcgtgcagg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2178 - 2194	(+)	1.000	0.899	gcgtgcagGGGCgtgga
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2179 - 2195	(+)	1.000	0.959	cgtgcaGGGGcgtggaa
V$SP1F/TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth response gene alpha (EGRalpha)	0.83	2182 - 2196	(+)	1.000	0.868	gcaGGGGcgtggaag

V$E2FF/E2F1_DP1.01	E2F-1/DP-1 heterodimeric complex	0.81	2183 - 2199	(+)	1.000	0.812	caggGGCGtggaagtcg
V$EGRF/EGR3.01	Early growth response gene 3 product	0.77	2184 - 2200	(+)	1.000	0.787	agggGCGTggaagtcgg
V$ETSF/SPI1_PU1.02	Spleen focus forming virus (SFFV) proviral integration oncogene Spi1/transcription factor PU.1	0.96	2184 - 2204	(+)	1.000	0.966	aggggcgtGGAAgtcggcggc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2199 - 2215	(-)	0.750	0.835	tccCCGCgcgcgccgcc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2200 - 2216	(+)	1.000	0.792	gcgGCGCgcgcgggaa
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	2200 - 2210	(-)	1.000	0.963	gcgcGCGCcgc
V$ZF5F/ZF5.01	Zinc finger / POZ domain transcription factor	0.95	2203 - 2213	(+)	1.000	0.966	gcgcGCGCggg
V$ETSF/ETS1.01	c-Ets-1 binding site	0.92	2205 - 2225	(+)	1.000	0.920	gcgcgcggGGAAgcgggggag
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2208 - 2230	(-)	1.000	0.936	cccggctCCCCcgcttccccgcg
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2209 - 2217	(+)	1.000	0.991	gcGGGGaag
V$EGRF/NGFIC.01	Nerve growth factor-induced protein C	0.80	2213 - 2229	(+)	0.785	0.809	ggaaGCGGgggagccgg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2234 - 2246	(+)	1.000	0.959	cgggGAGGcgaga
V$EBOX/MYCMAX.03	MYC-MAX binding sites	0.91	2245 - 2257	(-)	0.789	0.914	gggccaGGCGctc
V$P53F/P53.01	Tumor suppressor p53	0.73	2266 - 2288	(+)	1.000	0.759	catccCATGcccgggcccgggcc
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2270 - 2290	(-)	0.958	0.889	GGGGcccgggcccgggcatgg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2284 - 2304	(-)	0.958	0.907	GGGGcgggggaccgggggccc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2288 - 2310	(+)	1.000	0.932	ccccggtCCCCcgccccgtccca
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2289 - 2305	(-)	0.953	0.971	cggggCGGGggaccggg
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2291 - 2313	(+)	1.000	0.874	cggtcccCCGCcccgtcccatcc
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2293 - 2305	(-)	1.000	0.892	cggggcGGGGgac
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2293 - 2307	(-)	1.000	0.997	gacgGGGCgggggac
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2294 - 2310	(-)	1.000	0.936	tgggacGGGGcgggggа
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2295 - 2311	(-)	1.000	0.888	atgggacgGGGCggggg
V$E2FF/E2F.02	E2F, involved in cell cycle regulation, interacts with Rb p107 protein	0.84	2326 - 2342	(-)	1.000	0.896	gctccccgcCAAAcccg
V$NF1F/NF1.01	Nuclear factor 1	0.82	2328 - 2348	(+)	1.000	0.838	ggtTTGGcggggagccgggcc
V$NF1F/NF1.02	Nuclear factor 1 (CTF1)	0.81	2328 - 2348	(-)	0.750	0.810	ggccCGGCtccccgccaaacc
V$E2FF/RB_E2F1_DP1.01	RB/E2F-1/DP-1 heterotrimeric complex	0.71	2329 - 2345	(+)	0.795	0.759	gtttgGCGGggagccgg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2330 - 2342	(+)	0.866	0.901	tttgGCGGggagc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2334 - 2342	(+)	1.000	0.991	gcGGGGagc
V$NRSF/NRSE.01	Neural-restrictive-silencer-element	0.67	2345 - 2365	(+)	0.782	0.681	ggccggccgCGGCccgcgcg
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	2361 - 2383	(-)	1.000	0.772	tgggccCCCAgcccctccgcgc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2362 - 2378	(+)	1.000	0.911	cgcggaggGGGCtgggg
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2364 - 2378	(-)	1.000	0.822	cCCCAgccccctccg
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2364 - 2386	(-)	1.000	0.917	gtctgggCCCCcagccccctccg
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2366 - 2380	(+)	1.000	0.895	gaggGGGCtgggggc
V$SMAD/SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	0.99	2378 - 2386	(-)	1.000	0.993	GTCTgggcc
V$HICF/HIC1.01	Hypermethylated in cancer 1, transcriptional repressor containing five Krüppel-like C2H2 zinc fingers, for optimal binding multiple binding sites are required.	0.93	2397 - 2409	(+)	0.869	0.933	taggcTGCGcggc

V$STAF/ZNF76_143.01	ZNF143 is the human ortholog of Xenopus Staf, ZNF76 is a DNA binding protein related to ZNF143 and Staf	0.76	2399 - 2421	(-)	1.000	0.783	tcgcCCCAgccggccgcgcagcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2408 - 2424	(+)	1.000	0.892	gccggctgGGGCgagca
V$CP2F/CP2.01	CP2	0.90	2411 - 2429	(+)	1.000	0.920	ggCTGGggcgagcagagcc
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2427 - 2449	(-)	1.000	0.949	cggaccgCCCCCgggccgcgggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2430 - 2452	(-)	1.000	0.885	ccacggaCCGCcccgggccgcg
V$AP2F/AP2.02	Activator protein 2 alpha	0.92	2432 - 2446	(-)	0.905	0.922	accGCCCcccgggccg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2432 - 2448	(+)	1.000	0.868	cggcccggGGGCggtcc
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2435 - 2449	(-)	1.000	0.956	cggaccgCCCCcggg
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2436 - 2450	(+)	1.000	0.894	ccggGGGCggtccgt
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2441 - 2463	(-)	1.000	0.900	ccaggccCCGCcccacggaccgcc
V$EGRF/EGR2.01	Egr-2/Krox-20 early growth response gene product	0.79	2443 - 2459	(+)	0.751	0.887	cggtCCGTgggcggggc
V$SP1F/SP1.02	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.85	2447 - 2461	(+)	1.000	0.966	ccgtGGGCggggcct
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2449 - 2461	(+)	1.000	0.899	gtgggcGGGGcct
V$NOLF/OLF1.01	Olfactory neuron-specific factor	0.82	2458 - 2480	(-)	1.000	0.834	cgccccTCCCcggagcgccaggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2466 - 2488	(-)	1.000	0.882	ccccgaaCCGCcccctccccggag
V$SP1F/GC.01	GC box elements	0.88	2467 - 2481	(+)	0.876	0.933	tccggGGAGgggcgg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2468 - 2484	(+)	1.000	0.903	ccggggagGGGCggttc
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2469 - 2485	(+)	1.000	0.963	cggggaGGGGcggttcg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2469 - 2481	(+)	1.000	0.969	cgggGAGGggcgg
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2471 - 2485	(-)	1.000	0.944	cgaaccgCCCCtccc
V$SP1F/GC.01	GC box elements	0.88	2472 - 2486	(+)	1.000	0.887	ggaggGGCGgttcgg
V$PLAG/PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally regulated C2H2 zinc finger protein	0.88	2473 - 2493	(+)	1.000	0.936	GAGGggcggttcgggggcggg
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2474 - 2488	(-)	0.750	0.837	cCCCGaaccgcccct
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2474 - 2496	(-)	1.000	0.957	ggccccgCCCCCgaaccgcccct
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2477 - 2499	(-)	1.000	0.979	gccggccCCGCcccgaaccgcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2479 - 2495	(+)	1.000	0.935	cggttcggGGGCggggc
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2483 - 2497	(+)	1.000	1.000	tcggGGGCggggccg
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2485 - 2497	(+)	1.000	0.931	gggggcGGGGccg
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2488 - 2504	(-)	1.000	0.797	gcaGCGCcggcccgcc
V$NRF1/NRF1.01	Nuclear respiratory factor 1 (NRF1), bZIP transcription factor that acts on nuclear genes encoding mitochondrial proteins	0.78	2489 - 2505	(+)	0.750	0.788	gcgGGGCcggcgctgcg
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2494 - 2516	(-)	1.000	0.935	cgcccccgCCCCCgcagcgccggc
V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2497 - 2519	(-)	1.000	0.956	gcccgccccgCCCCCgcagcgcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2499 - 2515	(+)	1.000	0.991	cgctgcggGGGCggggc
V$ZBPF/ZF9.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type zinc fingers	0.87	2502 - 2524	(-)	1.000	0.885	tccccgcCCGCcccgccccccgca
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2503 - 2517	(+)	1.000	1.000	gcggGGGCggggcgg
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2504 - 2520	(+)	1.000	0.892	cgggggcgGGGGCgggcg
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2505 - 2521	(+)	1.000	0.961	gggggcGGGGcgggcgg
V$MAZF/MAZR.01	MYC-associated zinc finger protein related transcription factor	0.88	2505 - 2517	(+)	1.000	0.916	gggggcGGGGcgg

V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2508 - 2524	(+)	1.000	0.887	ggcgggcGGGCgggga
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2508 - 2522	(+)	1.000	0.976	ggcgGGGCgggcggg
V$EGRF/WT1.01	Wilms Tumor Suppressor	0.92	2510 - 2526	(+)	0.953	0.932	cggggCGGGcggggagg
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2512 - 2526	(+)	1.000	0.934	gggcGGGCggggagg
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2514 - 2530	(+)	1.000	0.921	gcgggcGGGGaggaaag
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2514 - 2526	(+)	0.866	0.904	gcggGCGGggagg
V$ETSF/PU1.01	Pu.1 (Pu120) Ets-like transcription factor identified in lymphoid B-cells	0.89	2517 - 2537	(+)	1.000	0.901	ggcggggaGGAAaggggcgg
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2518 - 2526	(+)	1.000	0.991	gcGGGGagg
V$MAZF/MAZ.01	Myc associated zinc finger protein (MAZ)	0.90	2519 - 2531	(+)	1.000	0.910	cgggGAGGaaagg
V$ZBPF/ZNF219.01	Kruppel-like zinc finger protein 219	0.91	2519 - 2541	(-)	1.000	0.937	cccaccgCCCCctttcctccccg
V$NFAT/NFAT.01	Nuclear factor of activated T-cells	0.95	2522 - 2540	(+)	1.000	0.970	ggaGGAAaggggcggtgg
V$ZBPF/ZBP89.01	Zinc finger transcription factor ZBP-89	0.93	2522 - 2544	(-)	1.000	0.946	ctccccaccgCCCCctttcctcc
V$EGRF/EGR1.02	EGR1, early growth response 1	0.86	2524 - 2540	(+)	1.000	0.865	aggaaaggGGGCggtgg
V$ZBPF/ZNF202.01	Transcriptional repressor, binds to elements found predominantly in genes that participate in lipid metabolism	0.73	2525 - 2547	(-)	1.000	0.775	cctctcCCCAccgccccctttcc
V$GLIF/ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-paired homolog, Drosophila)	0.89	2527 - 2541	(-)	1.000	0.937	cccaccgCCCCcttt
V$RREB/RREB1.01	Ras-responsive element binding protein 1	0.80	2528 - 2542	(-)	1.000	0.820	cCCCAccgcccccctt
V$SP1F/SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription factor	0.88	2528 - 2542	(+)	1.000	0.911	aaggGGGCggtgggg
V$EKLF/KKLF.01	Kidney-enriched kruppel-like factor, KLF15	0.91	2533 - 2549	(+)	1.000	0.958	ggcggtGGGGagagggc
V$SREB/SREBP.02	Sterol regulatory element binding protein	0.80	2534 - 2548	(-)	0.750	0.838	cccTCTCcccaccgc
V$MZF1/MZF1.01	Myeloid zinc finger protein MZF1	0.99	2537 - 2545	(+)	1.000	1.000	gtGGGGaga
V$BNCF/BNC.01	Basonuclin, cooperates with USF1 in rDNA PolI transcription)	0.85	2545 - 2563	(+)	1.000	0.887	agggccgcgcTGTCccgag
V$CDEF/CDE.01	Cell cycle-dependent element, CDF-1 binding site (CDE/CHR tandem elements regulate cell cycle dependent repression)	0.87	2546 - 2558	(+)	1.000	0.886	gggcCGCGctgtc

24 matches found in this sequence.

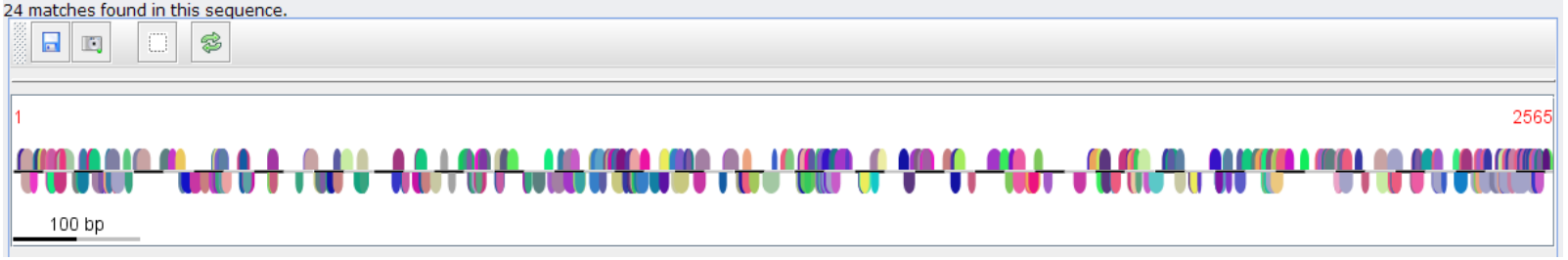

Table A.4 Transcription Factor Response Elements in the Pln Promoter Sequence The table below represents a list of potential transcription factor response elements in the human and mouse Pln promoter regions. The list was compiled by comparing the MatInspector data and researching signaling pathways relevant to prostate cancer tumor growth and metastasis.

Transcription Factor	Iozzo Promoter (counting) Start = +1, numbers are all negative	Iozzo Promoter (MatInspector) (-2565 = 1)	Human Promoter from Ensembl (-2565 = 1)	Mouse Promoter from Ensembl (-2566 = 1)
NF-CTF1	2527 – 2512 (AP2/NF-CTF1) 1947 – 1935	38 – 58 (-) 1655 – 1675 (+) 2329 – 2349 (-)	55 – 75 (-) 1665 – 1685 (+) 2328 – 2348 (-)	1460 – 1480 (-)
NFkappaB	2469 – 2460	95 – 107 (+) 137 – 149 (+) 138 – 150 (-)	112 – 124 (+) (c-Jun/ATF2) 154 – 166 (+) 155 – 167 (-)	99 – 111 (+) 339 – 351 (+)
GATA-1	2392 – 2387 2240 – 2235 2109 – 2104 2058 – 2053 2000 – 1995 1840 – 1835 1830 – 1825 1727 – 1722 1558 – 1545 (GATA-1/CEBP)	170 – 182 (-) 321 – 333 (-) 504 – 516 (-) 561 – 573 (-) 733 – 745 (+) 743 – 755 (-) 835 – 847 (-) 1004 – 1016 (-) 1712 – 1724 (-) (Lmo2, GATA ½ site)	187 – 199 (-) 338 – 350 (-) 471 – 483 (-) 521 – 533 (-) 578 – 590 (-) 750 – 762 (+) 760 – 772 (-) 852 – 864 (-) 1022 – 1034 (-)	445 – 457 (+) (Lmo2, GATA ½ site) 479 – 491 (+) 1111 – 1123 (-) 1635 – 1647 (-)
AP-2	2527 – 2512 (AP2/NF-CTF1) 2375 – 2368 1701 – 1694 1489 – 1476 (AP2, H-APF-1) 1362 – 1355 1036 – 1029 317 – 310 303 – 293 (2 AP-2) 271 – 263 (AP-2/Sp1) 259 – 252 157-150 132 – 122 (AP-2/Sp1) 73 – 66	1642 – 1656 (-) (AP-2α) 1690 – 1704 (+) (AP-2) 2431 – 2445 (-) (AP-2α)	1652 – 1666 (-)(AP-2α) 1700 – 1714 (+) 2432 – 2446 (-)(AP-2α)	1352 – 1366 (+) (AP-2) 1352 – 1366 (-)(AP-2α) 2407 – 2421 (+)(AP-2α) 2483 – 2497 (+)(AP-2α)
Glucocorticoid Receptor	1901 – 1896 512 – 507	2043 – 2061 (+)	--Not present—	829 – 847 (-) 1486 – 1504 (-)
c-Ets-1	1802 – 1795	965 – 985 (+) 2205 – 2225 (+)	983 – 1003 (+) 2205 – 2225 (+)	1239 – 1259 (+) 1355 – 1375 (-)
Sp1	1688 – 1683 1125 – 1117 1071 – 1066	873 – 887 (-) 2293 – 2307 (-) 2366 – 2380 (+)	890 – 904 (-) 2293 – 2307 (-) 2366 – 2380 (+)	2334 – 2348 (+) 2355 – 2369 (+) 2413 – 2427 (+)

	948 – 940 917 – 909 698 – 690 271 – 263 (AP-2/Sp1) 232 – 227 197 – 189 132 – 122 (AP-2/Sp1) 35-29	2435 – 2449 (+) 2446 – 2460 (+) 2485 – 2499 (-) 2503 – 2517 (+) 2508 – 2522 (+) 2528 – 2542 (+)	2436 – 2450 (+) 2447 – 2461 (+) 2483 – 2497 (+) 2503 – 2517 (+) 2508 – 2522 (+) 2512 – 2526 (+) 2528 – 2542 (+)	2509 – 2523 (+) 2528 – 2542 (+)
CEBP	1558 – 1545	653 – 665 (+) (CHOP, C/EBPα)	670 – 682 (+)(CHOP, C/EBPα)	2034 – 2048 (+)
TEF-1	811 – 803	1801 – 1813 (-)	1310 – 1326 (+)	138 – 150 (-) 255 – 267 (-) 1651 – 1663 (-)
Pu. 1	763 – 758	487 – 507 (-) 1797 – 1817 (+) (Pu120) 2059 – 2079 (+) 2184 – 2204 (+)	504 – 524 (-) 2062 – 2082 (+) 2184 – 2204 (+) 2517 – 2537 (+) (Pu120)	614 – 634 (-) 1729 – 1749 (+)
ATF/CREB **Tax/CREB**	729 – 722 451 – 443	52 – 72 (-) (c-Jun/ATF2) ~~53 – 73 (+) (ATF2)~~ ~~357 – 377 (+) (ATF)~~ 751 – 771 (-) (Tax/CREB) 1829 – 1849 (+) (CREB) 1832 – 1852 (+) (ATF) 1849 – 1869 (-) (Tax/CREB)	69 – 89 (-) (c-Jun/ATF2) 768 – 788 (-) 1856 – 1876 (-)	511 – 531 (+) (CREB only) 871 – 891 (+) 1580 – 1600 (-) 2395 – 2415 (+)
GC Box	119 – 106 99 – 81 (2) 62 – 49	2466 – 2480 (+) 2471 – 2485 (+)	2467 – 2481 (+) 2472 – 2486 (+)	2453 – 2467 (+) 2489 – 2503 (+)
TCF/LEF-1	--Not identified--	1026 – 1042 (+) 1305 – 1321 (+)	1044 – 1060 (+) 1318 – 1334 (+)	428 – 444 (-) 607 – 623 (-) 810 – 826 (-) 1304 – 1320 (+)
Consitutive Androstane	--Not identified--	1236 – 1260 (-) 1357 – 1387 (+)	1368 – 1392 (+)	803 – 827 (-)
Smad3	--Not identified--	1238 – 1246 (+) 1247 – 1255 (+) 2378 – 2386 (-)	1264 – 1272 (+) 2378 – 2386 (-)	1106 – 1114 (+) 1762 – 1770 (-) 2277 – 2285 (-)
Elk-1	--Not identified--	849 – 869 (-)	866 – 886 (-)	78 – 98 (-) 193 – 213 (-) 1125 – 1145 (-) 1826 – 1846 (+)
CKrox	--Not identified--	1819 – 1835 (-)	1828 – 1844 (-)	2524 – 2540 (+)
RREB1	--Not identified--	2364 – 2378 (-) 2473 – 2487 (-)	631 – 645 (-) 2364 – 2378 (-) 2474 – 2488 (-) 2528 – 2542 (-)	2264 – 2278 (-) 2425 – 2439 (-) 2542 – 2556 (-) 2550 – 2564 (-)
GFI1	--Not identified--	1186 – 1200 (-) 1291 – 1305 (-) 1398 – 1412 (-)	1204 – 1218 (-) 1304 – 1318 (-) 1335 – 1349 (-) 1408 – 1422 (-)	1569 – 1583 (+)
Androgen Receptor	--Not identified--	89 – 107 (-) 110 – 128 (+)	106 – 124 (-) 127 – 145 (+)	139 – 157 (+) 139 – 157 (-) 866 – 884 (+) 969 – 987 (+) 1675 – 1693 (-) 1719 – 1737 (-)
PBX1	--Not identified--	1303 – 1319 (+)	1338 – 1354 (+)	1564 – 1580 (+)

				heterodimer 1746 – 1762 (+) homodomain
Nkx3.2	--Not identified--	259 – 273 (-)	276 – 290 (-) 1936 – 1950 (+)	480 – 494 (+)