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(54) Titre : METHODE DE DIAGNOSTIC DU CANCER DE LA VESSIE.

(54) Title: METHOD OF DIAGNOSING BLADDER CANCER.

(57) Abrégé/Abstract:

The present invention relates to a method of diagnosing cancer in a subject comprising detecting in the DNA of said subject at least one hypermethylated CpG island associated with said cancer, wherein an elevation in the level of methylation in said CpG island of said subject, relative to the level of methylation in said CpG island of a control subject, is indicative of said CpG island being hypermethylated.

Abstract

The present invention relates to a method of diagnosing cancer in a subject comprising detecting in the DNA of said subject at least one hypermethylated CpG island associated with said cancer, wherein an elevation in the level of methylation in said CpG island of said subject, relative to the level of methylation in said CpG island of a control subject, is indicative of said CpG island being hypermethylated.

Title: Method of diagnosing bladder cancer.

FIELD OF THE INVENTION

The present invention is in the field of bladder cancer diagnosis, and in particular the methods for predicting the progression of bladder cancer tumors. The invention provides diagnostic methods and diagnostic compositions for use in such methods. The invention further provides therapeutic targets for treating specific forms of bladder cancers.

BACKGROUND OF THE INVENTION

Bladder cancer is the fifth most common cancer in the western world with an incidence of 20 new cases per year per 100,000 people in the U.S. Unfortunately, these statistics do not include superficial pTa bladder cancer, which represents the most common type of bladder cancer. In the Netherlands, the incidence of both superficial and invasive bladder cancer is estimated as about 30 new cases per year per 100,000 people. This is in accordance with data from global cancer statistics for the western world. Superficial bladder tumors are removed by transurethral resection. However, up to 70% of these patients will develop one or more recurrences, and it has been estimated that 1 in 1,450 people is under surveillance for bladder cancer in the United Kingdom. Cystoscopy is an uncomfortable, invasive, and expensive procedure, but currently remains the gold standard for detection of recurrences. Because patients have to be monitored perpetually and have a long-term survival, bladder cancer is the most expensive cancer when calculated on a per patient basis.

Hence there exists a need for an inexpensive, noninvasive, and simple procedure for the detection of bladder cancer. Cytology done on voided urine is a noninvasive procedure with up to 100% specificity. Unfortunately, this method is limited by its sensitivity, which is especially poor for low-grade

tumors. Because of this limited sensitivity, alternative methods need to be developed for the detection of tumor cells in voided urine.

SUMMARY OF THE INVENTION

The present inventors have found that the methylation of a number of specific CpG islands (CGIs) in the DNA of cells shed in the urine of a subject is indicative of the presence of a tumor, in particular a bladder tumor. Thus, aberrant methylation of these CpG islands in the DNA of a subject may be used as diagnostic and/or prognostic marker as well as a therapeutic target.

The present finding has been found to be particularly advantageous in the case of bladder cancer diagnostics (including disease prognosis and prediction of disease recurrence and progression), since the detection of methylation may occur in DNA (of cells) in a sample of urine obtained from the subject to be diagnosed. In particular urothelial cells present in said urine sample are used for this purpose. The skilled person will understand that diagnostic methods as indicated herein may make use of any body sample in which DNA comprising the aberrant methylations as defined herein can be detected, including biopsies of cancerous tissue, or tissue suspected of being malignant.

The present inventors have demonstrated the suitability of using methylation of specified CpG islands as diagnostic markers in bladder cancer diagnostics, such as for:

- detection of recurrent cancer in DNA isolated from patient urine, and
- detection of primary cancer in DNA isolated from patient urine.

Thus, in a first aspect, the present invention provides a method for diagnosing cancer in a subject comprising detecting in the DNA of said subject at least one hypermethylated CpG island associated with said cancer, wherein an elevation in the level of methylation in said CpG island of said subject, relative to the level of methylation in said CpG island of a control subject, is indicative of said CpG island being hypermethylated. The presence of a

hypermethylated CpG island might indicate that the subject is at risk of, or suffering from, a cancer.

Preferably said CpG island is selected from the group consisting of the CpG islands listed in Table 1, Table 2, Table 3, Table 4, Table 5, Table 7, Table 9, Table 10 and Table 12.

In a preferred embodiment of methods of the invention, said cancer is bladder cancer.

In another preferred embodiment of methods of the invention, said method comprises detection of recurrent forms of cancer in DNA isolated from patient urine and wherein said at least one CpG islands methylation associated with cancer selected from the group consisting of the CpG islands listed in Table 1, Table 2, Table 3, Table 4, Table 5, Table 7, Table 9, Table 10 and Table 12.

In yet another preferred embodiment of methods of the invention, said method comprises detection of primary forms of cancer in DNA isolated from patient urine and wherein said at least one CpG islands methylation associated with cancer selected from the group consisting of the CpG islands listed in Table 1, Table 2, Table 3, Table 4, Table 5, Table 7, Table 9, Table 10 and Table 12.

In still a further preferred embodiment of methods of the invention, said DNA is obtained from a urine sample of said subject.

In another preferred embodiment of methods of the invention, said bladder cancer is non muscle-invasive bladder cancer. Alternatively, said bladder cancer is muscle-invasive bladder cancer. In a further preferred embodiment, said method provides detection of differential methylation of one or more of the genes provided in Table 7. Differential methylation of one or more of the genes provided in Table 7 is used to discriminate between subgroups of bladder cancer, such as between NMI-wt and MI and NMI-mt groups.

In a preferred embodiment of methods of the invention, general inflammatory cells in urine, preferably lymphocytes, are detected by

methylation of at least one of the CGIs listed in Table 9. Table 9 indicates a number of CGIs methylated in blood but not in bladder cancer. The differential methylation of these CGIs, which can be detected in DNA (of cells) in a sample of urine obtained from the subject to be diagnosed, and in particular in urothelial cells present in said urine sample, are useful for the detection of lymphocytes in urine, or in general inflammatory cells in urine, which is indicative of cystitis. Positive detection of the presence of inflammatory cells in the urine can be used to diagnose infection or non-infective inflammation of the urinary tract and kidney.

In a preferred embodiment, said method comprises detection of recurrent cancer in DNA isolated from patient urine. This method entails the detection of specific CpG island methylations associated with recurrent forms of the cancer.

In another preferred embodiment, said method comprises detection of primary cancer in DNA isolated from patient urine. This method entails the detection of specific CpG island methylations associated with primary forms of the cancer.

The present inventors have further demonstrated the suitability of using methylation of specified CpG islands as prognostic markers in bladder cancer diagnostics, such as for:

- prediction of disease course based on analysis of tumor-derived or urine derived DNA, including:
 - prediction of invasive potential of non-muscle invasive urothelial carcinomas;
 - prediction of urothelial carcinoma-specific survival, and
 - prediction of presence/absence of lymph node and distant metastases caused by urothelial carcinomas

Thus, in a second aspect, the present invention provides a method for the prediction of the recurrence, progression or prognosis of cancer, in particular bladder cancer, comprising detecting in the DNA of said subject at least one hypermethylated CpG island associated with said cancer, wherein an

elevation in the level of methylation in said CpG island of said subject, relative to the level of methylation in said CpG island of a control subject, is indicative of said CpG island being hypermethylated. The presence of a hypermethylated CpG island might indicate that the subject is at risk of cancer recurrence, progression of a cancer, and/or poor prognosis. A preferred method for the prognosis of a risk of cancer recurrence, progression of a cancer, and/or poor prognosis comprises detection of one or more methylated CpGs in CGIs of the genes listed in Table 12B, whereby the CGIs are preferably chosen from GPR103, DBC1 and/or GATA2 genes. Said cancer is preferably bladder cancer.

In a preferred embodiment of said method for the prediction of the recurrence, progression or prognosis of cancer, said CpG island is selected from the group consisting of the CpG islands listed in Table 1, Table 2, Table 3, Table 4, Table 5, Table 7, Table 9, Table 10 and Table 12, preferably from Table 5 and Table 10.

In aspects of the present invention the methylation of dinucleotide in or methylation level of a CpG island may be determined by any method available to the skilled person. Preferably said method comprises methylation-specific PCR (MSP). Alternatively, or additionally, use may be made of a multiplex ligation-dependent probe amplification (MLPA).

The present inventors have further demonstrated the suitability of using methylation of specified CpG islands as markers in bladder cancer diagnostics for prediction of therapeutic response, such as for prediction of failure or success of (neo)-adjuvant therapies.

The present inventors now envision as part of their invention the use of demethylating agents capable of specifically demethylating the CpG islands associated with tumor, in particular bladder cancer, as defined herein. They may also be of use as priming therapy for chemotherapeutic regimes.

Hence, the present invention provides a method for the treatment or prevention of cancer, in particular bladder cancer, comprising administering to a subject in need of such treatment a therapeutically effective amount of a

demethylating agent capable of selectively demethylating at least one of the CpG islands methylations associated with cancer as described herein.

Clinical outcome of demethylating agents may depend on specific methylation profiles.

The present invention further provides pharmaceutical compositions comprising demethylating agents capable of selectively demethylating at least one of the CpG islands methylations associated with cancer as described herein.

The present invention further provides diagnostic compositions comprising PCR primers and reagent or probes capable of selectively hybridising under stringent conditions to hypermethylated CpG islands as defined herein.

DETAILED DESCRIPTION OF THE INVENTION

As used herein the term "CpG island" refers to genomic regions that contain a high frequency of CG nucleotides. In mammalian genomes, CpG islands are typically 300-3,000 base pairs in length. They are in and near approximately 40% of promoters of mammalian genes (about 70% in human promoters). The "p" in CpG notation refers to the phosphodiester bond between the cytosine and the guanine. CpG islands are characterized by CpG dinucleotide content of at least 60% of that which would be statistically expected (~4-6%), whereas the rest of the genome has much lower CpG frequency (~1%), a phenomenon called CG suppression. Unlike CpG sites in the coding region of a gene, in most instances, the CpG sites in the CpG islands of promoters are unmethylated if genes are expressed.

As used herein the term "CpG island methylation" refers to a methylation of at least one CG dinucleotide in a CpG region as defined herein. Hence, the methods of the present invention include the detection of at least a single CG dinucleotide being methylated in a CpG island as defined herein.

As used herein the term "hypermethylated CpG islands" refers to a CpG island exhibiting an elevation in the level of methylation, relative to the

level of methylation in the same CpG island of a control subject. Again, the level of methylation includes the presence of a single methylated CG dinucleotide in the CpG island as compared to the control situation, in which the same CpG island is unmethylated. Also, methods of the invention include embodiments wherein the methylation of a single CG dinucleotide in a CpG island as defined herein is detected among other methylated sites.

As used herein, "cancer" shall be taken to mean any one or more of a wide range of benign or malignant tumors, including those that are capable of invasive growth and metastasis through a human or animal body or a part thereof, such as, for example, via the lymphatic system and/or the blood stream. As used herein, the term "tumor" includes both benign and malignant tumors or solid growths, notwithstanding that the present invention is particularly directed to the diagnosis or detection of malignant tumors and solid cancers. Typical cancers include but are not limited to carcinomas, lymphomas, or sarcomas, such as, for example, ovarian cancer, colon cancer, breast cancer, pancreatic cancer, lung cancer, prostate cancer, urinary tract cancer, uterine cancer, acute lymphatic leukemia, Hodgkin's disease, small cell carcinoma of the lung, melanoma, neuroblastoma, glioma, and soft tissue sarcoma of humans; and lymphoma, melanoma, sarcoma, and adenocarcinoma of animals.

The term "bladder cancer" as used herein refers in general to urothelial cell carcinoma, i.e. carcinomas of the urinary bladder, ureter, renal pelvis and urethra. The term includes reference to the non muscle-invasive (NMI) or superficial forms, as well as to the more dangerous muscle invasive (MI) types. Also included in the term is reference to the primary forms as well as to recurrent forms of the cancer.

The NMI types may further be subdivided into FGFR3⁺ and FGFR3⁻. Mutations in the fibroblast growth factor receptor 3 (FGFR3, indicated herein as FGFR3⁺) occur in 50% of primary bladder tumors. It is known (e.g. Van Oers et al. 2005 Clin. Cancer Res; 11(21), pp. 7743-7748) that an FGFR3 mutation is associated with good prognosis, illustrated by a significantly lower

percentage of patients with progression and disease-specific mortality. FGFR3 mutations are especially prevalent in low grade/stage tumors, with pTa tumors harboring mutations in 85% of the cases. These tumors recur in 70% of patients. Efficient FGFR3 mutation detection for prognostic purposes and for detection of recurrences in urine is an important clinical issue. Thus, in preferred embodiments of the present invention the method of diagnosis includes further the step of detecting an FGFR3 gene mutation. This additional step may be performed prior to, during or after the step of detecting the hypermethylated CpG island as indicated herein. The detection of the FGFR3 gene mutation as indicated in Van Oers et al (this reference is expressly referred to for the methods and mutations to be detected as described therein) indicates the cancer is very likely of the non invasive type.

"Subject" as used herein includes, but is not limited to, mammals, including, e.g., a human, a non-human primate, a mouse, a pig, a cow, a goat, a cat, a rabbit, a rat, a guinea pig, a hamster, a degu, a horse, a monkey, a sheep, or other non-human mammal; and non-mammal animals, including, e.g., a non-mammalian vertebrate, such as a bird (e.g., a chicken or duck) or a fish, and an invertebrate.

A method of the invention can be performed on any suitable body fluid, such as for instance on abdominal fluid, pleural fluid, bronchial fluid, pericardial fluid, blood, serum, milk, plasma, sweat, tears, urine, peritoneal fluid, lymph, vaginal secretion, semen, spinal fluid, cerebrospinal fluid, ascitic fluid, saliva, stool, sputum, mucus or breast exudate. Preferably, a method of the invention is performed on blood, serum, plasma or ascitic fluid, more preferably serum. Depending on the methods employed, the skilled person will be capable of establishing the amount of sample required to perform the various steps of the method of the present invention. Generally, such amounts will comprise a volume ranging from 0.01 μ l to 100 ml or more. Preferred samples are urine samples.

In even more preferred embodiments of aspects of the invention the cell fraction of urine, preferably tumor cell fraction, is used. Urine cell fractions may be obtained by filtration or centrifugation. The cellular DNA may subsequently be analyzed, for instance upon extraction of the DNA from the cells, although *in situ* methods performed on whole cells are also envisioned.

The skilled physician or biologist will be familiar with the various ways of providing a sample of a body fluid from a subject, in particular an urine sample. Urine collection and preparation of the sample for CpG island methylation analysis suitably comprises for instance the collection of a urine sample were collected into a 50 ml centrifuge tube. The sample may optionally be used for additional tests, such as dip stick tests for leucocytes, erythrocytes and nitrite as routinely performed in the art. The cells in the urine are suitably spun down for 10 min @ 3000 rpm; 4°C. An amount of supernatant is suitably stored at -80°C for later use. The cell pellet may then be washed, for instance by adding a suitable amount of PBS (phosphate-buffered saline), such as 10 ml, to the cell pellet. After mixing and centrifugation (e.g. 10 min @ 3000 rpm; 4°C), the PBS may be discarded. The cell pellet may then be resuspended in PBS (e.g. 1 ml) and transferred to a microcentrifuge tube. The suspension is then suitably centrifuged (e.g. 5 min @ 6000 rpm; 4°C). The supernatant can then be carefully removed and the cell pellet may be stored in a -80°C freezer until DNA extraction.

Commercial systems for DNA isolation from blood, urine and tissue are available from various suppliers of molecular biological reagents. Special reference is made to the DNeasy® Blood & Tissue Kit and DNeasy® 96 Blood & Tissue Kit available from QIAGEN GmbH, Hilden, Germany.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms. The

precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the polynucleotide or polypeptide compositions in the individual to which it is administered.

The present invention also pertains to pharmaceutical compositions comprising demethylating agents as defined herein.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as a polypeptide, polynucleotide, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally,

auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Once formulated, the pharmaceutical compositions of the invention can be (1) administered directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) delivered *in vitro* for expression of recombinant proteins.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into the nervous system. Other modes of administration include topical, oral, suppositories, and transdermal applications, needles, and particle guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Specific aspects of the present invention relate to the CpG islands indicative of certain forms of cancer emerging for instance from the following comparisons:

- A) CpG islands hypermethylated in non muscle-invasive (NMI) bladder cancer (BC) that are FGFR3 wild type, herein referred to as NMI-BC wt, vs. muscle-invasive (MI) bladder cancer herein referred to as MI-BC (n=31)
- B) CpG islands hypermethylated in MI-BC vs. NMI-BC wt (n=11)
- C) CpG islands hypermethylated in all bladder cancers (n=62)
- D) CpG islands hypermethylated in NMI-BC-FGFR3 wild type vs. NMI-BC-FGFR3 mutant (n=31), and
- E) Hypermethylated CpG islands predicting progression of disease or death of disease (resp. n=3 and n=11)).

The methods of the invention comprise the detection of

hypermethylated CpG islands in the DNA of a subject. As indicated, hypermethylation is a relative term indicating that the methylation level of the respective CpG island is higher than or elevated with respect to the methylation level of the corresponding CpG island in a healthy control subject.

The methods of the invention comprise the detection of at least one hypermethylated CpG island in the DNA of a subject. Since there are many CpG island indicated herein whose hypermethylation is indicative of cancer, in particular bladder cancer, the method preferably entails the detection of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 25, 26, 27, 28, 29, 30, or more, such as 35, 40, 45, 50, 55, 60, 65 or more hypermethylations in the DNA of a subject. In such instances, it is possible to speak of a CpG island methylation profile. In such a profile, the percentage of positively detected CpG islands is preferably at least 50%, more preferably at least 70%, more preferably at least 90%.

The CpG island methylation profiles may comprise of between 2-25 CpG islands for diagnostic purpose, such as determining whether a bladder cancer is present, and/or whether it is an NMI or MI type.

The CpG island methylation profiles preferably comprise of between 2-25, more preferably more, such as between 50 and 150, for instance about 100 CpG islands for diagnostic purpose, such as determining the prognosis of an NMI to develop into a more aggressive MI type of tumor. Thus, the present invention provides for a prognostic method for determining whether an NMI type bladder cancer can develop into an MI type.

It is also possible to use a method of the present invention to distinguish between a primary or recurrent form of the tumor.

The skilled person is well aware of the various methods that have been developed to analyze DNA methylation. Amongst these methods are restriction enzyme- and sodium bisulfite based approaches, as well as multiplex ligation-dependent probe amplification (MLPA) approaches.

Restriction-enzyme based methods are based on the inability of methylation sensitive restriction enzymes to cleave methylated cytosines in

their recognition site. The identification of the methylation status relies on Southern hybridization techniques or PCR and is based on the length of the digested DNA fragment. The inability to digest methylated sequences results in longer fragments, indicating a methylated CpG dinucleotide. Restriction-enzyme based methods are simple, rapid and highly sensitive and are suitable for genome-wide methylation analyses as well as marker discovery techniques.

Preferred methods for application in aspects of the present invention is sodium bisulfite (NaHSO_3) based detection of DNA methylation. Such methods are essentially based on the fact that treatment of single-stranded DNA with sodium bisulfite results in sequence differences due to deamination of unmethylated cytosines to uracil under conditions whereby methylated cytosines remain unchanged. The difference in methylation status marked by bisulfite reactivity can accurately be determined and quantified by PCR-based technology. Bisulfite sequencing techniques (such as described in Frommer et al. *Proc. Natl. Acad. Sci. USA* 89 (1992), 1827–1831) provide qualitative data on the methylation status of 5-methylcytosines in the amplicon between the sequence primers and thus requires primers specific for bisulfite converted, but not specific for unmethylated or methylated DNA. This approach provides detailed information on the methylation status of all CpG-sites.

A methylation-specific PCR (MSP) assay for determining the methylation status of CpG islands may be used. Such methods are for instance described in Herman et al. 1996 (*Proc. Natl. Acad. Sci. USA* 93 (1996), 9821–9826) and Herman and Baylin (*Current Protocols in Human Genetics* 10 (1998), 10.16.11–10.16.10). The MSP assay is based on the use of two distinct methylation-specific primer sets for the sequence of interest. The unmethylated (U) primer only amplifies sodium bisulfite converted DNA in unmethylated condition, while the methylated (M) primer is specific for sodium bisulfite converted methylated DNA. Using MSP, 1 methylated allele may be detected in a background of 1000 unmethylated alleles. MSP is very suitable for analyzing the methylation status of CpG dinucleotides in a CpG-island. The method may also be applied for high-throughput analysis of clinical

samples. The most critical parameters determining the success and specificity of MSP, i.e. bisulfite conversion, primer design and PCR as well as several post PCR validation approaches are discussed in Derks et al. 2004 (Cellular Oncology 26 (2004) 291–299). Methylation Specific PCR (MSP) is described in great detail in US5,786,146, US6,017,704, US6,200,756 and US6,265,171 and International Patent WO 97/46705.

Commercial systems for DNA methylation analysis using MSP are available from various suppliers of molecular biological reagents. Special reference is made to the EZ DNA Methylation-Startup™ Kit and EZ DNA Methylation-Direct™ Kit available from Zymo Research Corp. Orange, CA, U.S.A.

Use can also be made, alone, or in combination with any of the above, of the MLPA technique. The MLPA technique is for instance described in great detail in Schouten *et al.*, 2002 (Nucleic Acids Research 3(12) e57, 13 pp.).

Also, use can be made of a microarray chip to which DNA of a subject is hybridized. Such arrays for CpG islands are for instance commercially available from Agilent Technologies Inc., Santa Clara, USA.

Herein below are provided the following Tables:

Table 1. Coordinates of selected regions containing relevant CpG islands based on Homo sapiens full genome as provided by UCSC (hg18, Mar. 2006). These CpG islands are aspect of the present invention as hypermethylation of these regions is associated with cancer, preferably bladder cancer and/or certain forms of said cancer.

Table 2. CpG islands differentially methylated in NMI-BC wt vs. invasive BC. These 42 CpG islands are aspect of the present invention as hypermethylation of these regions is associated with either NMI or more aggressive MI forms of the cancer. Hence, these regions are particularly indicated for use in diagnostic methods wherein typing of the cancer is relevant. The table provides data on CpG islands hypermethylated in non

muscle-invasive (NMI) bladder cancer (BC) that are FGFR3 wild type, herein referred to as NMI-BC wt, vs. muscle-invasive (MI) bladder cancer herein referred to as MI-BC (n=31) as well as CpG islands hypermethylated in MI-BC vs. NMI-BC wt (n=11).

Table 3. CpG islands hypermethylated in (bladder) cancer. These 62 CpG islands are aspect of the present invention as hypermethylation of these CpG islands is associated with (bladder) cancer.

Table 4. CpG islands hypermethylated in NMI-BC FGFR3 wt vs NMI-BC FGFR3 mut. These 31 CpG islands are aspect of the present invention diagnostic markers for typing of (bladder) cancers and in particular indicate the relevance of FGFR3 mutations in bladder cancer. These 31 CpG islands may be used for diagnosis of FGFR3 wt primary and recurrent tumors in for instance urine. These 31 CpG islands may also be used for detection of FGFR3 wt tumors in patients with a FGFR3 mt (mutant) primary tumor. Alternatively, these 31 CpG islands may be used for the identification of recurrences that progressed to muscle-invasive disease or to stage pT1 or to high grade (WHO 2004 grading system) or G3(WHO grading system 1973). These 31 CpG islands may also be used to present specific targets for therapy in NMI-BC tumors that are FGFR3 wt.

Table 5. CpG islands potentially involved in progression and death of disease. These 14 CpG islands are aspect of the present invention as hypermethylation of these regions is associated with prediction of the recurrence, progression or prognosis of cancer of cancer, in particular bladder cancer.

Table 7 (including Tables 7A and 7B) indicates differentially labeled CGIs between subgroups of bladder cancer and/or between subgroups of bladder cancer and a reference sample (i.e. blood).

Table 9 indicates a number of CGIs methylated in blood but not in bladder cancer. The differential methylation of these CGIs, which can be detected in DNA (of cells) in a sample of urine obtained from the subject to be diagnosed, and in particular in urothelial cells present in said urine sample,

are – apart from the purpose indicated herein for diagnosing bladder cancer – also useful for the detection of lymphocytes in urine, or in general inflammatory cells in urine, which is indicative of cystitis. Positive detection of the presence of inflammatory cells in the urine can be used to diagnose infection or non-infective inflammation of the urinary tract and kidney.

Table 10 provides a list of hypermethylated CGIs that show 3 or more CpG dinucleotides highly methylated in a specific CGI. This list comprises 82 CGIs representing 71 genes and 11 CGIs not directly associated with a gene. A preferred gene from Table 10 is MEIS1, showing the highest degree of methylation with a fold change of 4.8 and an average fold change of 2.2 across the 10 probes that were present on the array for this CGI.

Table 12 (including Tables 12A and 12B) provides a list of CGIs that are differentially methylated between tumors and urine from non-bladder cancer control. These genes represent potential biomarkers for urine tests.

LEGEND TO THE FIGURES

Figure 1. Methylation pattern and expression of selected genes. (a) MEIS1, (b) NR4A2 and (c) HOXA9. (d), (e), (f) are Box plots representing the expression profiles which were taken from oncomine

Figure 2. Comparison of differential methylation between subgroups. (a) Unsupervised analysis performed on all probes present on the 244K array without selection: PCA showing the distinct bladder tumor groups cluster separately (Red-MI, Blue-NMI-mt and Green NMI-wt), (b) Venn diagram showing the number of CGIs that are differentially methylated

Figure 3. Semi-supervised analyses between bladder tumor subgroups involving hierarchical clustering and PCA. (a) Clustering and PCA of NMI-mt and NMI-wt tumors, (b) Clustering and PCA of MI and NMI-wt tumors, (c) Clustering and PCA of NMI-mt and MI tumors.

Figure 4. Most methylated gene-associated CGIs are targets of polycomb complexes. (a) Overrepresentation of PcG genes in BC methylated CGIs. (b), Venn diagram showing the overlap in PcG target genes between

bladder cancer subgroups.

Figure 5. A. Hierarchical clustering of GGMA data of all the investigated samples. B. Heat map showing the probes which are methylated in all tumor subgroups vs. blood and urine; C) Methylation of two CpGs in the MEIS1 CGI (black peaks: methylated CpG, red: not methylated. IM, in vitro methylated DNA; RT112, T24, J82: bladder cancer cell lines; PU: patient urine; NU: normal urine; NB: blood), D) KM curve for progression to muscle-invasive disease based on a combination of methylation of GRP103, DBC1 and GATA2.

TABLE 1. Coordinates of selected regions containing relevant CpG islands based on Homo sapiens full genome as provided by UCSC (hg18, Mar. 2006)

chr1:119333484-119333719	chr1:149638545-149639227	chr1:160220156-160220709
chr1:178464743-178471598	chr1:2072175-2072389	chr1:2106293-2106715
chr1:232106869-232108183	chr1:33385564-33385979	chr1:41122328-41122880
chr1:47672249-47672972	chr1:68288825-68289104	chr1:71284766-71286392
chr10:21828640-21829645	chr10:22804715-22807056	chr10:73437163-73438385
chr10:7449476-7449790	chr10:7489383-7495345	chr12:113657930-113659205
chr12:118612357-118612674	chr12:94776044-94776377	chr13:113930978-113931584
chr13:34950488-34951119	chr13:49595986-49600287	chr13:94152191-94153185
chr14:36205192-36206099	chr14:37746906-37747538	chr14:53488428-53488700
chr15:94688798-94689131	chr15:94696311-94696840	chr15:94705727-94706054
chr15:94712480-94712812	chr16:52873104-52882105	chr16:52873104-52882105
chr16:85098883-85102729	chr16:86294154-86294408	chr16:87372445-87372729
chr17:24303411-24303889	chr17:34157398-34159854	chr17:44074280-44075233
chr17:56827843-56838048	chr17:58865328-58865618	chr17:73932992-73933361
chr17:75377960-75381951	chr17:75531280-75531546	chr18:5186244-5187389
chr18:68359955-68362770	chr19:4059891-4060207	chr19:42586165-42586705
chr19:63420090-63420541	chr19:63784504-63785085	chr2:104835284-104839920
chr2:105864220-105865009	chr2:111591678-111597436	chr2:115635091-115637285
chr2:124498611-124499725	chr2:156892636-156892878	chr2:156893736-156894685
chr2:171384729-171385226	chr2:176737610-176738187	chr2:19424445-19425131
chr2:43251514-43251780	chr2:45249374-45251726	chr2:63134470-63134933
chr2:66525936-66527222	chr2:70984709-70985764	chr2:72224630-72228512
chr20:22505518-22507240	chr20:22510737-22514165	chr20:22514762-22515148
chr20:35582018-35583550	chr20:54012011-54014085	chr20:60061693-60062033
chr21:33316999-33322115	chr21:36990008-36995832	chr21:37857725-37858416
chr21:43350621-43351134	chr3:129688131-129694023	chr3:148591199-148594390
chr3:62330280-62330608	chr3:62331767-62332398	chr4:111780013-111780343
chr4:122520930-122521740	chr4:155881084-155881434	chr4:177159356-177159814
chr4:40134579-40135662	chr4:9756136-9756429	chr5:115810975-115811393
chr5:122461778-122463450	chr5:134390896-134393045	chr5:135442969-135443206
chr5:140724146-140724826	chr5:174091287-174092335	chr6:101023927-101024343
chr6:1549606-1560865	chr6:21704622-21705099	chr6:26312699-26313302
chr7:121727243-121727884	chr7:1481682-1482268	chr7:155266364-155266696
chr7:155288454-155292175	chr7:156895132-156895886	chr7:2082782-2083345
chr7:27164708-27165039	chr7:27219187-27220360	chr7:2724511-2724848
chr7:27251165-27252762	chr7:32768010-32768497	chr7:55040457-55041024
chr7:8449587-8450236	chr7:96488158-96489591	chr8:132985505-132986242
chr8:142288380-142288718	chr8:57520625-57522095	chr8:65661156-65662687
chr8:9798161-9799053	chr9:121170908-121172141	chrX:39749470-39754050
chrX:50040955-50041296		

7; I vs SW; chr1:41122328-41122880; 1; chr1:41122606-41122650; Unknown
CGGATGTGCGCTGGACTCTCGGGGCGGGCGGCCGCTAGTCTCCCTCCTTCGACACCCCGCGCCCTGGGAAC
CTCCTCGCGCGGTTTGGCCACTCGTGCTCTGCGAGTAGGGGGCTTCGGGCGCCCGGCTGTCCCAACCAAG
GTATCGGGATGCGGAGTTGATGGGTGCGGGGCGCTGGGAGGGGGCAGATGAAACGGGCACTCGAAAGG
GGGCGATGCGCGCCGACGCGACGCGGGGTCATTAGCGCGCGGGTGTCAGCGCGCGGGGCGAGGCTTATCGCCC
ATCAGAGCCTGGCGGGGCGGGGCTCCCGACGCGGCTGCCGCGCCCGCGGCGACAGGGCGACGGCGGG
TTCCACGCTCGGGCCCTGGTTTCGGGGGCGTTCTCGGGACGGCGTGCGCGCGCTCACCACCACCGCGGA
GGCGGGGCTGTAAATTAGGATAATTGCGCTGCTCCAGCCTGGGGCAGCTCAGGACCGGGCTGCACCGCGC
TGGCCCGGACGGGCGGGGCGAGGGGTGGCGGGGCCGAGCGATACAGCCCTGGCGCAGTCCG

61; I vs SW; chr10:73437163-73438385; 10; CHST3; INSIDE
CGCCAGACCGGCGGTGCGGGGCCCCCGGGCCACGTGCTGCTCATGGCCACCACGCGCACCGGCTCCT
CTTCTGTTGGGCGAGTTCTTCCACAGGACAGGGCAACATCTTCACTCTTCAGAGCCGCTTGGACATCGAGC
GCACAGTCTCCTTCGAGCGGGGGGGGCCAACGCCGCGGGCTCGGCCCTGGTTACCGCGACGTGCTCA
AGCAGCTCTTCTTCGTGGCAGCTGTACGTGCTGGGACCTTATCAGCCCGCTGCCCGAGGACCACTGAC
TCAGTTTCATGTTCCGCGGGGCTCCAGCCGCTCCGCTGCGAGGACCCGCTGTGTACCGCTTCTGCAAGA
AGGTCTTCGAGAAAGTACCATTGCAAGAACCGCGGCTGCGGCCCTCAACGTGACGCTGGCCGACAGGGC
CTGCGCGCGGCAAGGAGCACATGGCCCTCAAGCGGTTGCGCATCCGCGACCTGACTTCTGACGCGGCTGG
CGGAGGACCCCCGCTGGACTCGCGCTATCCAGTGTGTCGCGACCCCGGGCGCTGTGCCCTGCG
GCATGGTGGCTTCGCGCGCAAGTATAAGACCTGGAAGAAAGTGGCTGGACGACGAGGGGCCAGGACGGCC
TGAGGGAAGAGGAGGTACAGCGCTCGCGGGGCAACTGCGAGAGGATACCGGCTGTCCGCGGAGCTTGGGGCT
CGCGCAAGCCGCGCTGGCTGCGGGGCGGTACATGCTGGTGGCTACGAGGATGTGCGACGCGGGCCGT
GCAGAAGGCCCGGAGATGTACCGCTTCGCGCGCATCCCCCTGACCCCGCGGTGGAAGACTGGATCCAAA
AGAACCGCAGGCGCGCCACAGCGGACGCGGCATCTACTCCACGAGAAGAACTCTCGGAGCAGTTTCGA
GAAGTGGCGCTTACGATGCGCTTCAAGCTGGCCAGGTGGTGACGAGCGGCTGCGGCTGCTGCCATGCGC
CTCTTCGGCTACAACTGGCGGGGACGCGCGCGCCCTACCAACCGCTCAGTCAGCTGCTGGAGGAGAG
GGGCACTTCTGGGTACGTAGGGGGGCGGGGGCCCGTATGCCCTCTCTGTGAAAGGCCTGCCCGCTC
TTTCTCGCGCAGCCTCGACAGAGGGCGGTGACAGCGCCATGACGGGCGAGCGCTCTGTAGCAGTAGG
GCCCCAGCAGGCGTCCAGCCAA

97; I vs SW; chr12:118612357-118612674; 12; CIT; INSIDE
CGGGGCTCTACGGCTCCCGCAGGCGAGCGGCCCTGCTGCTGTCTTCAAACAGCCTCCCGGGGGACCGC
TCTCTCGCGCTGCTGAGCATCCGGCGGGGGACTTCTCTCGCTCCAGGGGGCGGCCAGAGACTTGTCCCT
CGCGAGCTCGGTCCGCCCCCTCGCGCGTACGGTGGGTGTGCTTGGCTCTCGCGGGTGGTGCGGCTTC
GGCGGCGCTTGGCTCGGAGGCCACGCTTGGTAGTGTGCTGTACGTGGCTGGGCTTGGCTTGTTC
GGGCTGTGGCGACACAAGAGAACGTAGGGAGCTGCG

162; I vs SW; chr17:34157398-34159854; 17; PCGF2-PSMB3; DIVERGENT_PROMOTER
CGAGAGGACCCGACCCCGCGGGGAAGGGCGCCCTCCCCCGGCTCGCGGCGCGCCCAAGACATCC
CTTCTCGCGGCCCAAGTCCCGCGCGGTCCACAGGGCGCCCTGTGCCACGGGAGAGCACCCCGGCCAG
ATGGAAGAGGGGTAGACCGGCGAGAGCGAGGGCGCTTTGGCTCGTGGGGAGCGGCGACCAACCCA
GGCGCATCCCGCAAGCCCTCCCGGTGCGCCGGACCTTCCCCCTCGCTACCTCGGAACAGGGTCTGCC
GGGGGCTGCTGCACAAAGAGGGGTGGTTCGAGGAGAGCGCAAACTGTTAAGACGGGAGCGCGTTCG
CCATCTTGGAAGAGAGAGAAAGGGAAGGACAGAAAAAGGAGAACCGGACCGGACCAAGC
TGGGCTAGGGAAGTACGCGGGCGCGGGGGTGGGAAGGACAGGATCGGCTCAGAGCCCCCTCCCATCGG
GGCTTGGCAAGACCGGCGCGCCCATCCCAATCCCGACAGGCTTACAGGAGCGGAGAGCGGAAGGCGAG
GGGAGTCCGCTCCGCTTACTGGGTTCGGGTCCGGTCCGGGTCTCGAGGAGGGGGGATGGAAGGAGG
GAGGGAAGGAGGGGAGGGGGCGCGAGCGCTGTCGCTCGCCCGGGCGGGCGGAGGGGAGAAACCTACG
GTAAGAAAGAGAGTTTGTGAAAGCGGCTTGGGGTGGGAGGAGGAGGGGAGCGGAGGGGACCGAGGGGG
AGGGGAGGGGACCGGAGTGTGGGGGGGAGCAAAATGGCTTTTCTCCAGACAGGAGTAGCTCCGCCC
ACCACTACCCACGTCACCTATTCTTCAGATGCTGGCAGAGAGGGAAGAGAGGGGAGGCTGGC
GGCGCCCTCCCGGCCACCGGCTGCGCGGTCCCTAGCCAGGACGACACCCCTTCCCTTCCATCGGCGCG
CCCCACCCCGGAGGATGGATCTTTATGTTAACCCTCCGCACTAGCCCCCTCCCTTCAAAATATGGGTTC
CCCCACTGACATGTGATGCCCATCCCTAACTGGGCGCCTGAAAAATGGTGAATGGGAATGTGGGTG
AAAGGTGGCTCGTGTCTCCACGCCCGGCTAGACCAAAGGGCGCGGGGTCCGGCGGGGACGCGAC
GCCTTACGCCAGGCGTCCGAGCGATTTTCATT

169; I vs SW; chr17:56827843-56838048; 17; TBX2; INSIDE
CGGAGGGCGGCACAGCTGGAGCGCGGATTTGTGGCACGCGCTCACCGTGTCTGCTCCGGGGAATCCCGACCC
GCTCCCTCGCAAGAGCGTTTCCGAACCGCAACCCAGAGCTGTGAACGCGCGCGCAAGCCCCACTTCCCG

ACCGCCGCCCGTCGACGGTGGGCCCCGTCTAGGGGTCCTTCCCTGCGCTCTACCCCGTCTCTCAAGTCACT
CAGTCGATCGCCCCGTTTACGCTCCCGTGATCCAGACATCCATAACCACGATCTCGCCTCCATGCACATC
CAACGCACGACGGTGACAAACGTGCACCTGACTTCTGCGGACCAGGTGTCTCAAGCGTACAGCGGCCACC
CGCGAACCCGCGCCCCGGGCCAGTGAGTCGTCTGCAGCTCCCCGGTTAGGGGATTCCCCAGAACTCC
GGGAAAGTCACCCGAAGTCCATCCGGGATGCGGCCCTTGGTTCTCGGCCGCGTATCTCGCCCTTAGGTGCA
GAACGACGCCCTTCCAGGGCCACAGCTGCCAGGCTGGGCCCTTGGCCTCGCATCCCCCGGAAGACACAGG
GACGGGGCCACACAGGCCGTGGCTGCGGAGACGCTTCCCCGGGCCACCCCGCGACAGGAGGGAGTCTGA
GCCGCCGCTCTCCCGCGTCCCCGCCCATCCAGCCAGTTGGCCCCACCTGCGCGGGATAATTGGGA
CGGGAGGGAGGCGACGGGAGGGCGGGCTCCAGAGAGACTGCGCGCTGTACGCGCAATTTGTTAA
GTGACGGGACGGGCCGGCGCTGCGGGCTGGGGTACCGAGGCCGCGCCCCACCCAAACGACACT
GGGACCGCGGGGAGCCCGGTCCGGCCGCTAAACCGGGCTGGCTGGCGCCAGGGCTCCGGGAGGTGCG
GTCCGGCGGGGAAGCCGTGATGGGAAGCGACTCTGTCCAGGAGTGTCTTACCACCACTCCTCACG
TCCAGGCAGTGATGACGGCCTGGCGGCACCTCACAGCGGGCCATAGCACGGGGCCACACAGTCCCTT
GAGCTTAGCTGGGCACATTGCTCTGCCACCGAGGGCTTAAGCCAGTCTGCAGCCCGCGCCCGTCACTC
GGACGCAAGTCCGTCTGCTCCGCTCTGCCACGCGCGCACAGCCCGCTTCTGCTGCCCACTGCCCGCG
GGTACGCAACCCCGCCCTGCACA

270; I vs SW; chr21:37857725-37858416; 21; chr21:037857850-037857894; Unknown
CGATTTCCGCAGATTTCTGCTGGAACGTTCTCTCGGGCTCAAGTTTCTGAGAGGACGACGTGGAGA
GTGAGACAAAGATGCTCAAAAGCCAGGAAATCGCAGGCTCGGAAGCCCCACGCATCTCTGAACGCAG
GCCATCTCGGGGCTGCGGCGGGACCAAGCGGACGCTTGCAGGCTGTCGGCGCGGGGCGCGAGCC
GCCGGCGTAGGCCGCTCCAGTGGAAGACCCACCGCTAGGGTTCCAGGGGGCTGCGGACGCTTCCGAG
GGGCCAAAGCGGAAAGAACGCGCCCGCTTGTGCGCCACGTGACCGTCCCCGTCCGCGTCCGACGCAAC
ACGTGACTGTGCGTCCGCGCGCTCGATTGACTGGGAGCTCCCTGGCCACGCCCTAAGCGCCAGCCCCGGG
CTTCGGGGGGCGGTGTGCTGCGGTGGCATGGCGCTTCCGAGCGCGCAGGCGGGGCCAGAGTAGCT
TTTCGGGTATTTGCTACCGGCTCTCGGTAGGGCTGGTCACTTTGCTTGCTGAGCTTCCGCCCTCGCTCC
TTTGGTCCCCAGCAACTTGACGGGACGCGTCCCTCATGAGGCCCTCCAGCGAATGCCCTAAGCTCCGA
AGTTGCTCCGAGGAAACAGGCTTGCTCCGAGGGTGACGCTCCTACTGCCCGTGACGTGC

271; I vs SW; chr21:43350621-43351134; 21; CBS; INSIDE
CTGCTGCACTTGTAAAGTGGGTGCTTCTCAGCTTCATGGTTTGAGGGGTGCAGCCAGCTTCGGCCTAAGT
GGTGTGAGGGTCGAGACCCAGCACCCACACGGGAAGCGCGGTGTCCCGCTTCAGGCTGGAGTACT
CTGGCACCTCTGGGGTCCCGAAAGTGCCTGAGTACCTGTTTGAAGCCGCTGTAGGTGACTGCGCACCTGT
TTGAACTCGCTGTAGGTGACCGCGCACTGTTTGAGCTGCCTGTAGCTGACCGGGCACCTGTTTGAGCTG
CCTGTAGGTGACCGCGCACTGTTTGAGCTGCCTGTAGGTGACTGGGCACCCGTTTGAGCTGCCTGTAGGT
GACCGCGCACCCGTTTGAGCTGCCTGTAGGTGACCGGGCACCCGTTTGAGCTGCCTGTAGGTGACCGGGC
ACCCGTTTGAGCTGCCTGTAGGTGACTGGGCACCCGTTTGAGCTGCCTGTAGGTGACCGGGCACCCGTTG
AGCTGCCTGTAGCTGACCGCG

283; I vs SW; chr4:40134579-40135662; 4; FLJ20273; INSIDE
CGCGTTGTAGGGGTAGCCGTAGTAGGCCAGTGTGTAGGGGTGCGAGGAGTACACCTAGCTGGGCTGCTG
CGCTGCCTCAGCCGCGCGCCGCCCTGGCTGCCTTCTGGTAGCGCGAGTACTGCTCCTGTCCACGGGCT
TGGCCAGCGTGACCTCCAGGCACGAGCCCTCCAGCTCAGTGCCGTTGAGGTTGTTTCATGGCATGCACGGC
ATCTCGCGGCTGGTGAAGTGACGAAAGCGTAGTTCGCGGATCTTCTTGACGCGCTGCTCACGACCGGGG
TTGAACCTGCCGAAAGCTCTTTGATGGTGTCTCGGTGGTCTCGATCATGAGGTTGCGCACGTAGAGGAT
CTTCACGGTCTCCATCAGTCCCTCGTCCAGCTCGATCTCAGGTTCCGCCAGTCCACGGGATCTGGTGGC
CCCACAGCTGGATGCGGCCAGGCATGAGCTTGGCGCGAGCCATGGCAGCCGGCGCTGCTGCTACTCC
ACGAAGGCGAAGCCGCGGTTCTTCATCTTGTGCGCCGCGCTGGCGTAGACGATCAGCTCCAGCACGCCCT
CGGTGACCTTGGCAATCTCCTCCAGGATTTCTCGCGCTTCTTCATCTTGGGGATCCCGCCGATGAAGAGG
CGGCAGTTGTCCCGCTGCAGCACACGCGAGCAGGCGGCCCGGGCGGATCTCGTAGTTGTTGAGCTCACG
CACTGCGCGCTTGGCCTCGTGTGTTGGCAGTACATGACGAAGCGGTAGCCGCGGTTCTTGGCGTCAAAAG
TCCATCATGAGGCGCAGCTCGTAGATGCGGCCACGGCCCTCGAAACGGGCACAGCTCGTCTCGTACAC
TTCGCGCGGGATCTTGCCACGAAGACCTCGCAGCCACGCTGCGGGTGCGGGCCCTCCCAGCCGGGCGG
TGGGCCGCGTACTTGGCTGCGCCGTTCTCTTGACCATGCTGTAGCCGCTGCGCTCCATCAGCGCCAGC
AGTGCTGTCTGTTGGGCGCGCCCGCCACGCCCTCGGGCACCTTGGCGGAGGACCGGGCGCGGAGTCACT
TGCTCATGCTGCGGTGGAATCCTCTGCG

357; I vs SW; chr7:27219187-27220360; 7; chr7:027219187-027219246; Unknown
AAGTCTGGAGATAATTATGTCGTACAGTCGAAACATTATTCCGTTCTTACTGTAAACGGCCCCCGGCCACC
TTTACGAGAAACAGGAACTTCTGAGAGTTACTAGCAGCGTTTACGCGGGCAAACGAGTTCTTTTCTTT
CTCTCCCGGATTGTTCGAAGTATCTATCGGGCGGCTTCGATGCCAGGTTTCAGAGGCGCGCCAGGGAGAGG
GCGCCCCGAGAGGAGCGCAGCGGAGAGGCTACGACGTTCCCGGTGCCCGCGGCCCTCGGAGGCCGG
GCCCTGCGTCTTGGCCAGCACTGGGTGGCAGCTGAGGCTGGTGGCCCGGAGCCCTCGCGGCCGCGGGCA
GGCCCTTCTTGGGCAAGGTGCGGCACTCCCGCTGTCCAGGGCTCTTCGGCACCTCTTCCAAATCAGGT
CGCTCTCCCTGCTCCCCAGACTCAACTCCTCCGAAGCTGCTCCAGCTTGAATGTGACCGCTAGGCCGACT
CCCTGGGCCCGCGAGCAGTTCTCGAAAGGTGCGGACTGAGCCCTTCTGGGGTGGGGTGGCGGTTGGTTT
TCGCAAGTGTGACCCAGGGTGAACCTTCTATTTGGGTCCCGGGTGTGTCAGGGCCAGGAGAACAGCTGG
GATGGGGGACCCCGCTCCACCCTCGGGCCGGCAGCTCCGCGCCCTGTGAGTCCCCCTCCCTCTCTAT
GATGGCCAAGGCGTGGCGCAGGGCTATCCGGGAACCTTGTAAAGGCTCGTGTGCGCACCTAACCCCACTC

GCGGCACACTTCCTCTATGTAGTCTGCGGCCCCGCTGCCAAATAGAGTGACCAGTGCAGGGACAGAATG
CCAGGCTGGTGGCCGACCGCCTGAGGGACAAAGGCGAGCATTCACAAGCCAACAGCAGACCCCTGCCCCC
CATATTTCCATTTCGCTCAGGCTTTTAGGACAAAATCAACAAGGCGCAGAGTGGTGCAGGCGCTCACCCC
GGGTGCAGCCTGGGGAGCCACTGGTTCCGCGACCCCTGGGCATGAAACTCCTCAAGGGCGGCCCTCGAGA
GCAGGGGAGAGGATGCTGCCGGCGCCTGCCGAGGGCTTCTTGCGGGAAGCGGGCAGGCACCCACC
GGAGTCAATTGCCGGGACCCCTCAGCGCAACGCGGGCTGTTCTCTCG

373; I vs SW; chr7:156895132-156895886; 7; DNAJB6; INSIDE

CGGAGATGGCGCGTCTGGATTACGGGAGATCGTGCGGCCAGCTTCCCTCCCTCTGCTCTGGATGGGGGCC
GGCCGCCGCGCTCACTCACGGCTCTCTCTCCCGCTGTGCTGCAGGTGTGGCCGCGACGATGCCCTC
GCTGAGGAGCGCATGCGGAGAGGCCACAACGCCCTGCCAGCCAGCCTGCCGGCCTCCGCCCCCGGAAG
CCGCCCGCGCTGCCTCGCTGCTGAGACACGCGCTCACTGTCTCTCTGAGGAGAGGGCGGAGCAGGACC
GACCTCGGGCACCCGGGCCCGGGACCCCTCGCGTCCGCGAGCAGGTGTGCAAAGGGAGGCAGCCGTGGA
GCAGGCGCAGAGTGAGACTTCTCTGGGTGCCAGAGGACAGCGAGGACAAAACCGCGCCTGGGCTGCTG
TGTTCTGACCTGAGCGGGCGTGGGCGGTGGGGCGGGGAGGAGGTAGCCTCCTCTGCTCCTCTCC
GCTCGCGGCCCCACGCCACGGTGGCTCCGGGCCCCACCGTTAAACGGGGTCCGCGTGTCTGTAC
GCAGCGTGTGTCTCCGCAAGGATGACAGAGCTGCCACGGCAGTGCGAGGTGCTGCTTTTACCGTAGACG
TGCTTTTTCGTAGCTTTAGCGTAGAGCTTGAGGCTGTGGCTTAGGCCGGGTGCTCGTGTGTGGGG
TGTGCGTTTGCCTTCCCTCCGTCAGCTTCACTTCTCGTGCCTTCTTCTGCG

389; I vs SW; chr8:132985505-132986242; 8; chr8:132985506-132985550; Unknown

CGTAACGGGCGTGGGTGCTCCGTGCGCGCGCCCGGCGAGGAGTGGGCTGGCGCGGTAGCTGTGCCCCG
CTTGGTTGCGTGACCGCGGGTCCGCGTCCGCTCCCTCCACCCTTCGCCCTTCGCCCTCGCCTCGTTCCG
GCCTCCGCGGCCAGCAACGGCGCTCATGGTGCCTGCGCGCTCCCTGCGCGGCCCGCTGAGCCTCGGT
GCGGCGGCGAGCGCGTCCGAGATCGCCATGCCTACCCGTGAGTGGCCGCGCGAGGGCGCGGGCGTTGG
GAGGCGACTGCCTGCGCGACGGCTTGGGCGGGTACTCCTCCCGGGCGCTGGGGAGGCTGGGCGCGC
TGAGCAGAGCCAGGAAGTGTCTGCGAGCGCGGAGTTAGTTTCGTTTCGGCTTAGCCTTCCGAGATGGC
GTGAGCCCGTTGCACGGATCGGGAACCTGAGGCCCGAACGTTAAGGGAACCTGCGGGACGCGCTGTTAGG
AGGCGGCAGAGCTGCTGCTAACCTGACCCGTGGGATTTCAAAGTTAAAGCCCTTTTCCACGGCCACACG
GCTTCGTGGGACTTTATGGAATATGAAAATAACTGCGGTACCATTTGTCAGTCCCTTCTCACCTCGGGCC
GGAGCTCGTAGTGAGCGCGCGCCCGAGTCCCTTCCCGCGCGCCAGACAGACCCCGACAGCCTAA
CTCGGCGTCCGTATCGCCGTGCGGGCGGCTGAAGTCC

12; SW vs I; chr1:68288825-68289104; 1; DIRAS3; INSIDE

CGGAGGCACGAACCAAGCAGCCTAGAAGACAAATGCGCTGCTCGGAGAGACTGCCGCGGCAACCAACTG
GACACCCCAAGAGCTCACTCCTCCGCGGTTTATATTCGACTTGCGCACAGGAGCGGGTGCAGGGGCGC
AGGAGAGTGTGGTAACAGGCATAGATTCCGCTTCCGCAATACGTGGTAAGAAACCAGCTGTGAGGGGCTG
GCCAACGCAGAGCGCGCGAGGTCCGCTTGGCATCTACAACAATCGAGGGGCTAGTCCAGAAAGTTCAAG

15; SW vs I; chr1:71284766-71286392; 1; PTGER3; INSIDE

GCTCAGCTAGTAAGTGAGGAGCTCAGCTCTGAAGCTGTAACCAAGACCGCGCGGGCAGGAGGAAAGGAC
ACTTCAGCGCTCTGCGGTTGCAAAACACACCCTGCGGGTGCTGCCACTTAGCAAAGTCTAGGTTCCCGCTT
ACTCGCACACGCATCCTGACTTCCCCCAACCTGGAACCTACCTACCAGGAGCGGAGACCAGCAGACCGAC
AGCACGCACATGATCCCATAGCTGAATGGCGCTCTCGGTGCTGATGCGGCCCACTGGGCACTGGACT
GAGATGCCGTGGCCTTGGCCGCGAGCGGGACACCAGGGCCCTAATGTTGGCCAGGTTGCAGGAAAAGGT
GACTGTACAGCCCAAGAGCCCCAGGAAGGCAAGGCAGAGGCCAAGAAAAGGTTGCCCCAGTTATGCGA
AGAGCTAGTCCCGTTGCCCTCGCCGCGTGTGATGAAGCACACCGTCCCGGCCACTGGACCGGTGACT
GGCCACGCCAGCAGCGGCAGCAGGGCGAAGGCGAGCACGGCCAGCCACAGCCGAGCAGCACAGCGC
GGTGGCACGCGTCTTCATGTGGCTCGCATACCAGTGCGGCGCCCTGATGGCCAGCGCCCGCTCGACGGC
CATGGCGCTGGCGATGACAACGAGGAGAGCCCGAAAACAGTCAATGGTCAAGCCCGAAAAGGTGCAGAGC
CGCCCCGACGGGTGATGTGCTCCCAACGCTGCTTGACAGGTACACGACGATGACGACCGGGGTGTGA
GAACTGCCCGACCGGTGCGGTGAGCGCCAGCCAGCCGATGCACAGCAGAAGGACTTCTTGCGCTTGCTC
TCCCGCGCGCGGTAGCTGCGCGACACGAGCAGCATGGCCAGTGGCTTGCCACGAAAACAGTGAACAGC
ATGGTGTATCGGGAAGGCCACGGACACCGATCCGCAATCCTCGCCAGACCCCTGAGGGGCGCGTGAAGTTG
CCCCGCGCTCGGGGAACGCTCGGGCGGCCACATGCTGTAGGAGTGGTTGAGGCGGGTGCAGAAAGG
GGGCATCCCTCCGTAGCCCCGGGTCTCCTTCATGTTGCTTCGAGGTGAGGAGGGATGCGCTCCAGAG
AGCCGCGAGCGGGAGGGGCGAGACGCGCGCGGGCGGGCGGAGGTGGCGTTTACCGCGGCTGGGGCT
GGGTGCCCCCATGTTGCGGGCGCAG

21; SW vs I; chr1:119333484-119333719; 1; TBX15; INSIDE

ATTCTTAATTCCACACCTCTTCCCAAGTTACGCCACCGGTGCGAGGACGGCAGGAGACCCCGAGTGCAG
AGAAAGCTCAAACCGGCAGCGAAGTGGTCTTAGCCAAGCTGAAAAACGTTCTCGGATTCCGGGACAGCG
GCCTAGACACAGCCCGATCTTCCAGTCTAGTGCCCTGGTCGAGACGGTTCTATCCTTTTGCAAAAGAACCG
GAAAGAGCTGGGTCCCGGGGCG

26; SW vs I; chr1:178464743-178471598; 1; LHX4; INSIDE

CGGGGTGGGCTTCCCGCGCTGCAGCCCGGAGGCGTGCAGCGCTGATGGAGCGTCAGAGGAGACCTCG
TCCAGCGTTGGGCTTCTGTTGTATTTCTGCCAGAACTCGCGTTGAGGAGAAATTGTTTAAAGCGTTTCT
CTACCTGTCCATGCTCTCGTAAATACAGTAAGCATGGCAAGCCCTTTCGCTGGTTAACCCCGCGTCCGT

GTGCTCACTGCCGCCCTGCACGCACGAGGTTCGCGGATGGTTCAAAGCACCCGCGGTGGCAGCCGGAGAG
GCAGAGCGGGCTCTAGGCACTAAGACAGGGCCGAGCTGGACGACTGCTGGCAGGGCGGCCGGGAGGCC
CCGCCGCGGGGAGGTTTGGGCCCCCTACCTGCGGAACCTGGAGGCAAGTGCGGACTCCGGCTGCAGGCC
GCGGTCTCGCGGGACGCGCGCGGGGCGCCTGCGTCCCGCCACCTCCGCGCACACCCCTGGTCCCTTCC
CCAGCCCGGGCGCGCGCGCCCGCGCGTGACTCGCGCGTTCCGGGCCGAGTACGGGCTGTCCCTTGGC
CCAGCCTCAGCCAGACGCGGGGAGAGAGAGCAGGGGCTGGGAAGTGCCGGCAGGAAAGGAATTGGCCA
GGGGAAGAGGAGGAGGAGATAGATGGAGTCATCGGTTACGGAGCGCGCTCCGTCGGCGGAGCGAAGC
CGGGACCGAGAGCGCGCAAGGCGAAGACACAGCGACGACGCCCGTCCCGGCCCTCCGGACCGCTGC
CCCGCTCGGCCCGGCTCGGCTCCGCCCGCCCTGGGTCCGAACGGAGGAGGAGGACACGAGCCG
CGCGGGCTTGAACCCACGAAGACCCGCAACCCAGGGCGCGCGCTCTCCGACCACCTGCTGCCGCGG
CAGGCCATCAGCAGAATTTATACCCAGGGCGCGAGCCCGCCACGGCTGGGCGGAGGCGGAGGCGGAGG
GGGAGGGGGGGGGTCCGGCTTGCAGGCCCCCGCCCGCTCCCTGCCGCCCGCCCCCTCCGCC
GCCGGCTCACTCGGGGCGCGGGACCCCACTCCCTCCGGGTGGGTGCCCGCGCGGGTTGGGG
ATGTGCCGAAGGGCGGCCCTCCCTGCGGAAAGCGACGTACGGCCGCTCCTCAGTGTGAATGAATCAAAA
CGCCCGGTGACCGCGCCCTCCCGGGCGGCC

40; SW vs I; chr10:7449476-7449790; 10; SFMBT2; INSIDE

AAACCACTCTGAAAGAACTGTGAGACCTTTGCACTAAGACCATTAGGGATTCTACGCAAGGTTCTCTCTGC
TCCTTGCAAAATTACAGGCGTCATGAAGGATGGCGGCTCGTAAATCGAAGCCTTTGAACAGGGCTCACC
GTCCGGCGGCATCAACACCTTGTGTCTGTGTGCACACCCACGCGGTGCAATCCGCGATGACTACG
TCACACGAGAAGTCGGCCCTGCGGTCTCCCCGTAACCGCAGTAGCGCAGAAGCAGCAGCTGCCCGCACG
TGATAATGATCGTGCCACCAGTACGTGTCCG

41; SW vs I; chr10:7489383-7495345; 10; SFMBT2; INSIDE

CGGCAACCGAGCCAGATCCAAGAGGGGTGCGCCTCGTCTAAATTGGTTTCCACCAATGGCCTCGGATCA
GCCGCGGTGTGCTGCGGGAGCCCTCAGGACGCGGCTGGGGTTGGTGCGGGGGCCCGAACCCTAAAC
CCGGCTCGGTTCCGCAAGGTTTCAGGAGACAAGGTAGAGAAAGGCTGGGGTGAGCGAGAAGTCGCGCGG
CGATCGTCAGGGCCACGAGCCTCGCCTTGCCCTTCTTGAATCCACCCAACTTTAAAGGCCAAAGATCCT
GAAAATTCGAAAGCGAAACGCGAGCTGGTCTCCAGAAGTTTGAGAACGGTCTCCAGGCTTTCCAGCGT
CGTCCCGGGATTCTCGCACACCACAAACGCCATCAACCACGAGCACCAGGTGTCCTGCTATTGCCCCGA
ATGGTCCCATCCGCGTCCCGGGAACCTCCCTCGGCTTTTCGCGCATCCAGGCCCAAGCCCACTG
GTGCGCCCCGAGCCCTAGGTGCCAGAGCGGTGGTCCGCGGGCTCCTGCCAGTCTCGGCTCCTCCTC
TCCCCCACGAGAAGGAAAACTTGGGCCCTTCGAGAACCCTGTGGAATGTTCTTTGTAATCAACTGTACAT
CCGCTTCCACGGCGGCCCTCGTCAAAATCGCGGCTTTTCGGGGCTTGGAGCAAATTGCGCTTGTGAGC
GCGACGTACAGGAGCAAGGGGAGGGGTTCGCGGCTGAAACTGCAGCTTCGAGCAGACAGCCATTTTA
GGTGTCTCCACCTCGCGGGGCCATGGGAAAGCCGCGCCCGGGAGGCGCGCCAAACGCAGGCTGGA
GGAGCCACGACGCGTCTGCGCGGCGTTCGCCATCGTTCAGCCTCGCTGCCAGGTGGGAGGGGTCA
CTGCGCGGGGTCTCCAAGCCAGTGCCGCTTGTCTCCCGGCCCAACCCACTGACAGCAGCGCGTCCGAG
TGACCCTGTCAGCCTCGTTCGCGCTCCTGCAAAACACGTTGCTGCGCTAACTACAAACCTGGCCAAACATG
TCTTTGTAACCTATCATTTAAAAACGCTTCCAGGCACCTGGCCGCTGCCAGATCAGGTTTCGGGGGCCCG
AGGAGTCTTCCACCTGCCCGCCAGCCCGGGGACCGCGCGGCCCTCCGTGTGGCCCCCGCCCAAG
AGGTCCCTCGGGCAGGAACCG

112; SW vs I; chr14:37746906-37747538; 14; SSTR1; INSIDE

CGGAAAACTCGAATGTCGCCCTGCCGTTCTCGGGTTGGTGACAGGTCTGGTCATCGCACGGCGGCAGC
TCCTCACTGGATTTAGAAAGAGCTGGCGTCCCGCCCGCCCAAGCCTTTAAACTCTCTCGCCAGAACCCG
CCAACTCTCCAGGTTACAAAGTACAGCAGGAGCGGGTGGAGCCCTTCAAGCGCGCAGCCTTATCTT
TCCCGAGTGAACACCTAGGTGGATTCCCAACACCGCGCCTGGCACGTTTCTGGAGGGAGTCTCAAGCTCC
TCCAGAGTCCCGAGTCCCGTCTCGTTCTGTCAGTCGATATTCCTGTGGGAGACACGGGGGCTCTGAG
CGCTACGAGCTTTATTAAGAGATTGCGAATGGTTCACTCAGGTCCCTGAACACTCCCAATAGCCTAAGCT
GCCTGCTGTATTATAGCGCAGAAGCCCTAACGCACGGTGGTTGCTCTTCTCTATAACGCTCGCAGCTT
AGGGCCAGTTTCCGCGATTCTAAGAGTAATTGCGTGGGCACCTGTGCTGGGCGCAGGCGCAAGAGGGA
GTTGGTCTGCGCGAAGATCTCAACCTGCTAACAGACCGCACATGCACCTTTCACCGACCATCTACG

118; SW vs I; chr14:53488428-53488700; 14; BMP4; INSIDE

CGGTAAAGATCCCGCATGTAGTCCGGAATGACGGCACTTTGCTAGGCTGCGGGCGGCGGCGCAGCCCAA
ACATCTGCAGAAAGTGTCCGCTCGAAGTCCCGCAGGAGCTCATGGCTTGCCTGAGCGCGTCTCCCGCG
TGCCCTGAATCTCGGCGACTTTTTCTTCCCGCTCTCAGGTATCAAACTAGCATGGCTCGCGCCTCCTAG
CAGGACTTGGCATAATAAACGACCATCAGCATTCCGTTACCAGGAATCATGGTGTCTCTG

147; SW vs I; chr16:52873104-52882105; 16; IRX3; PROMOTER

CGCGAGGATGGGCGGGCTCCACGTCTGGGGGCGTGTGAGCAGGGCCAGAGCGAAACCTCAGTCTGAGT
TTACGAACTGGGAAGGAGCCTGAACCCAGAAACACCGTTAACAAGAGGGCGAAGCAGCGAGGCCGAG
GAGACGTCTCCTTGGCCTCTGGGGAAGGGCTGGAGGAGCGAGCCAGCTGAGAAGCGGCTTTGCCGGGT
GTCCACTAGCGGTTCCGACGCCCTCTGTGCGCCCGCAGAGTGACGAGAGGCCGACACAGTCCCTCCCC
ACTGCCCTTGGGGCGCGCGGACCTTGATCACCCCTTCGCGGAGGGAACTTCCAAAGGCGCGCGCTGG
CCGCTGGGTCCGATGGCCAGTCTGTGCGGCTCCGCTCTGCTGCCGCGAGCTTCGAAGGTGTGAGT
GTTGAGCCGTGTCTGTTCCGTGGCTTCGAGGGGTGTGCGCGCTTCTATACCTCCCGGAACGCGCGAGA
TAGTCACACGCGCACTTTGAGGGTCAACACCCCGCATCTGGCCACACTGTACCTTTACTAACGTGGGGA

GGGGGCAAAAAAATGTGTCTCTCTCTTACCCCGAGGTGTCACTCGCCCAAACTCCCTACAAC TTCTT
CAAGTCAAACTTGTGCAAGTTTGGCTGCTGACTGCGGAGAGAAAGAGGGCGCGAGGGGGCGCGCG
CGCGCGCGGGTGTAGAGGCCACGGGAGGCGAGGCGCGGAGCTGCCCTTTGTCTGTAGAGGAAGCTCCA
GCCCCAAATTTCCCTGCTGCTCCTCCCCCGCGCCGCCACCCAGGCCCGCTGGAGCCGAATCCCGGCTGG
AAAGGTGCGGGCGGTGTGACACCCCCGCAACCCCGCGCGCGGGGCTTACAGGATGCTCTTCTTAGGGCA
CGTGGGAAAAACCCACAGGTGCCAAGACGCACAGATGCTCCAGGACCCGGGCTCCCCAACTCTCAACT
AGAGTGTGGCGGTACACATCATCTAGAGGATATGTACCCCTAGGCGACCTCTCTCCATATCCGCTCC
ACCGTACCCCCACACCTTGGCATCTATAAAGAGGGAAGGGGGGCAACCGGGTTGGAAGGAGGATGGAAT
CTGGGCTTGCACGCCTCTTATAGCTAACAGTGAGAAAGCCTAACTGTGTGCGATCAAGAATGGGGACGA
AGGGAGTGTGAGAACACGACC

151; SW vs I; chr16:85098883-85102729; 16; FOXF1; PROMOTER

CACACACACACACAAAAAGTTGGGAGAGAATCTGAGAATGCTTGTGTTGCTGGACGCGTGCGCACGTAT
GAGCGCGCGGTACCTTATGATTATTGGCGCGTGGCGCCTGGCTATGCGTGGCGGCGAACGCGAGTGGAGAACCA
TGTGGGCGTGCATGAAGTGTGCACTTAAACCAAAGTGTGCCCTCCCGCTTGGGACAGCGCTGTGTGTTGGT
CCAAGGGTTGGGAGCGCCTGACCTGTCTGAGGCTCGCTGGGAAGGGTGTTTGAGCGCCGTGGCGCGTGCG
GAGCGTGTCTGTGTGCGCGGGGCTGAGCTGGTTGTGTGAAGTGGTAGCGGGTGTGCCAGAGAGCGGTTTAC
TCGCGTGAATGCACAACCACTACCGGTACGCTCCACCACTCAITCTTCTTCCCTAGCGCGGCGAGCTT
GTCTGCACGCGGAGACCCAGAGAGGCCAGCGGAAGGGCAGCGCGGGAAGGCGCTCTCTTCTCCCGGAG
CGCAGATCTGGCGGAGGAGGCGGCACTAGCCGCGGACGGCTGCGCGCGGAGCGCCCCAGCTCTCTC
CGACGTGCCAGCGCGCCGGAAGGCGACAGGCGCTCTCCCGCGCAAAAGTGAAGGCGTCCGAGCGCAGGAAGG
TGGGGCGGGTAGTTAGGGGAGACAAGGAGTCCCGAGAAAACCGAGAGGCGGGTAGGCTTTGAACCGCG
CGCGCGCGCGGGCTGTGCTGCGAGCCCGGACACGCTCTGCCCCAGCTCGCGCTGGGGCTTGGCCTCTA
GGCTCTTCGCGATGACCCGCGAAAAACCCCTCGCCCCCTCTTCTCAACCGGAACCTGGAAGGAGAG
CGCGCGCCCGCCAGCAGTCTGCTGCGAGAGCAGCACTCACCTGGGTCTGTGCGCGCCGCGATGCGCCGG
GCTCTTGGCTGTCTGCTCGCTCCGCTCTCGGCAACCACTTTCGTGGGTCCACCCGCCGCCAGCCGCA
GAGCGCTGAGGTGCAAGGGCAGGCTCTGCGTGCAGGCCCCCTGCGGGTGGCAGCAGGTGCGCGAGGG
CGCCCTTGCAGGCGCTCCAGACCCGCGCTGTCTGTCTCAGGAACCTGGCTTGGCGCGCAGTGTACAGG
CCCCGCGGCGGGCAGGCGGACGCCACAGGGGCAATTAGGCCAATCCCCCTCCCGCCCTGCGCACGG
GAATTCCTATTATTATTATTAAGAA

180; SW vs I; chr17:75377960-75381951; 17; CBX8; DOWNSTREAM

CGAGCAGGAGCAGGCCGCGGCCCGGATGTGGAGCCAGGCTTTTCGGGAGAGCCCATTTCTACAGGGATTTC
GGCCCGCAGCGGTGACGAGGCGCAGCTGGCTCGCCCTTTGTAGTTTCGGCGCGCTGATTGATCGCCTAAT
CCAGTGAACCTGAGAAGACAGACTGGGCTGCCAATGCCGACCCACGCGCGCGACGTCGCCGA
GGGCACCGGGAGCGATGGGTGCGGAGGGGCTGGGAGGACGGTCATCCGGGCGGCTGGACCTCTCCTTCC
TCCCTTCGCCCTTCGTGGCTCGGCGCGGGCTCAGGAGGACGACAGAGGGGGCGCCCTGGCGGTGGG
CGCCAGCGCGTACCTTTGGGTGCGGGGAGGTAAGGCTTTCTCAGCTCGGTTTCGGAACCGAAGGCCAC
CGGCCCGCGGGGTAAAGGGTGGGCGCCGCGACCCGGGCCGACGCGGCCACCTCAGAGGGCGCGCG
CGTCCCAACCAAGTGGCGCGCGCCCTCGGACCGGACGAGGAAAGCGACCGCGCGCTCCAGGGTGC
CCGAGACTCAATCGCACCACTGCCACCCGCGACCTCCGCTCCGAAGTCTCAGGAGGAAGCCCGCAG
CCAGCCCGCAGCCTCTCTCGCGGTTTCAGGACCCGAGGCTGCGGGCAGCGCGCTTCCACGACGGACAGCA
CGGAGTCCCGCGCGGCCCGGAGCCACGCCAGTCTCGGACTTCAGTCTGGGTCCGAGGCTCTCTCGGCGCTG
GAGGCTTTTAGAGGAGAAGCAAGAAACAGCAGACAGGCCGCCAGAGGCCGACAGGTCTGTGCGCCAG
CGGCCCGGGCGCATGCCACAGTGCCTGGATCAGGATTGGTGGGAAGCCAGCATCAAACGGACAGAAAAT
GAATCCGATCCGACACTTAGGAAGAGCATGAACCTTCCAATTCCAACCAATGTTTGTGGCAGGCGAGGTTT
CCCGCGCGGTGGCCACAAGCAGCCCTGTCTCGGACGCAAGTAACCACTCCGCTGAGGCGCGC
CAGCGACGCTGTCTCTGACAGTTGTCGGGATTCCACAGGACTCTGCCCAGGAAATGGAACCCGTGAG
GCGCTCTCTCAAAGCCGAGGTTGGTGATGCCAGCGAAGCGAAAAAGGCGAGGGTGGGCGCCTCCCA
TCCGCTTAAGCAGTAGCCCATCCACTGC

187; SW vs I; chr18:68359955-68362770; 18; CBLN2; INSIDE

CGCGCGCGCAGGTCCCCGCCCTCTCCCCGGGTGCGGGGCGGGGTGGGCAGGCCGACGGCTGACCTGGT
CGAAATAGATGGTATCATGGTGCGGTTGCTCATCTCGGACGGCTCGTGTTGTCTCGGTGGCGAGAAAG
GCCACCTTGGCGCTGCGCGAGCGCACGGATGCTAGGAGAGGTTGACGGCGCCCTCCGCGACGGG
CTGGAGTCGCACACCACAGGCACCTTGCCTCCAGCACGATGGGCTCCGTGTCGTTCTGCGCCCGCACGG
GGCAGCGCGCGGGCAGTAGCACAAACGAGGGCCAGCGCCACCCCGAGGAGGATCCGACAGCCGCCCGG
CATCGCGACGGCCCCCGCGCCCGGCATCATACGCCGACGCCGAGTGGCCCCCGCGCGCGCTCT
CATCGGAAGTGGTGGGAGGCGCGCGCGGGGTGGAGGCGCGCGCGCGCGAGCGCGCGGAAGGGCG
CGAAGGAACCGCGGAGCTCGCAGCAGCCTCCGGGGGCCCTTCGTCCCGGCTCTGACAGCTTCAAGGCCAC
GGTCGTTCTCAGAAGAAAGGCGCTGTGAACCTGTACGGCGACAGAAAGCCCTTACACCGGGAGGT
GGAGCCACCGGGAAGAGGGGATGGGAGCAGGTGCTCGCGGTGCGGGGTCTCCCGAGAGGCCACCC
CCTTGGTCCCGCGCACAGCAACCCGCTTCCGATCTGGCACAAACAGCTCCGAGAAAGCCCGCGCGCA
GCTGGCAGCGCATCCCTGAAGGCTCCCGAGACGCGCGGGGCTCGCAGCGAGGAGGGGCGCGCTTCT
CGAGTCTCTCTCGCTAAGACGGGCCCGAGACCTCAGAAGCGGTACCGCGACCCCGCCATTACCA
GCGCGGAGGGGCGCTAAGACGAGGCAAGAAAGAAACCTACGAATGCTTGCCCTTCTCGCCTTCTCACAG
CATTTCTTGGAGCAGCAAGGAACCTTTCTTATCCCTTGTTTCCCTGCTATCTCTATTTTCAATCT
TCGAGATGTTTTTAAAGTCCATTAAAGTCCCTTTGGTACAGCAATTTATCTGTTTTCACCCACAGAAAT

CCCAGGAATCTCCTTGGGGCGAATAAGATTACTAGGGGGGAAATACACCACACACACACACACACACA
CACACACACACACACACACACA

200; SW vs I; chr19:42586165-42586705; 19; ZNF569; DOWNSTREAM

GGAAGTATCTTGGCCTGCACGCGGTTTACATCATTGGGAGCACAGGCCTCGCCCTCCGAACTACGAGGCC
CAGAGCCCTTCGCGCCGAGCGTTTCCCGCCTTCCCTGTCTCAAGTCATTGCCAGGGCCACTGCGGGC
CGTTTCTGCTGTCCGTGGAGCTGCGGCCCGCTGTTCACAGGGTGAACGAGCACGTGCGAGGCGGTGGT
GCTTGTATCCGGGATAACCAGGTAGGGCGGCTGCATGCTTCATAGAGGCCAGCCTGTGCCGACCGGGAGC
TGTAGGACGGTCTGTGTCTGGGCTGCTTATGGGTATTGCGGTGCGTCTGCCGGTGCGCGGTCCGAGCCTA
CTCAGGAGCGGTGTGTGTCTTCTGTCTCGTGTGCTATGAGGTTTGCATCTGTGTGGCTGGAATAGCT
TGTTTGTGGGGGCCCGCGCTGACCTGTCTGTGCGTTACTGTGTGTCTAGGCAGGATAGTGACGGGGC
GTGTGACTGTGACGCCATCATCAGGTTGGTGAGATGGCGTGACCGC

207; SW vs I; chr19:63420090-63420541; 19; ZNF274; DOWNSTREAM

CGAGGGAGGACGACAAGCGGGGACGTTGGCGGAGGGGTTAATGGCGGAGTCGCGATCCAGCCGAGCCCA
CAACTCTGGGAGGCTGGTTCTGCTCTCTCCGAAGCGTCGCCCGGCTAAGCTTCGAGACCAGGACACAC
AACC GCCGACTATTCAGAGCCACAGTCGGCTTCACGCTGGAGGCCGGAACGACACCTCCCCAAAGCC
CGCGCGCGCGGCCCGCAGAACTGACCTACCCAATCACCACCGCTGCGATCAAGCGCGACACACGTT
GCCGGGTAAGAGTCACGCTTGGCAAAATAAGCAACCTGCCCTCATCCAATCAGCGTCTCGCCTGCCCGTTA
GTTCTCTGTCTTGCCTAACAGATTCTTGCTCTCCATACCGCTACTTGCGTGTGCCGGTGCTGGCCCA
ATCAGCGTCTTGCGCTCTTCTCGCTCCCG

223; SW vs I; chr2:72224630-72228512; 2; CYP26B1; INSIDE

CGCTTGTGTGCGGTGGATGTGCGCAATGGAATTGGACACCGTGTGGGGCCAGCAACATGCGGGTGTGCG
GAGGCCACTCGGTGCTCACGAGGTGGTGTCTGCCCATGAGGATCTTGCGCACGTTCTCGCGCCGGTCAAG
CGTATCAGCGGCCGCCCAACAAATGCGTCTTGAACACGTTGCCATACTTCTCCCTCCGCGACGACTGGAA
GCCAGAACCCTGCGGGAGCCACACCCGGGTCTCTCTCAGGGTGCACTTCTGCGAGGGGCCCGGAGGGA
GGGGCGCGCGGACCCCAACCGGGGTACAGTCACCTGCCCCCTCTCCCAACCAACACACTCACACAGACGA
GCACCGAGGTTTTATTTTTCATAGCGTGCACAAGAACTGCGAAGTAGGGCTAGAGGATAATAAATAATGC
AAGGAGGCGGAGGCCAGGGGACCCCCAGGAGGCTGTTTTTGGTAATGCTTTCGAGAGGAAAGAGGTA
TCCCGGACAGCTGGACCCGAAGCGGGAGTCTCCGCCCCACCCCCACCCCCACCCCCACCCCGCGCTC
GGGAGCCTCTCGGAATAAATATTTCCAGGCTCCGGGCCACGGGCTGGCGAGACCCCGCGGGGTGGCCGC
AGGCCAAAGATTATATAGCGGTAAGCGGTGCGGTGCCGGAGGCAGCAACTACAGATGGGGGTGGAGTT
TCCTCCGCTCTCCGGTGTGGCCCGCGCAGGACCCGGCGGCCCTCGAGGACTCTGCAGGGCGGGGTCA
CGGGCCCAGAGCCGCGATTTTCTTAATGCATTTTGCCCTGGAATAACGGAGACGGACTTTGGTTGCCGCC
CTGGAGTTTGAACCCGAGCGCGGGCGGGCGGGGACCGGGCAGGGCGACCCGCGCAGGTAACCGATC
CCCGGTGGTGGCGGCGCAAGCCGAGGATGGCGGGCGGGCGGGCCCGGCGGACTCTGAAACGGCTGGCG
GAGCCGGCCCGCGCGGGTACCGGAAACCGTGGAGACCTCAGAGGGCGGGGGGCAACCCGCTCCCGTCA
CCTTTGACGTGCGCACTAGTTACCCACCCCAAGTTAACCTTCTCCTGCGGGGCGAGCACCCGCGCGAA
AGGGGAGGGGCGCCACCTGTCTAGCCGCCCGCCTGCCAGCCAGAGCGTACCGACTCGGGCTCCAGAT
CTACCCGCTCCTGCACCCCGAGG

227; SW vs I; chr2:104835284-104839920; 2; POU3F3; PROMOTER

CGCTCGGCAGAGGCACGATACAGCGGGAGAGAAGGGCAGGCCCGTTACATTTTAAATCGGAGCGCACCG
GCGGCCGCTCCTCGGTGCGTCTGGGCTGCCGCTCGGGGCTCGGGACTGCCAGATGCAGTCTGGCTGG
GGCGCGCGCGCAAGCGGGCGCACCCCGCAGCTAGGGGTGCGGGGTGCACGCACACGCAACGCTATTAA
GAGCCATGTATTTATTGAATGTCCGAGTTGGGTAGTTTCAATTGGAAATCCCCGAGGAGGGCTCAATTTGCC
CTTGTTTCTGTTGCCACTTCTTTTCTTGGTTGCTGAGGTTCTCTGTGCAGCGTTTCCGCTTGCGCG
CGTCCCCCACCACCCACCCACCCACCCCGCTTCTCTCGCTACCGGGTGCACTCCCCCTCCCATCCCC
TTAACTCTTTCAGCTGGGTAGAGCTGAGAAAGCAATTTGTGCGCGCCAGCCCATCCACCAAGCAAAATGCAT
CTGAGACAGAAAGGAAAGAAAAAAGCACCACCATGCCTAAGAATAGAGAGCGAGCAAAACCCCCACC
GCTAATCACACACACACACACACACACACACACACACAGGAAAGCGGTGGAGCAGAGAAAGGGCG
CGCTAGCCGACCCGTTCTTTTCCCGGCTCCTGCTGCCACAGGGAATTCCTAAAGCCATTGGGGTCCGA
ATACACTTACGATGAATCTATGGGGGAAGGTCCGACTGATTGCTTTTCAAATACATCGCACGGCTCCGCTG
ACCGGCACCTCCAACTCAAAAGGGCACGCACGCTACTTGCCGAATCCCAGAGGAGGGAGGGAGGAGG
AAGGGAGGGAGAGCGAAGGAGGGAGAGAGGGGGTGGAGGAGCCAGGGAGCGCGGCGAGCGAGCGGTCC
GTCTCGCACGCGCGGGCACCGCGCTGGTCTGGGCTGCAGGTTTCCCAGATGATGGCATCCGAGAACTTA
AACAAAGGGGCTGCCCGCGCGCAACGGCTGCGGAAAGTTGCGGTGGCGGATTTCCAAGGAGCGGTGG
CCACGACCAGAGCTTTGGCGATGCGAGCCCCGCTTCCACCCCGCGATCAGAGAAGGGGGCGGTG
GGTGAAGGGAAGAGAACTTTGAAACCACTGGGGACACACTGTCTATAGGTATTAGCTTGAATGGTACA
TCCGTGCCGCGCGCTTTACA

235; SW vs I; chr2:124498611-124499725; 2; CNTNAP5; PROMOTER

GACTCTCATCACTACCACACCCATGTGTCTTCTCTCTCCGTCTCCCTGAGACGCCAGTGAACCACTGG
GCTTGGAAATCCAGAGCCCCGGAACACCTTGCAGTACTTGCCCGAAGCAACGCGCCACAGCGGGAGGGA
CGCAGACGCAAGACCCGCGAGAGGATGTGCGGTGGGAGTAGTGTGCGGGGTCTGCAAGCAGGGAGCGG
GCACAACGTTAAACCTTGAACACAGAAATCCCGATCCTATCGAGACCCATCAGCTTTTCCCATTTGGGAAC
GAGCGCAGGGGAAATTAATGCGTAATTCAAGCTCTGTTTCCCTCCCTCCAAAGGTGAGGTGGGGGAA
CGCGTCTCGTTAGCTCATTACAAAGCTTCCGTGGGAAATCCCTCTTCTTAATGCGTCTGTCTTCAACT

CCTATTAGCATCCTTCGACAGCGGCCCTTTGAAAATCTCCTTTAAATTTTCATACCTCTACTCGTTTCCCAAT
 GGGGGGAAGGGAAGAGAAAAGCCGGGGGTAGAGAGAAATTCCTTCCCCTTCCCTCCCAGGTAGCCAAAG
 CGCACCGCAGCGGCTTGGCTTCTCGGAGGAAAAGCGCCGAGCGGGGCAAGACCCGCCAGGCTGCTC
 TTATAGGCGACGCGGGGCGGGCCTGGCTGGGGCGGTGCCGCGCGGCCCGCTCGCCTATAAGGAGCTG
 TCCGCCACCCGGGTGCTGATTCCAGCTCTCGCGCCGACGAGGTGATTGCTGCCACCGAGCTCCGG
 CGCCTGTGCTTAATTGGGTTTGGATTGACACCGTTAAGGAGGGGGAAGAGAAGAGAGCGGGCGAG
 GAAGGCGAGTCCAGCTAGCGGCTGTTGCGGGGACCGTAGCCCCAGCTGCAGCTCCGAAGAATCCCCCGCC
 ACGGTTTCGGTGGAGCGTCTGGGCACGGGATGGAGTGAAAGAGCGAGTGCCTCTCCAAGCGGGGTGGG
 AGGCGGCAGGCTGTGCAGAGGAGAGACAGCGAGAAGAAGCCCGGCTGGCTACTCGGAATTTGGGAT
 TCGATTGGGAGGGACCGCTCACTCGGGGAAATGGATTCTTACCACGGCTGACCAGCG

257; SW vs I; chr20:22505518-22507240; 20; FOXA2/C20orf56; DOWNSTREAM

CGTACCCGGCTCTCAAAGGCACGGCACCTTTGAATTAGGTTGCGGAGTGGCCTGGGCGAGGGGACCCGG
 GGCCATCAAAGGCCCGAGGGAAGGCCGTGGGGCGACACCCGTCTAATGACAAGTAATTAAAGGATTGACG
 CGCGCATTACCAGCGGAACGGGAGGCATTAATTATTAAAAACGATTAGCCTTCCGCTGTGTCTCGTGC
 GCGTCCCATCATGTTTCAGCGAAGATAACCAGCCACCCGAGGCGAGCCGGGGCTCGGAGGGCGGGGGCG
 CGCTCCCAGCAGGCTTCGGGGCGGTGGACACGGGCGCACAGCCCAAGGCACCGGGAAGGAGAGGAGG
 GCGCACCAAGGGTCCACACAGGAAGGTGACTACATAACACTGACCCTGCTGAACAAACGAAACAGATT
 CTGCCACTTGGGTTTCGAAGTCTGGTGACTGCGGCGCAGATGGGAAAAGCTTTCGGTGGGGGTGGTGGG
 CAATTTCCATGTGCCAGTTCCCTGTGCGATCAGACCAAAGACCCAAAGTAACCCAGCCAGGCACGGGCT
 CTCACAGTGCTGTACCCAGGCGTTTAAAGAAAAGACCCAGAGAGAATGTGGATCTGGCGTGGGGGCA
 GGGATTGGGGGGGGGCTGGTAGACACCTGGGGAAAATACAACCTTTATGAGGTTTCAAGGGCGCAGCAGCA
 GAACTACTATTTTCCGAGGTCCACGCCCTTTCGCGAGGCGGCGGAAAGACGCGGCTGTTCTGTTGGGT
 CTACAACTCGCGTCTCCGGAATTCGAGGGCAAGCCCGGCACGCGCAGCGTGTCTCTGCCGTGGAA
 GGGGGGAAATCGGCGACTGGGTTGACAGGAGAATGCGATGATAAATGGCCCTGCGCTGTCTTCTGACTT
 TCTCTCTGGACCCAGCTCGTAACCCAGAGGCTCCCAACCTGCCTGCCGCCAAGCACGGCTGTGCGCA
 AAAGGCCACACCGCTTCTGACGCCAGAGCTAAGGTTCACTCGCCTCTTAGAAAGGCGCGGCCCTCCC
 CTGCTGTGCTTGATGACGATCCCCATCGTCTCTCGGCCCTGCTGTGTCCGAGAAAGATTGAGACTGG
 ACTCGAACCCCTGCGCGCAAGGGGAGGGCGTCACCATGCTCGCCTCAGCCTCTTCAAACCTCCCATGCA
 CCACGCACATCATTTTCTGCTGA

262; SW vs I; chr20:54012011-54014085; 20; CBLN4; INSIDE

CGACGTCCAGGGACAGGTGCCCTTCGGCTCCCGCCGACCTGTTGCTCGAACTTGCCCTGAGCTCTCGC
 TGGCGGGCTGTGGGCTCCCAAGCCTCTCCCCCGCCGCGCAGCAGCCTCTTTAGGGCCCGGAAGAAATG
 GGAGCCGGGGCTGGTGAGAGGGGTAGGAAGAGGGACCGTAGAAGTTTCAGACCCAGGCATATTTGGGAA
 GCGGAGTGCTTTACATGATTCCCCATTTCCCAATCGGACAGCTTAGCCTGGGCAGGCAGCCTCGTGCTG
 AGGTGCTGGAGACCGCCACCCCTAGGTGCTTCCCCCGGGTCTGACCTGATCGAAGTAATGAT
 GCGCGTCTTGTGCTCATCTCGGATGGCTCGTGGTTGGTGTCTCCGACCCGCGAGAAGGCGACCTTGGAG
 TTGGCCGCGCGGACCGATATCCCCAGCGGGGAGGAAGAGGAGCCCTTGGAGTCTGTGGCCGGGTTTCGAGT
 CGCACACCACAGACACTTGCCCTCCAGCAGATGGGCTCCGTGTGTTCTGTGCCAGACCGGCAGCCC
 CGGCAGCGTGAGGACCAGCAGCAGCGCCGCGACCGCGGACAGCGCCCGGCGCCCGGAGCCCATGGTGAG
 CCGTGTGGCAGCCGCGCGCGGTGGCGCTGGTGTCTCGCCCGCTCGCCTCCTACCCCGGATCCCGGTG
 CTCGGGAAGATGCTAGCGGCTAGGTGACAGCGCTGCAGGAGCGACGGCGGCGGCGCGCGCACACTTC
 CACCAATTCTGTGGCTTGAAGTCAAAGTCTCCCTCGAGCTCTCTCGCTGCTGTGTTACTCTTGTCTTAA
 GGAGCTCATGACGACCCCTTTACCTACTCTCCTCCGCCCAAGAATCAGCCCTGCTGGGGCCCTGCACC
 CACTCTGGTTCTTAGACATCTGAAAGTCATCAAACCTCACATTACACCTCAAGGCAAAAAATAATAATA
 ATAATAAATCTACCCCAAACTCAAGCACCACAGCTAAACCACGGAGCAGGAACAAAAAGAGGGACTC
 AAAGAGAAAGCCACAAGGGTGGCGGGTGCCAGCGGCGGGGTGCCAGTCTGTCTGGCTTGGCGCAGGG
 ACGAGTTACAGAGGCAGAAGTCTTCCAGGCTGAGAAGACGCGAGGCTGTGTTTCATGGCCAGGACGCC
 AGCGACTCCCACTTTCGCTG

268; SW vs I; chr21:33316999-33322115; 21; OLIG2; PROMOTER

CGGTGCCGGGAGCCTTGCTTCCCGCCGACCCCTGGTCACTCTGCGCAAGAACGTGTTCTGTTTGGC
 AGCCAGGCCGAGACGACGCTGAATGTGAGCAGGAACTCGGAGAAGGGAAGGAGAGATCAGAAAGAAG
 GCGCGGGAGGACCCGGGAAGCAGTGGGAGGTCTGCGCCCTGGAGCCCCGCGAGAGCCCGCGGTTTGG
 CACGGGCTCTTCCCGGGCCGCGCGGCGTCCAACAAAGGCCGCCCCGACACGCAACCCGCTCTTTGTGG
 GAGAGAAACACAAAGAAGAGGAAAAACACGGAGGAGGCCAACAGCACCAGGACCGGGGGGCAACCAGG
 AACTCCCGGAGCCGGGGCCATTAGCCTCTGCAAATGAGCACTCCATTCCCCAGGAAGGGGGCCCGAGCTG
 CGCGCGCTGTTGGAAACCGCAGTGCTTGGGACCCGCGGAGTCCGCCACCCCGCGGCGCGGCGCAGGAC
 CCGGACAAGTCTGGGGACGCTCCAGGACGCACAGGGCAAGCTTGGGCACCGGGATCTAATTTCTAGT
 TATTCCTGGGACGGGTTGGGGAGGCATAGGAGACACACCGAGAGGTACTCAGCATCCGATTGGCACCAG
 GGCCAAGGGAGCCCAGGGCGACACAGACCTCCCCGACCTCCAAGCTACTCCGCGCAGCGGAGATGTT
 GAGCGAAGCCTGCCAGTTGAAGAAGGGGGCAGCAGCAGCAGAGCTTCCGACTTTCCTTCCAGGCTCT
 AGACTCGCGCATGCCAAGACGGGCCCTCGACTTTCACCCCTGACTCCCACTCCAGCCACTGGACCGAG
 CGCGCAAGAACCTGAGACCGCTTGTCTCACCGCCGCAAGTCCGTCCGAGCAGACACCACTGGGCGAG
 CAAACAAAAAGAAACCGGGTTCCGGGACACAGTCCCGGCGGCTGGACTAACCTCAGCGGCTGCAACCAAG
 GAGCGGCACGTTTCGCTGTGGTGTATTAGCTACACTGGCAGGCGCAACTCCGCGCCCCGACTGG
 TGGCCCCACAGCGCGCACCACACATGGCTCGCTGTGTTGGCGGGGTAGGCGCGAAGGAGGCATCTACA

AATGCCCCGAGCCCTTTCTGATCCCCACCCCCCGCTCCCTGCGTCTCCGAGTGACAGATTCTACTAATTGA
ACGGTTATGGGTCATCCTTGTAAC

276; SW vs I; chr3:148591199-148594390; 3; ZIC4; INSIDE

GGCCGGCCCGCCCTTCCTTCCTTCCGCCCTCGCCCTTTCATGCCTCAGAAACGTGGCCCTACTCTGCATTCCG
GTGTGTGCGGAAGCAGCAATCACAGAGGCAGCCCTAATACCGGAGGCGCGCGCGCAGCAGGGCCAG
GTGGTAGCTCGGGGCTGAGGATCGCGGCGGGGGCAGCCGCTATGGGGGCCAAGCCCTGACACACGTACC
ATTCGCTCAAGTCGGCGGTACGCGCGGCCACCGCCGCGGAGGAGGCCACCTGGGACTTGTGGCCGCGAGTC
CGACGAGGGCGACACGAGGGAGACGGTGTAGCCGAATCGTAGCCAGAGCTGGGCGCGCGCGAGCGCCCG
TGCACCTTCATGTGCTTACGCAGCGAGCTGGGGTGGCTGTAGCACTTGTGCGAGCCCGCACCTTGCACG
TGTATGCTTGTGCTAGTGTGCACGTGCGAATGCTTCTTACGGTGGCTGTGTGGCGAAGCGCCGCTCG
CAGCCCTCGAACTCGCATCTGAAGGGCTTCTGCGCTGGCGGAGGCAACGCAGAGACATTAGTGTGTGG
GTCGTGTTCCTCGTCAAGTGTGCTGCCACCTCCCCCATTCGTCTCTCATTTTCTGGAAAAAGAACTACAAAAT
ATTTTCAGAAATCCTTTCACGCGCGCTCAGGTCGAGCACCCCTTTCCTCTGTCAGAGAGCGCCCGCGGT
GCCCTCTCTTGAACGCCCTCCATCCTCCCGCTTCTCCTCTGGGCTCATGGGAGGGTATGGAGGAGGA
GCGACAGTGACTCCATCTTAGTCGAGTTTCCATCCTCGAAAAATCCGATCCACTCGGGTGTGTTTCTCCAAA
TTTTCTCCACTTGAACCCAGAACCTCTGCTCGGAAATACATTACCGGAGGAGCTCACAATATAGTTAA
CGGGGAAGCTCACATCTGCTCGATTAAAGTTGCTGTTTCACTAATCTCTGCGCTACCCCGCCAG
GGTTCATCCCCCCCCACCCACCCCATCCTGCGCCAAATTTGTTTCTAAAGTAGGTTTTGCGCAACCGCAA
AGCGATGAAATAATTAAAGGATGCGCAGCCGATGCACATTGTGTGTGCATAAAGTGGATTGCTGCTGAG
GGAGAGGTATTCTGAGCAATGATTCACTTCAGAAGGATTTTACAGGAATGGAGCCCCCTCCCTCTTCTCT
TCTACCCCTGAGG

285; SW vs I; chr4:122520930-122521740; 4; GPR103; INSIDE

GAAATGTTCTGGAGCATGGTGACGGGAATGCAGAAAGAAGGTGATGAGCAGGTCACTGAGCGCCAAGGAG
CAGATAAAGATGTTGGTGACGGTGCGCATGGCCCTTGTGCGGGTCAACACGTAGAACACAGAGCATTGCC
AAAGAGCGCCAGGGCGAAGATGAGCAGCGCGGTGAGCAGAGGGCCAGCTTGGCGCGTCCCGCAGCTC
TGGGGGTGTAGACGAGCGGTGCGAGCCGCTACAGAGCGATGAATGCTCCCGCTCAGGTTGTGGTCCCGC
AGCAGCCGAGAGAACTGCTCCGGTAATGTTAAGCGCTGCATTGCTGTGCGCTCCCGGGACGCGGGGCC
ACCGCCCGCTACTGGCTGGCCATCCGCATCTGCGGGGACGCGAGGGCTTGGGGGACACGCGGAGGGCC
GCCTCCCTTCTCTACTCTGGAGTCAGCCGCGCGGGAGGGCTTAGGCTGCACCCGGGAGGTTTGGGAAA
GGAGAGCAGCTCAGGGATCAAACCCACGATAAAGAGGCGGGAAGCCAAAGCACTGGGAGACTCGATCTC
AGTGACCAAAAAATGTTGCGGGTTCAAATAAAGTTCTTCCCTTGGCTTCTCCCTAAGCGGAGGCGCGCCAG
GGTCTGGGGTGTCTGGACGCCACGCGAGGGTCTGCGGCTCTGGCTCCCGCTTCTGGCCATCGCATGC
GGACGCGGACCCGCTTGGGGAGCGGTGGAGGGTGGGGCTGAACTCGGTGACGCCCTCCCTCACACCCAG
CTTCAGTGCGGCCAACGCGCTTCCCGCACCTCAGGGCG

293; SW vs I; chr4:155881084-155881434; 4; LRAT; PROMOTER

GAAAGATGAGGTGCAGAACTAAGCTGGGACCTCTGAGCCTCAATTTGGGCCCTTCTTCTGCGCTGACACCCAA
GCGGATCTTGTCTTGGCCTGTATGCGTTACTGGGGAAATGGACCTGGGCCCTGAGCGCGCAGGTGCGGAG
GGCTGCCCGGGGGCGGACACCCCTGCGGGGACACTGTAGCTGTCAATTCCTTCTTCTGAGCGGGTAGG
GGAAGCGGTGGCCAAAGTGGGAGTCGACCGCTCAGCACAGTCTGTCTGAGTGTGACCAAGGATCCAG
GCTCTTTCTAAATCTCGCCGAGACCTGGTGACGCATTTCGCATGTATTTAAGGCGTTTGCACGCAGAACG

296; SW vs I; chr4:177159356-177159814; 4; GPM6A; INSIDE

CTTTACTCTTGGAGAAATCCCTCACAACAAAGGACAAGGAGCAAGGGGAGGGGCGCCAGTGGAC
TTGGCTGGAAGAAGTGAGCGGGCTGGGGTTGGAAGAGTAACCTCGGGCTGCGGGCTGACGCAGTCGGCAA
CCGCGGAAGACGAGCATCTCCCTGCGCTGTGATACGCCAGTCCAGGGATGGCGAGTGCTTTCTCCTC
CCAGCTTCTCCCTCGCTCTTCGAGGTGACTCGTGGGACCTGCGTCTAGTGTGGGTGTGAATCGGCT
ATTTACACCCAGTTCTTCCCCCTCCGCCACACGCAGTCACATTCTTGAGCTATTCCAAGCTGCGCTCCG
CTAAGCACCAATAAGCGGACCTGCTGGAACCTTGAGCGAAGCTGAACTGCGCCGAATCCACCGTCC
AGTGACCCGAGCCAGTGTGGACGCCCTTTAATCACG

317; SW vs I; chr5:140724146-140724826; 5; PCDHA5; INSIDE

CGCTGTGCGAGCCAGGATCCGGGCAGATCCGCTACTCGATGCCCGGAGGAGCTGGACAAAGCCTCCTTCGT
CGGCAACATAGCCAAGGACCTTGGGCTGGAGCCCCAGGAGCTGGCGGAGCGCGGAGTCGCATCGTCTCC
AGAGGTAGGACGCAGCTTTTGGCCCTGAACCCCGCAAGCGGCAGCTTGGTCAACCGCGGCAGGATAGACC
GGGAGGAGCTCTGCGCTCAGAGCCCACTGTGTGTGGTGAACCTTTAATCTTGGTTGAGAACAAAATGAA
AATTTATGAGTAGAAGTAGAATAATCGATATTATGATAACTTCCCGCTTTCGGGATGAAGAGTTAAA
AGTAAAAGTTAATGAAAATGCGGCTGCGAGGACACGGTTAGTGTCTTCCCTTCCGCGGGGATGCGGATGTG
GGTGTGAACCTCTCTCCGAGTTACCAAGCTCAGCTCCAATCTGCACTTCTTGGATGTGGTAAGCGGAACT
GATGGACAAAAGTATCCGAGCTGGTGTGGAACAGCCCTAGACCGCGAGAAAGAGACTGTTACAGACC
TCTCCTCACAGCTTAGATGGCGGAGACCCGTAATCTCCGACACCAACGCACATCCGTGTTACGGTCTCT
GACGCAACGAAATGCGCCCTGTTACCCCATCCGAGTACAGCG

333; SW vs I; chr6:101023927-101024343; 6; SIM1; PROMOTER

CGAATCGGGAATTGGCATTCCGTAAGGGAGCGGAGGGCCTCAGGCCACTAGGCAGCTCCGAACGCGGGG
AAGCGGGAGCAAAGATGAGCTCAGAGCGAGGGTTGCGGCGCCACCTGGGGTGGCATGAGGGGCGGT
GGACCGCCCCGAGACTCAGTGACAGTCCGAGCTTAACCCGCTTGGGGGCGCGCCCGCTGAGGTGGTT

GCGTCTCCAAGTCGTGAGCCTCCAATAGCTGCTCCCGCTTTTCGGTTCGCAACCCACAGGACCCCGGGAAAT
TACCACCTGTGCTCGTCTGGGCGGAGACCCCGTGCTTCGGAAGCCTGGGGCACATGCCTGGCTCCACCCCT
AGACTCACCGCCTCTGGGCCCCGAGACATGGGAATCTGCCCTTGAATATCTGGGCGCCTTTGTGTGA

367; SW vs I; chr7:121727243-121727884; 7; FEZF1; DOWNSTREAM

CGCTCCACAACCCGGAAGGAGCTCAGGCCGACCTTGGCGTGAGGGTCCCTGCGGGGTGGGTACCTAC
CCGTCCGCGATCACCCACAGGGCTGTTAGTAATCTCCCTGCTTCCTAGGCCGTTGAAAGCACTCAGGTC
ACCCACTCTCGGTGACCAGAGCGGTCACTCTTTCCCGCCATGAAATGTGAGTTCCGGTGGCAGCCGCCG
CGCCCTGCACTGTCCCTGCACATCTCCGGTCTCGGTCTCGCCTTTCTCAGCTCCGCGCCGCTTTCTCT
GGGCGCCGACGACTCATGAAGTGAGGCGGGGCCACAGATTTAAGTTTATTTCCCGCAACTGTCCGGGCG
GTCCCGGAGCTGGTGAGGACGCGCTACCGTGGGTGCAGAAAGGAGATCCCTGGACTCTCTAGAACCCTGG
GCCCGCGGTGTGGACCGATGGTGGATTCTCCGCGACAACAGCCCTGGAGGGAGAGTGCGCCGGGGGAG
GGGCCACGGGGCCCTGAGGCTTGGGGGTGGCCGCACTGGCCCCGGGCTGGCGGGGTGGTGGAGTC
CGAAGCGGCGAGGCGAGGACCCCGGGGCCGCTCCCCCAGTCCGCTCCCGGATGTGGCCCCGCTGC
AGTAGCACTACG

376; SW vs I; chr8:9798161-9799053; 8; hsa-mir-124a-1; PROMOTER

CGGGCTCCGCTGCGGGACAGGCAGCCGAGGAGCTCCAGACCCCTCCCTCGCGCCCGCGGCCGCTGC
CGGAGGTCTGCGGAGGGCGCCTGGCTCGGTCCGTCTCCTTCCCTGGCGGGCCCTCCCGACCCACGGT
GCTCAGCCAGCCCCATTCTTGGCATTACCGCGTGCCTTAATGTATGGACATTTAAATCAAGGTCCGCTG
TGAACACGGAGAGAGAGGCCTTTCTCCTGAGGAAGGAAAGGAGGAAGGAAGGAAGGTGAAAGAA
AGGAAGAGGGGTGGGTAGAAATGGAATAAGAAAACAGGAAAAAGAAATAAAAAGCGGCGCTGTGCGGT
GCGCACTGACAGCGGGGAGAGGGATGGGGTGGGAACGCCGAGGAAGGGACCACAGCATCTCCCCG
CCGAGCTCCCCAATCACACAGACAATGAGATAACAGCGACGCTTTCCAAAGGTCTTTGTCTCCCCAT
CCTTTTCGATCCAGGCTTTTCTCTGCAAAGCGGAGGGGTGGAGGGATGGGGGTGTGGGTGGAAGTGGG
AGACGGAGGGGTGCCTCCCCGTGTTAATTACCCCGGCTCCCTCGCCCCCTTTCCCGCGCCTCGCCTCC
CCTGCAGCTCCAGACATGAAAAAACACATCGACCCACCTCGCCCGAGCGCAGCAACCCACCCACCCAT
GTGCCCTCTGCTTCGCCCGAGGAACTGAAGGGGACTAGGAGGAGGAAGAAGAGAGCGAAGGACAAGGA
GAGCAGCGGGGACTCGGCAGCGGAGCGGGGCGAGGGCGCGGCGGCCCTCTTTTACCTCCATCGCTG
AGTGGGGGCGCAGCCGGGCGGGCGCTGCCGACGGGCGAGTTGCCCGCGTCCG

380; SW vs I; chr8:65661156-65662687; 8; BHLHB5; DOWNSTREAM

CGCGCGCGCGCACCCGACGCACTCTGCAATGCCCTCACCAGTCCCGCAGCTGGGCAACCCCTCCAA
GACCTGTGTTACGCTTAAATTCCTCTCCCTCCTATCGTACCCACCATCCATCCTTAAGCAGGGAGGCGCA
GACTCACAGAATTCCTTCTCCACCAACTCGCACTTTGGTCTAGCACGCGGAAACCGCAACCTTACGCG
GGCCCGACCTTGGCATGTCTCCAGCATGAGTGGCATTGACTTTTCCAAATGTAATGACTTATGAAAGATATA
ATCATGTGTTAAATGATCCTCCGTTTAACTGTTAATGGTGTCTCTGGGCACATTTACGTAATTTGATGCTA
TGTTAACTAATTAACCACTAGAAAAAGGATAATACACTTCCAGACTTTGAAAAATAATCATGAGTTCACT
TCCCGGCTCGCAGCACATCGTGGCGGCCCTGCCGGGAGGAGCGAGAAACGAGTGGAACCCGAAAGTGT
GCTCATGGAATGCAGGAGGTAATGAATCCTGGTCAGGTGAGACTACTTAGTCAAACCTTTAATGAAAAAGT
GATTTCACATGGAAAGCAGGAGTGGGAGGGGAACAACACTACACAAAGGTGCCTTTAAACAAATTAATGGCA
AAACCTGCTATCAGAAACATGAATAGGTTTCTTTCAATTAATGCAAGGTAAGACTAAATATCCACGTGC
CAAGCAACTTTACATCAATTAACATTTTTTTGTTGTGTGGGCAAGTAAATGAGCCCGGCTCCTGTGCTCT
CTGTATTGCGATATACAACTTGAAGTCTCTGGATTTCGAAGCCAATGAGCTGAGGTTTATTTAAATTCG
GCCTTTTAAATCAAACTTTAGACACAGTAGGTGGAAGGAGGGAAGAGAAGGAAAAACAAGGAGTCAGTA
ACTTCAGTTTAAAGTAGAAACAACCTTTACGGGTGAGAGTCTTTTTTGCCTCGGCAAAATCTCTGGCTCTCTG
ATCGACTGTGTTTGAACCAAGGTTCCAGTAACACAGGGCTGGGTAGGATAACGAGGAGAGTGTGTTGTGC
TGGACCTGGCAGGACTGGAGGAGGAAGGAGCGCCTTCCAGCAGGTCCAGCATCCCTAGGTTGCAAAAC
ACACCAATGACGTCCACGCACTCGCCCCACCGCGCTGTTTTTGTCTGCGCAGTGTCCCGAAGGGA
TTCCGGGATC

398; SW vs I; chr9:121170908-121172141; 9; DBC1; PROMOTER

CGTCGGGAGCGCGGGGACACACGCCACTCACTCAAACCCGCAATTAGCCCTTTGAGCCCCAGGCAC
AGGAACCCCTCCCTAGAACTGGAGAAGACTTGGAGGCGGGGGCGGCCAGGTGAAAGCGGACAAGGG
TGCCGGTAGGGGAGGGGAGAGGAGCGCGGGACGCCCGAATGCGGCCGGGGCGGGTCCAAGGG
CAGCGGGCTGCGGGGCGCTGCACCCGGCGCGCCTTACCTGGAGTCAATGCTCCGTCTTTGCGGAGAG
CTGCGGGAGGACGCTTTTATTCTGCTCGGTGGGAACITGGGAGAGCCCTGCGTGCAGCTCGCATTCCGGG
CAGCGCGCGGGGACTGCAGGCGTGGGGGTACCTGGCTCCTAGCAGCCTGGCTCATACTCAGCCGTAAGT
CCCTTCTGCTGGTCCCGAGGACAGGCATGAATCCCGGCTCCGGAAGCGGCTCACTCTCCCTCTGCTCCC
GGCTCTCTGCTCTCGCTCTGCTGTGCTGTGCTGCTCTCTCCCTCTCTCGCGGCTTCCGCTCGCTGCG
TCTCTCTCTCCCGCGCGCCAGATCAGTTTCAGCCGTGGGGTCCGGGAGCGAGGCGGCTGGCGAATGGA
GAGGGAAGTCCAAGTGCCCGCGTCTCCGGGCGGGGAGCGGCGGAGGCGGGCTACGCCGGGGGAGGG
ACTTAGCCGCGACGCGGAAATGAATGGGGAGCGCGGGCGGGGCGGGCGGGGAGGAGAGTGA
CGCCGGGGTGTCTTCCGAGGAGTGTGTTGTACATCTTTAGCGGAGGAGGAGAGAAGCGAGAGGAGGAG
AGAGCGGAGGCGCCTCGAGGGAAGCGCGCCCGGCTGGGCTCGGGCTGAGCCCTAGGAGCTTTCTGTGG
GTCTGGGGCGGTGAGGGTGTGTTGTCTATGCGCACGAGCATCCAAAGGAGCCGCGCATACGCGCAACCC
GGAATCCTGGTGCCTAAGCGTGAAGTGTGTTGTGTCGCGAGTACCTGAGTGTCTGCGGGCGGAG
GTGTTTCCACGGCCGCGTGGATCCATCGAGTGTGGGTTTTGTCTCGGGAGTTGCCCGTGTGGGTCCGTTT

GTGTCTGCGCGTCTCTCTGTGAGTGTITGACACTGTTTGTTCCTCTCGTGTGTAGGCGAGAGCCCACGTAA
CCTCCCAGAAATGAAGCAAGAGCTTCTC

403; SW vs I; chrX:50040955-50041296; X; CCNB3; PROMOTER

GCGTGTGCGCAGCTGTGCACGCTGATTGGTCCTCTGCTGGCCAATCACCCTGCACTTCATGACGGCTGTA
GTTTTCAAAATCCCAACTGGGCTGGTGGAGGGTCGCAGGTGTCAGGTTGAGACGGACCGAGTCGCTATAG
TAAGGAGCTCCGTTCAATTCCTTGGCCTCTCCTGGTCTAGGGGTGCGTCGATGGTCTTTGCTGTCTGTCT
CGATCTCGGTGTGAGGTAGGCGCCTTTGGGCAAGTACTGCTGGCTCCAGCGTCCGGCTCTGTGCGCTGCC
AGTGGGTCTTGGGCGTCCTCCAGCCCCTTGCTCAATTCTGTTGCTGGGATGCGCGGCG

TABLE 3. CpG islands hypermethylated in (bladder) cancer. Provided for each are: ID; Comparison; Coordinates of selected regions containing relevant CpG islands based on Homo sapiens full genome as provided by UCSC (hg18, Mar. 2006); Chromosome; GeneName; Location relative to gene Sequence.

2; ALL; chr1:2072175-2072389; 1; PRKCZ; INSIDE

CGGGCGGGAGCTACGCCAAGGTTCTCTGCTGCGGTTGAAGAAGAATGACCAAATTTACGCCATGAAA
GTGGTGAAGAAAGAGCTGGTGCATGATGACGAGGTAGGTGCCGCTTCTCATGGGGCCGGGGCCCCGGGA
ACGCGCTGCCCTGGGGCTCCTCCGGGCTTTAGCGGAATTAATCCATGCACGAGAGACCTAGCCTCACGT
TGACG

3; ALL; chr1:2106293-2106715; 1; PRKCZ/FP162; INSIDE

CGAGGAGTCCGTGTGAGGCCGCTGCGTCTCTGCTGCGTGGACACGCGTGATTGACCCCTTTAACTGTATCCT
TAACCACGCATATGCATGCCAGGCTGGGCACGGCTCCGAGGGCGGCCAGGGACAGAGCTTGCGCCGAG
ACCGCAGAGGAAGCGTCAGCGGGCGCTGCTGGGAGCAGAACAGTCCCTCACACCTGGGCCCGGGCAGG
CCAGCTTCGTGCTGGAGGAACCTTGCTGCTGTGCTGCGTCCGCGGGGATCCGCGGGACCTGCCGAGGG
GGCTGTATGCGGTTTCCAAGGTGCACATTTCCACGGAACAGAACTCGATGCACCTGCTCCGCCA
GGAAAGTGAGCGTGTAGCGTCTGAGGAATAAAATGTTCCGATGATGTGGAGCTCCTCTGATGCCTTTTTT
C

6; ALL; chr1:33385564-33385979; 1; chr1:03385935-03385979; Unknown

CGGACGTTAAGCCGCGTCCAGGGCTCCGTGCAGGCGCTGTACTGGTTGCCATCGTGCATCACGATGCAGT
AGAAGCCGCGGCTGGGCTGGATCTGGATGCTGCCCTTTCGGGCTTTCGGGCTTCGTGTGCAGCCCGATCACC
CACTGGGTCTTCTCCGCCACCACCTCCAGTAGTGGACGCCACTACTGAAGGCTTCAGAACCCAGCA
CCGACACCTCCACATCGAAGCGCTTTGGCGAGTCTGCACTGGCTGTGGGTGCAGTTGCCCTAAGCCACA
ATGCTGCAGTCCGTCGACAGGATCAGGCGCTGGTGGGCTGTGCCCGGTTCCAGGCTTAGGGCGGCTGGC
ACTGTGGGGTTGGAGGAGGAGAGAAGATGAGTGGGAGAGAAGGCTGTGGGCCACCATGCAGTG

8; ALL; chr1:47672249-47672972; 1; FOXD2/MGC12982; PROMOTER

CGCGCCGGCTTTGCCGCTTTCCCTGAGGGTGTCCAGTTTGTGAATAAAATTAGAGAAATCTGCGGGCGTA
GTTCCCCAAAGCCAGCTCAGGCTTCCGTTTTCAGCCCGCGCTGGCCGAGCTCGAACGCTGAAAAGGGCC
GCGTGCAATCGTTCGCTGTGCCTCAGGACAACTCCGCTTCAAGCCAGTGCCGCTCTCCGGCAGTTTCTT
GATTGACTTAATTAGATCCGCATAATCGCTGGAGGGCTTTTCTTTCCAGACCAGAGAACAGCTCATTTATG
GGGACCAAAAGGAAGAGAGGGAGAGACGACCCGGACGCCACTGATAGCAACGTACTCTTCGCAAAAAACA
CTCAGTAACTAGTGAAAAGCCCAACAGGCATCCCCCTCCGCCCGCAACGCTTCTCCCAATTGTTCTGGG
TTCGACGAGGGAGATGGCCGGGCGTGGAAACAGATGCAGAAGGAGGCCCGGCACGACAGAGACGCTGT
AACCAAGACCCGACAGCCTGTGGCTTCCGCTTTCGGCGGTGCAGCAGGCATGGTGTGGAGCCCAAG
GCTTCTGGGAAAGAGTCCAGGTTTTCGCGGAGGGAGCGACGCACTACGCGGGATCGCAGGCACTGCTG
CAAGACGCCGAACAGGCTGAGCCGGTAGCGGAAAGAGTAGGTTACAGAAAGAAGCAAGAAAAACGAAA
TAAATTCCGAATCCCGC

50; ALL; chr10:21828640-21829645; 10; C10orf114; PROMOTER

CGTCCGGGAGCCTCCGCAACTCGCATTTCCAGTCGCAACCCTGGGTCAATTCCTGCCTCCGTCACAGCTCC
CGGACAAITCCCCAAAGCCAAAGGCGTCGAGCGTGTACTGGCTCCACACAGCCCAATTAATATCAGCTTA
ACTCGTGGAGGCTTTGAGCCCCAGTGCTCCGTTCCCTGAAGCCTCCAGTGCGGAGCCGGCTCCTGCGA
GGACATCCTTTGGAGGGGGCGGGGGCGCAGGACGGATTTCTGGGAAAAATGTCGCTGGCGTGTGGCA
CCTAGAGGGCTGTGGGCAAGGAGCGACGCAACCAATGTCCCACTTCTGGGCTCTCAGATCCGGGATTCCTCC
AAAATCGCGACAGCCGCTCAGGTGCTGGGTGCTCACGTTGGCAGCACAAAGCGCAAAATGCACGACCCCGC
GCGCGCGCGGACCTCCACGCACACTTAGAGCCGAGGTGACAAGGGAAGGCGCGGGGTGGAGCCGC
TCTCTGGTGGAGCATGATCAATCACTTTAAAGGGTTCAAAAGTTCAAGTTCCCTTTGGAGGGGAGAGGTA
ATGCTTCCCGCGCCTGCTTCTCTGAGACCCGCGGGTTCCCGGCAGCCGCGCAACCACTGGGGATCTC
GGCTGCCGCTTGGGGAGCCCCCTCCGGGGAACACGCTCTCGGGCCGCGCAGCCGGGCGAGGTTGACGC
AGCTGCTAGGGGCGAGTTTGGCTTCCCGGGAGTACCGAGTGCCTCGGCAAAACGTGATCTCAGCCTG
CAGGGCCCGGGCGCGCGCTTTTCCCTTTCTCAGCAACGGGAAAGGCTGTGGCAGAGGCGCGCGGAG
TGCTGGCGGCTGGCGGCTGGAGGCTTCCGCGGAAACCTGAGCTCCCTGCGACCTGTTCTGCTAGCAGGG
GCGGGGAGAGCCCCAATAAGCCGCCAGAGGCGACCGTGCAATTTCTAAGAAAAAGCCTCTAGAAA
ACACCAAGCCCTTCCAAAAG

54; ALL; chr10:22804715-22807056; 10; chr10:022806090-022806137; Unknown

CGTCCGGCGTAAGCAGCTCTGGAACGGGCGAGACCCAGCTGTGCAGCGATGTCCAGTGTCCGCGCATCTG
CCCGCGGGGTGCAGCATGAGTCTTCTTTGTGGCGTGGGCTCCATCGGAACCGGCTTTCGACGACAAA
TTCTTTTTCCTCCCCCGCAGTTAACAGTTCTGGGGCAGAGGCTGGTGGAGAGGTCCAGAGCCCACTCAG
ACCGAGATGAAGATGAGGAAAAGCATGACGAGGAAGAGGCTGGCGGCTGCGGCGCCACAGGGAAGAGCT
CGGTGCGCGGCGCAGCTCCCGGACCCGCACTCCTGGGCTGCGTCCAGGAGCCGCTTGCATAGGAA
CCGTAGCGGCGCCCAAGTGAACCCCTGCGTTCCGACAGGAGAAGCTAACCGGGCGGCCCACTCCCACCCG

CGCTTCTCCCGCCCCACCGGCCGTGCGCGAAAAGCAGAGATCCGAGAACCGCGTGCGGTACAAACGG
 CAAAAGCTTCGCGCGCATTTTCGGGAGTTGAGCGCGCGCCGAGCGGGAACTACCGCTCTCAGGCT
 CCCAGCCCCGGCGCTACGACCCGTGTTGGCGCGCGCTGTGCAGCCCCCTCCTTCCAGCCCGCTCGGGCGCAT
 CCCCCAGGCCGGCCAGCGACGCGGGCACCGGGAGCCCTCCCCCGGTCCGGGCTTTGGCCACACCCG
 GGGACCGCGGAGTGGGAAAGGAACCAAAGCGCGCGCCTGGCCGACCGCGGACGAAATTCGAGGCGGGA
 GGGCGTTTCTTTTGTGCAAAATTCGCCCCAAAGCCAGGGCCCATGTACCTACTGTCTCCTTTGCCCCACAT
 GCTCCAAGAAAATAAGACACATTCTACCCGAGTCTTAATTATTGGGCCATTTCCTTAACGCGCGGTCTGT
 CCCCCTGGGCAGAAACATACTGCGAGATGCAGTTTGTAATTAACAAAGAGACGAGACCTAATGGGCTT
 CCGAAATGCTGGATACTGCGCGCGGGTCCGCCCGCATTCGGGCATCGCGCGTTCCCGGCCCTTCGGGACG
 TTCCGGCCCCGGCGACTTTGACCGCTGGCGAATTAGGAGAAACGAGAAGGCGGACGCTCCCCAATTC
 CCCATCGAGCCTTCTCCTCCGAGTCTGCGAAGCCCCGTGGCTCAGGAGACACCGGCTCCGCGCTGGGCC
 TGCAATCCGCTTCAGCGAGCGCAGGCCTGTGCGTCC

87; ALL; chr12:94776044-94776377; 12; SNRPF; PROMOTER

GTTACTTCCCAAAGGGCGTGTCTCCAAGAACTGCATTTAGCATTTTCAGATCAGAGTGACCCGAATCAAT
 AGGATTACGACAAAACTAGTGAGATTGAGATAACACCGTTACATCGAAAGTTTATCCGTGACAGAGGAA
 ATATTGCTTACGCCCTTAGGTAATTTCAAATGCACGTATGAAGGCCGTGCGGGTTTCTGAGGCGAAGCAA
 AAGAAAGGTGGGGCCGCGAGGTCGTGGGGCGGGGTGGGGCATGACACCTATCCAGACGCAACTCGA
 CCTCGTTTGCAAGAAATCTGTATCCAACCTCTCTCAGTGCGTTTCGCGG

94; ALL; chr12:113657930-113659205; 12; chr12:113657930-113657987; Unknown

GTTTCAGTGTTTATAGAAAATTTCTTTCTCTCTCTCAGGTCCACTAAGACCGAGAGAGAGAGAGAGTCTGA
 CTCTGGCACACCCGGCGAGGGGCTGCGGGGATTGGGAGCTGGCGCGGTTGATTTTCCGAGAATCCTC
 CACTTGGGGTGACGTCGGGCAGCGCGCGCGGGCCGTGAGGTTAATGCCAGGCTTTTCTCTAAAGCGTCC
 GGAATGATCCGGCGAATAAAACGGGTGTCTGCAAAAGTTAATGAATTGTACAGGAGGCTGAGGGTGGGA
 CTTTCGACCCGGGAGCCAGAGGCGGTTCTGGTGGACGCTTCCCCGTGCGCCTAGGGGTGCGCTGGGCTTT
 CCCAGCGAGGTCGTGAGAGCGCACCGCGTGAGCTTCATCGATCTCATCTTCTTCCAAGTGGGAGGAGGT
 GGAGATGCTGGGAGAGTTGTGGGGAGTTGGGAGTGGGTTGGAGGGGAGTGTCTAGATTCTACTCTGGA
 GGATCCAATCACGTGCTGTCTTCCCTGCCCTAGAACTTCAAGGTTTCCAACGGTTTGAATAAAACCCAAA
 CGATGCCCGATGTCCAACGAACGAATGATCTAGCCTCGCCCTACTTCTCAGGACTTAGCTTTGTCCCTGCC
 CGCGACTTCCCGCTGGGAACGTCGTCCCCCGCCACCACCGCTCTGCTTAGGTTTGAAGTCTGGGCCACTTT
 CCTACTCCCTCTGCTTTCCAGCAGGAGAAGCGCTTCGGAGGAGGGGCTAGGGCGCTCAACCTCCCGGG
 TTAGAGGAAATGCAAGTTGGGCCAATTTCCGCTCCAGACTCCGAGGCGGATAGGCCCAGGGGGCAGCGG
 CCTTGCCCGCGGCCACTGCCCTCCTCTCCCCCGCGCCCTGGCTAGGCTTTGAAGAGCTCATTTTAAAG
 AACTTTTCCATTTTCCCTTTTGGAGGCGTGTGTTCTTCTCAGTCACCTCGCTTTTCTTTTATGAGCTTC
 AGCGCTGATCTGCACGTTCTTCCCTCCGTTGAATTTCAATTTGAAGTCTCCCCAGAGCGGCCCTTTCCCTCT
 TGTTCCTGCCAAGTCGTTTAAAGCTAAGCAACATTCTTCTCCCTCCCGTCCGCGGAGCTCTCGGTCTA
 CACCCGCGAGGGGAGGCGGAGCGGTTACTCCGAGAGTTCCGCTGGGTTGGAGCCTTTCAGCAGCGGCC
 TTCAGACTGTTTGGGAGCGGAAAAGCG

99; ALL; chr13:34950488-34951119; 13; MAB21L1; PROMOTER

CTTTGCCGTCATCGCGGGTGAATGCACCACTACCTTTTGGCAGTTGGAGGGGAGACCCATCAGAGCCGGA
 GAACCTGCAGCCACGACGGCGAGGATGTGCAGTGGTCTCTGGGGAACGCCGCTTCCGCCCTCACCOCGGC
 GCGTGTGGCCTGTGCCGTCCGCTCGCCCTCTCTCTCGCTGCTCCGATTCGCCCTTCTACTTTTCT
 CTCTCTGGGCTCAAGATCGCTACGCTTTATTTCTGCGTGAGCTTATTTGAAACCTTACTTGGTGTCCCGGC
 TTAATCTCCACGTCTGCTCCAGACCAGGCTCTGCCACGCAACCCCTCAGCCTGCACCGCCACGTCGGGCC
 CAGGTGTGTCGAGCCAAGCCCCAGCGCGGGCCCTGCGCCCTGGCTCTCTCCCTTGGGTTCAAGCCA
 GAGATGCTTGCCCAAGACCTCGCCCTTGCCTTCTTGGGCCACCTGCAAGAACCCCTTGGTTGTCAAGGA
 CGTGAGACAGCCGAGGACGGGGAGGCCCGAGGGCTGTTGGGGACCTTAAGTGGGTCCAACGGGAAGGA
 CGCGGCCCTCGAGGGATGCCGTGCGGCTGGCTGGAGCCAGCGCGCAGGTGGCGCATCTTCG

102; ALL; chr13:49595986-49600287; 13; chr13:04959159-049599206; Unknown

CGGGCGGACGAATGGACGGATTTCGAGCGAAGCTTATTTCCCTTCTCCTAACGCATCTACCTATAAATAGCG
 CTCACCGCGCTGAGTCACCAAAACCCGAGTTTCCCCAAATAGCGCGTAACGACTGTGGGATCGCGTCCC
 TCGGGGCTCTGTGACAGACTCCAACCAACACCCGCTGGGCTGGAAGTGGGGCCACACGGCCACAGCGG
 GTCTCTACCAACCCGGCGCCACAGGACGCGGGCGAGGCCGCGGTGTCCGGACGAGTTCAGACGCGTCCG
 ACTTCCCGCGCGGACGGCGCTCTGGGGAAGGAGGAGCCGGCGGGCGGCTGGACCTGGCCTTGACTGC
 GCGGGGTCCGCCCCCGCCCTCGGGAGCGCAGAGTTGCGGGGGCGCGCACAGCTCCCGCCCTGCGCC
 GCCGCTCACACAATGGGACGCTCGGAGGGGGCGCGGCTCCCATTTCCGTTCCGAGGGCGGGA
 CTCCGGGCGGCGGAGAACGACTCGGGCTGGGGCCAGAAGGAAACCCCTCTCCCTCTGCCACTCAAA
 CTGCGAAAGGGCTCCAGCCGGCGGTGCCAGGGGCTGGGAGCAGCTGGGGAGGGAGCGGAAGTGCCACC
 CCTGTCAGTCAAGGGTGGTGAAGTCAACCCCTGCAGCCAGCCTGTAGGGGGTGTCTGTACATCACATGAC
 CCGGCCCCCTCTCCCCCGGAAGCCCGCGCGCGCTCTCTCCCCAGCCCGGACCTCCACCTCTCCCC
 CGCCCCCTCTCCCAACTTTGCGCTCCCGCTCCGCGACCGTGTCAACAGCGCCAGCTCCGCCCCCTCCC
 CGCGCCCTGTGGAACCGCCACGGCGCGCGCGGGCGCTCGCGCTCAGGTCCGAGGCTCCGAGAAGCGA
 GCGTGCCCCGGTTTCAACCTGCCCCCCAGCTCAGTGTCTGGTGGGTGGGACCAAGCCAGGCGCA
 CGGCGCGGTGCAGCGACAGCGCTTCTGTCTCCATCTCCACAGCAGTTAGAGGACGAAGCTGAGGCGC
 CGGGTCCGAGCTCGGAGGGAGCGAGCGCATGCAAGGCTCCGGGCCCTGACGCGTAGCCTCCGGGGGT

CGGCCACGGGCGAGAGAAGCAGCCGGGAGCCCCCTCTCGACCCAGCAAGGCGGCCCGCGCTCCGCT
CTCCCTACGCCCGGGTGGCGCAGCCAGTCCCCGTCTTTGGC

103; ALL; chr13:94152191-94153185; 13; SOX21; DOWNSTREAM

CGGAAGCCTCATCCCGCAAGCCTTCGCTCCTCGCTGAGACTCTGAGCTGCGCTGGGGTTGGCGGGCAC
CCGATTCCGCCCGCGCCAGACCGGTCACTCAGTGTGTGCATATGAGAGCGGAGAGAAGCGACCTGGAGG
CCATGGGTGGGGGCGGTGGTGAAGCTGCCGAAGCCTACACATACACTTAGCTTTGACACTTCTCGTAGG
TTCCAAAGACGAAGACACGGTGGCTTCAGGGAGACAAGTCGCAAGGGCGACTTTCCAAAGCGGGAGATGGT
GAAGTCTTTGGACGTGTAGTGGGTAGGTGATGATCCCCCGCAGCCGCTGTAGGCCCGCAGACTTCAGAAA
ACAAGGGCCTTCTGTGAGCGCTGTGTCTCCCCGGAATCCGCGGCTTAAACATTCTTTCCAGCTGCGGGG
CCAGGATCTCCACCCCGCGCATCCGTGGACACACTTAGGGTTCGCTTTGTTTGGCGCAGTGATTCAAGTTG
GGTAACCCCTTGCTCAACACTTGGGAAATGGGAGAAATCTCCCCCGCAACCTCCCGCACCCAGGTTT
CCAAAATCTGAATCTGTATCTTAGAGTGGAGGCGCTCTAGAAAGCAAAGAAACGGTGTCCAAAGACCC
CGGAGAGTTGAGTGAGCGCAGATCCGTGACGCCGTGCGGTAGCTAGGGCATCCAGGCTAGGGTGTGTGTGT
CGGGTTCGGGGGGCGCACAGAGACCGCGCTGGTTTAGGTGGAACCGCAGTCCCGCCGATCTGGAACG
AGCTGCTTCGCAGTTCCGGCTCCCGCGCCCCAGAGAGTTTCGGGGAGCGGTGAGCCTAGCCGCCGCGG
CTCATGTTTATTACGCGGCCTTGAGCAGCGGAGCTCCAATCCATATTAATCAACCGCTCGACCTACACAA
GTCTAAGTTTACGGGAGAAAACCTAGTCCCCGAAAGGAAGAACGCAATCCGGACAAGCAGTTGGCGCCT
TTGTCCCG

107; ALL; chr13:113930978-113931584; 13; chr13:113931540-113931584; Unknown

CGACCCAGCCCCGAGGAGAACCCAGAACCCAGCCCCGAGGAGAACCCAGAACCCAGCCAGCCCC
CCGAGGAGATCCAGAACCCAGCCAGCCCCGAGGAGAACCCAGAACCCAGCCAGCCCCGAGGAGATCC
CAGAACCCAGCCAGCCCCAATGAGATCCACAACCCAGCCAGCCCCGAGGAGATCCAGAACCCAGCC
AGCCCCCGAGGAGACCCAGAACCCAGCCAGCCCCGAGGAGAACCCAGAACCCAGCCAGCCCCGAGGA
GATCCAGAACCCAGCCAGCCCCGAGGAGATCCACAACCCAGCCAGCCCCGAGGAGACCCAGAACCC
GACCCAGCCCCGAGGAGATCCAGAACCCAGCCAGCCCCGAGGAGATCCCAACCCAGCCAGCCCCG
AGGAGATCCACAACCCAGCCAGCCCCGAGGAGAACCCAGAACCCAGCCAGCCCCGAGGAGATCCAC
AACCCAGCCAGCCCCGAGGAGACCCAGAACCCAGCCAGCCCCGAGGAGATCCACAACCCAGCCAGCC
CCACGGAGAACCCAGAACCCAGCCAGCACCTGGGCAACATTCTGC

111; ALL; chr14:36205192-36206099; 14; PAX9; INSIDE

TCAGAGAAATTTGAAAGGCCCTACTCTGAGGGGAGTAAAACTTCACCAGGCCCTGGGCTGGAAGCACAGGA
GTCGCGGCTGGGCCACGCCCTCGGGAGGCCAAAGGGCAGGGAGCCGACCCAAGGTTAAGCCCTCCAG
CTCTCCGTGCGGGTTTGGGTCCCGTCTCAAGAGTGGGGCGCGCGGGCTGGGCCTCCGGCTGACACCT
CTCTTCTCTCCATCAGTGAGCGACAGCTCCCCCTACCACAGCCCCAAGGTGGAGAGTGGAGCAGCTGGG
CCGCAACAACTTCCCGCCCGCCCGCGGTTGAACGGGTTGAGAAGGGAGGCCCTGGAGCAGGA
AGCCAAGTACGGTACGGTGAAGGAGGGGAGGGTCAAGGCCAGGTGGGCCGCTGCGCGGGGATTTAGGCG
ATGGAACACTTTGTGATGGTCCCTTTCTGAGCTTCCCGCAGAGAAGCCAGGCTGGCGTCCCTTTGCT
GCTACGAGCCAGATCTTCTGGAAGTGGGGCGAAGCAGAGCCCTGAGCTTGAAGGCGGAGCTGGGGCC
TCGACCCCGCCAGGGCGGGGAGCGCTCGTCAGGCGCTGGGGTCTGGGGCGGAGCTCCCGGGGGC
GAGGCTCTGGGAAGCGCTCCAGGCCTGTCCGGCTCCGGGAGCTTGGGAGGCGGCTCCCGAAGCCCTTTC
GGCGGCTCTCGTTGGGGGTAGAGTTAACCAAAGAAGGCGCTTCTGAAGGGCCGAGCGGAGCAGCCCTGG
GGCTCAGAGCCGCGCTTACGCCCGGAAACGCGCGCCCGGTCTCGGCCCCAGCGGTGCGACTGCGG
CTCGGGGCTCTCAGTTTCGACTTTCTCTCGGTGGCTCTCGGACAAACACGCTTGGCCAATCTCGG

130; ALL; chr15:94688798-94689131; 15; NR2F2; DOWNSTREAM

CGCTACGAATGTAAGATGAATTTAGTGGCGCGCTGCCCTCCCTGAATCCGAACGGTAATGATGGATTATC
AACGGGGATTGCGCTTCAGCCAGCGAGGGAGGTTTACTCAGCAATATGTCCGGCGGCACCCACCAAAT
GCAATCATTTGACCCCCCTGCGGACGATAGCTGCCGTGCCCTTCCACCGCTGGTCTGTGTGGCCAGGG
TCGCTGGGGGCCAGAGCCCGCGGATGACCAGAGAGGTGGCTCAGCGATCTTGGCTCTCGCCCC
CTCCTCTGTTTCTCTCTCAGCTTGAGGCTCTCTGGCAAGGGGATCGAT

133; ALL; chr15:94696311-94696840; 15; chr15:094696796-094696840; Unknown

CGGGGGGGTGGCGGCTGGAGGGCGGCTGAGTGCCTGCGCTGGCCCTGGCTGGGTGCGCACCCAGGCC
GCCAAAGCCGGGGGCCGCTTCTCGGCTGCTGAAGCCCGGAGTCAGTCAAGCGCCCTTGGCACCCGGA
GGGAGCGGCACCTCGCTCGTGCAGAGTTGCCCGACCCGAGCGGGAGGACACAGGACGCGAGGGCTC
CTGGCCTGCTGTGGCTTGGCTTGGCGCACTAAGCGCTCCCCATCTGCCGAGCTGGCCTCCGCGGCC
CTCTCGGCCAGTCTACGTTGTTAAGGACTTCAGCGCGAAGAAGAGCGAACCTGGCTAGAACCTGTTG
ACCTCTCTCTGGCTGGAAGTCCGCACAGCTCGTGGCAACACTGGACGACGCTTGTGAGGGGACGACC
GCGGGCAGGTGGGAGGAGGCTTGGTCTGCTCTGGATTCCACCTTGGGACGGAAGGGGAAGCGGAA
ACCTTGACCTCAGCCACACAAGGACACCTATCTGGCTGTCT

134; ALL; chr15:94705727-94706054; 15; chr15:094705808-094705853; Unknown

CGCTGCTGCTGCCGTGGGGCCGCTCCGAGGTGCCAGGAACCTCCGTAAGGGTCCCGCGCGCGCAGC
CCGCGAGTGGGCAAGAGGGGAACATGCGTGTATTTCAAAGAAACAGCGCGTCTCTGACTTCTCTGTCT
TCGCTCTCACCCCGCTCCCCCTCAACACACATAATATAACAGACGCGAAGATAATCTGCCATCTGG
CAAATCCCAAATTTGGTGACCAAGCTCGGAAAGCAACAGCGACGGCTCATCCCGGAGTAGGTGGCTGGTC
CTCGCGGACTCTCCGAGCTGGGGCAAGCGCCGTGGCTCTGCCG

136; ALL; chr15:94712480-94712812; 15; chr15:094712480-094712531; Unknown
 TAGGACCTGAAATTGCAGAGACATAGAAAATCAATACGTGGTCCGGAGTCAACTGCGCGCGACCAAGGGC
 TCTGCCCTCCCTCTCTCCGTTGATTTGGACGCTGGGAAGCTGCCCGCCGTCCTTCCACCCCTTTGCCCA
 GCCTTGGCAAGACCTCTCCGGAAACATACTCGCGTTAAGGAAGCTGGGAAGCTTCCCTGGCCCCGAGCTAG
 GAGCCCCGACGTTGGGGCTCCTTGCTGAGTGAGACGCTCAGTCCTGTGCTCCCGCCCCGCCAGGCGCC
 AGTCCCGCTGGGATCCATCTCCTCAGCCCCGTTTCCCGCTCTGCGAGCG

145; ALL; chr16:52873104-52882105; 16; IRX3; PROMOTER
 CGCGAGGATGGGCGGGCTCCACGTCTGGGGCGCTGTGAGCAGGGCCAGAGCGAAACCTCAGTCTGAGT
 TTACGAACTGGGAAGGAGCCTGAACCCAGAAACACCGTTAACAAAGAGGGCGAACGCAGGGAGCCGAG
 GAGACGTCTCCTTGCCCTCTGGGAAGGGCTGGAGGAGCGAGCCAGCTGAGAAGCGGCTTTGCCGGGT
 GTCCACTAGCGGTTCCGACGCCCTCTGTGCGCCCGCAGAGTGACGCAGAGGCCGACCAGTCCCTTCCCCA
 CTCGCCCTGGGGCGCGCCGCAACCTTGATCACCCCTTCGCGGAGGGAACTCCCAAGGCGCGGCGCTGG
 CCGCTGGGTCCGCATGGCCAGTCTGTGGGGCTCCGCTCTGCTGCGCGGACTTCGAAGGTGTGCAGTG
 TTGAGCCGTGTCTTGTTCCTGCGCTTCGAGGGGTGTGCGCGCTTCTATACCTCCCCGGAACGCGCGAGA
 TAGTCACACGCGCCACTTTGAGGGTCAAACACCCCGCATCTGGCCACATGTACCTTTACTAACGTGGGA
 GGGGCAAAAAATGTGTCTCTCTTACCCGAGGTGTCACTCGCCAAACACTCCCTACAACCTTCTT
 CAAGTCAAACCTGGGCAAGGTTGGCTGGCTGACTGCGAGAGGAAAAGAGGGCGCGAGGGGGCGCGGCG
 CGCGCGCGGCTGTAGAGGCCACGAGGCGAGGCGCGAGCGTCCCTTTGTCTGTAGAGGAGCTCCA
 GCCCAAAATTTCCCTGCTGCTCCCCGGCCCGCCACCCCGCCCGCTGGAGCCGGAATCCCGGCTGG
 AAAGGTGCGCGGTCTGACACCCCGCAACCCCGCGCGCGGGCTTAGCAGGATGCCTCTTCTAGGGCA
 CGTGGGAAAACCCACAGGGTGCCAAGACGCACAGATCTCCAGGACCCGGGTCCCCAACTCTCAACTA
 GAGCTGGGCGAGTCACACATCATCTAGAGGATTATGTACCCCTAGGCGACCTCTTCTCCATATCCGCTCC
 ACCGTACCCCAACCCCTGGCATCTATAAGAGGAAGGGGGCAACCGGTTTGAAGGAGGATGGAATCT
 GGGCTTGCACAGCCTTATAGGTAACAGTGAGAAAGCCTCAACTGTGTGATCAAAGAATGGGACGAA
 GGGAGTGATGAGAACGACCCCGCCACCGCGCAGGCTA

153; ALL; chr16:86294154-86294408; 16; KLHDC4; DOWNSTREAM
 CGTGTGACACTTTGGAACGCTTCTCTCGTTACAAACCAGCGTCTTTACTGAAGGTCTTCCGCTGCAGAGC
 TGGCAATGGATGTGTGGACAGAGCTAGTCGGCAGTGAGGCTCTCCTGGTTTTCAGCAGGAAACGTGC
 TGTGAGCAGGAATCGCGAGTGAGTTCCATGGCGTCCCCGGGTACGCGCGCTGCAGGAATCGCGAGTGA
 GTTCCATGGCGTCCCCGGGTACGCGCGGTGGGGTCTGTCTCG

155; ALL; chr16:87372445-87372729; 16; chr16:087372616-087372660; Unknown
 CGGCGGGGAATCGGGTGGCCACGCATCGGCCCTAAGGGGCCCTGGCAGCGCCCGGCAGGACAGCCGTC
 CACTGCACACCTCAGAGCCGGCACCCGGACGGTCAGCGTCCCCATGGGCCCGCACCCGAGCTGCCCA
 GATCTCAACCCGCACACAGGAAGGGTCTCTGCAACCCAGCGTCCACCGTGAGAGAAATGAACATGAACGCA
 AAAATACGGCTGCGGTGGCTGTGCGACCCACACAGAAGGGCGAGAGGCTCGTGGCCATCCACACACT
 GGGAG

165; ALL; chr17:44074280-44075233; 17; hsa-mir-196a-1; PROMOTER
 TTTCCGTAGATCATTTGTTAATTCTGGGAAGGAAGGACGCATCCGGGGAGAGGATCCAGGGCTGGAAA
 AGTGGGTGAGCGGCGCTGGCGCAGGCGGCCAGGAGAGCAGATGAACCGTTTCGTTAGAGCAGCGAGGT
 AGTCGTGAGCGCTGAGATCCAGAGACTAGGACCACTCCCTCTCTGAGCAGCAAAATGGGAAGAAGATGC
 TCACTCGGTAAGGGCGAGGGAGCCCGCATGGCGCCCCACACGGGCTCGGTCTTCTGCGCGCCAAGATC
 CCCTTGGGGCGAGGCGTTGGGTGAGCGTTTAGAGCCACTCCCTGCGCTGGTGGCTGGACATAGCCCTCC
 TATCCACCTCATCTTCCCCATCCCGACAGAGGAGTTGTGAATCTACGGCCCTTGACGTTGAGGCGTC
 GGAGGGCGCACCTTTGTAATTGCGGCCCTCCCTTCGCCCTTAAGTGCGGCTTCTGCGCGCCTAGGCTGGA
 TATGAAAGCCCCGTTCCTAATCCTCTGCTCTGGTCCCTCCTCTGACTGCTGGGACTCTAAGCTAGGCCCT
 CCCCAGGTTCCATCACTGCGCGCCAAACCCGCGGCTGGGCTGTCCGCAAGAGGGAGTTGAAGGCGCGCG
 GAATCCCGAGGTGCAGCTGACCTCCTCTCAACGCCGACTCGCCGCTCCCGCCCGGCCACCTCCTGTGCG
 GGCAGACTTCCTGTCTCTGCTCACAGCAGGAGGAGTCGCGAGCCGGTCAGCAGCGTGCACGGAGA
 TCTTCACTCTGCGCCAGCCCCGGGACACAGGTGCAGTCTCCAGCGGAGCACTGCGGAGTGCGCGCGCTC
 GAGCACTAGGGAATCCTACACGAGGACTTGGTCCATTCCACGCAGTCCCAGGCAGGTCCGACGCGGAGG
 GACGCAGCGGTCTCAACTCCTGGTCAAGCTTGGCG

172; ALL; chr17:58865328-58865618; 17; CYB561; INSIDE
 AGAGGAGGCGGAGACCTGACCCAGAAAGCAGCACTCAAACAGATGCAGCTGCACCCACGCGCCCGCT
 GCTGCCAGAGCCACTTCCGAGCCTGAGTCTGAAGACGCCTCAGCAGGGGCGAGGCAGAAAGACACCC
 GCGAACCCCGAGGGCCGCGGGCGCATCACTGGGAGCCGGGGCTATCTCCCTCCGTGAGCTCTTGAAG
 TCCATGGAGAGGGCTGCTCTTCCGCTGGGAAGGCCGCTTCCAGTCCGCCCCGCTCAAGATGTAGACAC
 CGCCCCACCG

176; ALL; chr17:73932992-73933361; 17; DNAH17; INSIDE
 CTTCTGCAGACAGACAAGAGCCCTCCTTACCTTCCATGAAGAGTCCGTACACGTAGGAGCCCTCTCGCGG
 AGGAGCGGTGATGCTCTCGGTTTTTCTTGGTCACTCGACAGACAGACATCTTTCCAGGGGCCACTC
 GTTCTTCTGGCCATGGAATGCATGATGGCGTGAGGAACGACTGGGGTTGAAGAAGCCGGCAGCCAC
 ACGGTGGTGGGAGGGCAAAGTCTGTCTGTCAGGCCCTCAGTTCTGCAAGGCACACGAGCCGCTAGGA

GGAGAGGACATAGAATGACATGGGAACGACCGGGCCTTGGCCGTTCTGAGCAGGGGTACGCCAGAACC
TTCCACGGGCACTCAGCG

181; ALL; chr17:75531280-75531546; 17; TBC1D16; INSIDE

CGCCTCACGGGGCCTGCCAGCAACGCGCTGTGTGTCAGCAGGAAGCCACGCCAGGTCTGACGGCTGCAT
CCTGTGTGTCTCTCCGGCCTGGCCGCTCAAGACACGCCACCTTTGATGCACACGCGCTCCGGAGGCACAG
GAAGGACGGGGCACTGGGAAGTCCATGTTAGTCTCCTGACGTCGACCACACAAACCAGACGGAACGGT
GTCCCCGGCCAGGCTGAGCGGAGCACACCATGAGGGCAGAGGCTACAGGTGATC

183; ALL; chr18:5186244-5187389; 18; chr18:005186349-005186393; Unknown

CGTCGGACGTTTACAAACGACCACGCTTTTCCCGCTTCTCGATTAGCCTGGCCTCCCTTGCTCCAGTGGG
GCGGACTCAAATGCGCACGCAACGACACGCGCCCAAGCCGTCAACCGCAGACAAACTGACTCTTCGCCA
ACTAGTAGCCACGGAGAGCAGCAAAGGGACCAAGGTCTTACCCGCTGCTCCAAAAAGACACGGCAACC
TCCAGCGGCGCGCAGTAGCTGCTCTGTGCTGACGCTCCGGTCGGAGTTTAGGTCTAATTCCTTAAGA
AGTATCGTCTCTGCCCTTCGTCTTACTCCCCITGGCTTCGCCCACTTCGCTCTCTCTCGGGAGGC
CAGGAGGACCCGGGTCACTTTGCCAATTCTGCGGAGGGGGAAGTAGCGTGAGGGAGATTCCACGCCAAGT
AGCCCGAAGCCCACTACTCTTTGCCCCACCTCTCCACTCTCTTGCCCGTGTAGGTGCCGCTGCTGCTGGCG
AAAGTCCCACTTCTTAAGGCTCCTGAGCTCGGAAGGGGTGTGAGGAGCCAGATGGGAAGAGAAGCAGCG
GGACGAGGGCGAGGAAGGGCTGGAGATTGTTAGAGGACAGATGGGGCGGGACTGGGGAGAGGGCGAA
GGCGACGCGCGGAGGCACTCTCCGCCCCATGAGCACAGACGTAACTCGAAACGCGCAGATGGGCCGTA
AGGTAAAGAGGCCTTTTTCCTCTCCTCTCCGCTCTTACCCTGCTCCCTCCTAGACACTTGGTGAAAA
AGCAAGGTGCGGTGTACCTGGAGCGAACCACCATGATTCTTCCAGCCGCTACGCCCCAGATTAAAGAGAGA
AAGACAGGCAGACGGAGGATGGGAAGAAGGCGGACTTGGCGGGTCCGGTGCAGGAGGGCGCGCTGG
GCGGGCGGGCGGGCGGGCGGTGACACCCCGGACGCTCCCGCGCTAGATCTGGGGCCGACGCTCCAG
CCGCCGCGCGCGCTCTGCTTCCACAATGCGGCCACAGCGCGCGGGAGGAGGAGGGTGAATCCCCGC
TCAGTCCATCCCTCATTCTGTGCCAGCTCGGGACGTACACTGCTGCTTAGGGAGCAAAGCACTTCCACCG
CTTTCACGCGACGAAGGTCG

193; ALL; chr19:4059891-4060207; 19; MAP2K2; INSIDE

GACCACAAAGCGCTTCTCATCCTTTTCTCGCCCTTTGATGCGCGCGCAACGTAAGTCTGCGAGCAGCG
GGCAGAGCGCCAGGTCTCCCTCGCAGGCGGGAAAGGGCTTCCAGGCGGGTGTGCTGCTGCTGGGTAC
ATGGCTACGTGGGGGCTTGTCTAAATTCACCTTCTGCTTTCATTACAAAAGTGTCAAAGGGGATCGCAGC
TTTGCAGGGTGTACCCCAAGCATTCGGTTTTGCAAACGACGCTGTGCGGCAGCGGTCTGATACCTGATG
AGCTCGGTGTGGCGGGTGGCAGCATTTCTCCG

209; ALL; chr19:63784504-63785085; 19; MGC2752; INSIDE

CGGTGTCTGGAGGAAGCGCGCGGACAGTCTCCCGCTCCACCGTGTGCGGGCTGAAGAGGCCGCTGAAC
GCTCGCGATTACTGAGGCATCTGGTAGGATCGCAAGGCCATCAACCTACAGGTGAAGCCGAGGCGCTGTG
GCGCTTTGAAGCCGGAGAGAAGCTCAGTAGAATCGGGAAGGCGCTGGGGCTGTCCAACTCCACCTTGGCC
ACCATTCTGTGACAACAAGGAAAAGATCTGGGCGAGTTCCAGGAGGCCACACTGAGGCGGCCACCAAGTT
GACCGGTGGCGCAGCCTGGTGTGGAGAACATGGAGCAGTGTGAGCATGCGGATGGAGGACCAGAG
CCAGCGCAACATGCCCTCAGTGTGTGCTCATTGCGGAGAAAGCCACAGCCGTTGAGAAACCGCAAGC
AGGAGCAGGGCGAGGGCGCTAGCCCGAGAGCTTCGGGGCCGCTGAGGGGTGATTGCTGGCTTTAAGG
CGGCCACAGCTTGAGCAGCATCGGGGCCAGCGGCCCAAGAAGCAGCTGCAAGAATCCAGCGTTAATGC
GCAGGCTGATCCCGAGGGCG

210; ALL; chr2:19424445-19425131; 2; OSR1; PROMOTER

CGGCGGTTCGGTGCTGCGGTATCCCATCCCCGCTGTTTAAAGAGAAATGATCACGTTAAGCGGGCCCT
GCGTGCCTGCGCAGTGCCCGACTACCGCTTGGATGGATTGACAAGGGAAGGACGCAGACACCTAAGAGC
AAACAAGGGTACTTTTAAAGCGAGGTTACATGTGTTTAGGACTCGCGAGGACGTACGTTTTCGAATTTGGTA
AAAGTCTCTGCTAGCTAGGACCCAACAGTTCTGCCCTCTCGAAACCAATGAGGTGACAAAACCTCCCATC
TCATTACTGGGAGTCCAGCGCACTCCGCCACCGCGGCTGCAGCTTCTGTAGCTCGGAGCCTGCGGACTC
CAGCGGCGCGAACTCCGCCCGCACTTTCTGGCTCTCTCGCTCACGCCTTCGGGGCGGAACCGGGGCG
GCCGAGTGGTCCCAGACTCGGCTGGGACCGGGCAGCCTAGAAGAAGGGTCCCTCAGTAGAGACCAGG
CCTCCAGCTCTCCGTCCGGGCTCCGCTCCACAACCCGCCAGTCATGTGAGGTCCGTCAAGGGAGCGATC
CCTCCGCTGCCCCGGGCTTCCGGGCTGTGGACCGCACTGAACCCAGTCCCGCAGCAAGCCCTGCTGCCG
CTTTCTGCGGCACGCTGCGGTGTGACGGCCCGCTGCTATGTCTCCACG

212; ALL; chr2:43251514-43251780; 2; chr2:043251514-043251559; Unknown

AAACACAGTGCCGAGTGAAAGTGGGACAAACGCGCCTGTGTGCATCCTGGCCGAGGTGCCGGAGGAAG
CGTGGTGGGGCAGAAAGTGTAAATGGGCCTTCTCTCGCTGCGCTGCGCGTGCAGTCTCTCGGTGCTC
ATCCCCGCTCCCTGAAATGCTCCCTTCCACTCAGGGCCAGCGCACTCCCTCCAGCTCCCTGGCCGAGAT
CTGTCTGCTTTGACAAATAACCCGCTCAGCCTTCGGGTTTATGAGTTTTCGCTCG

214; ALL; chr2:45249374-45251726; 2; chr2:045251412-045251456; Unknown

CGCTCCCTTTCCCGCACACGATTGCTGCCTCCTCTCGGGCTTGGTTAATGAGTCTGTGCGCCAAGCCAGG
TCGCTCCGGGAGTTCCGGCTTCCGCGCTCGGCACTCGGATGACCGTGTCTATTGTCTCTCTCGTGAAT
GTCGCTGAAAAAAATAAAAGTTTGTCTTAAGCCCGTGGCAITTCGCGCGCAGATGGAAAGGCAAGTGG
GAGAGGAGGGTGAGGTGCGGGGCGGGCGGGCGGCCCTTCAGGCGCGGGGTGGGCTGCCCCCGG

CCGGGAGCAGCTCCGCTCCGCGCACGTGGCTGTGGGCGCTGCGGACGGGGACGGCAGGCGGGGGACG
GCAGGCGGGGAGTGGAGGGTGCACTGCCCGCAGGTGCCGACGGCTTCTCCTCCAGACCCCTTCCGCCCGCG
CCTTGGCTGGCTGGTGGCGCGGGGAAACCATGGCAGCATTCGGCTCCGGCGGGCGGCTCTGCCGCGGG
GCCCCACCGAGCTTTCCGCGGAGCCTTCCCCGACCGCATGGGCATCTAGGGCGCAGAAAGAGTGGG
CGCCGAAACGGGTGTAGGCGCTGGAGGCCGACGGGAGGCCCCGGGCGGTACGGCTTCTCGGTAGAGAG
GGCGCTGCACCTCGCGCGCTGCGGGCTGAAGCGCGGGAGCCGCTCTGGGCGCGCGCGCGCGGCACTGG
AGGGAGGGAAGCGCCACGGCTGCGGGAACCGGGTGACGGGGAAGCGGGGGGTGGTGGGTGAGGT
CGGCGGGCAGCAGCCAAGTGTCTGCAGCTCCGAACCCCGCCACCCCTGGGCGAACGGAATGGCACCCG
CGGAGACGGCGGGGACGGGCGGAAAGCGGGTTTGCTCCGACCGCAAGCTGAGCCCGGTTGGAGGGCGA
GACCGTAGGCGAGAATGGCCGCGGGCTGGAGACCCCGGCGCTATGAGTGAAGTGGAGCCGCGGAG
GTAGGGTAGTTGGGATGTTAGTTGTGAAGACACTCGGACTTACGCTCCGGCAGACGAAACACCCGAG
CGCGCCAGGGTCCGTTTCTCCTTCTCTCTGCTTCCACACCACTGTAGATACGGAGCCAGCAGTCGGGC
TAGAGCGGAGGGTGAAGGTCGGGTTCCAAGGGCGGTTCTCTCGGCGGGGTCAAGCCCCACCCGCGGT
CGCGCTCGCTGGCGCTGTCTCGAGTTGAGCTTCCCCGCGCGCGGCC

217; ALL; chr2:63134470-63134933; 2; OTX1; INSIDE

219; AATG, CMT22411.1 (C.639.9997); CT, CTX13, CMT22412.1 (C.639.9998); TTTCTCCCACCTGTGGCCTCTCAGGCTCG
GCCGCCCCGAGGGAGTTTCTTTTATTCCEAGTTTCGGCTTTCTTTTGGGAAGCGCGAGCTTGGGCCCTGCCAGG
GGCCTCGCCCGAGCTCTATCGCGGGTCCACGTCGGCCACCAATGACCCGCGCGCCCGCGCTGTCCCCG
CGCCCACTCCGCGGAAGCAGCGCGGGGAGCGCACCACCTTCAAGCCTTCAAGCTTGGACCTGCTCGAGCG
GCTCTTCGCCAAGACTCGTACCTTGACATCTTCATGCGGGAGGAGGTGCGCTCAAGATCAACCTGCCG
GAGTCTAGAGTCCAGGTGCGCATCTCCCCGGGCTCCAGGGTCTGGGTAGGGAGCTGAGGCTGCTCGGGGA
AGGTTCTAGGAAGCTCTTGAGTAGTTCCTTGAGGAGCACCATC

220; ALL; chr2:66525936-66527222; 2; MEIS1; INSIDE

[illegible]

222; ALL; chr2:70984709-70985764; 2; VAX2; INSIDE

CGGGCGCATAACAGGCACCCCGCACATGCGACCGCGGACGACGATCCCTCCCATTTGTACCCTAAGGCC
TGAGAAGGCGCGCTCCACACCTCCGCGGTGCACAGTCCCTAGACCAAGTAGGGCGGGGAGGGAATCCTTT
TGTTTTATATTGGAACCTTTACGCCAAAGGACGAGGACGGAAGCAACAAAGGAACAACAGGCGGCTGAG
CGTGGCTCAAAACGACGACGAGGCGAGTGCCGAGGACACAGGCTTTTCGTTGGAGCGGGATACCGACGAGCA
GAAGAGGTGGACAACCTCTGACGCGAGACTCCCTACAACCCCGGATCGATGCTCCACTGCAAGCTCAAA
CGCACCTGTTTTCCCAAACTTAATCCAGACGCGGAATTTAACGACCGGACTTTGTAGATCCGGGAAATTTCTGTCC
ACCAAGCTGCACCAACACAGCAACTTTACAGACAAATGCGTGGCGTCCGTTCCCTGCTCACCCAAACCGGCG
CTCTCTTGGGCTGACAGCCACCCCTCGGGGTCTCAAACCCCACTCAAACCCCTCCGAACCCCTGTGTCTGG
GAGCAGTAGGGTGGGATGACTGCAGGATCCCTTGAAGAAGTGACTCGCTGCAACCCCAACCCACGACAGCA
AAAAACGCTTTACCCCGGAGCTGATCGGATCGCGCGATGGCGGGGGCTGAGGGGACCGGTGAAGGCCG
GCTCTCTTTGGGCTGGGCGATTCCGCGCGTGGGACGGTGGGATTGACCTTAGTGGAGTCCAGTCCTT
CGGAGAAATCCGCGGGCGAGTCCGGGACCCACGCTCCGGAACAACCAAGTCCGAACCTCGTACACACAGCAAA
TGGCGTGCAGCCGCGGCCCTAACTCCCAAGACGCGTCTGAAGAAGCCATACAAAGGGGCGCGAGCT
TCGGGGCTCTGGCTGGGAGGTTACTGCAAGGACAGCGCTCGCTCCAGCAGCCGGGTCAAGGCTCAGG
CGCGCGCGGCTCTGCTCGCTTTCTGCTTGATTACCAACAGCCACTGGGCTTGGGGAGATCGCGCGGGC
CG

230; ALL; chr2:105864220-105865009; 2; NCK2; INSIDE

226, AAG, Cmr2.10606422A105300000; 2, RCR2, 1135157
CGGCAAGACGCGCAGGAAGACCCAGCGCGGGATCGGTCCCCACGCCCAGCACGGACGCCGAGTACCC
CGCAATGGCGAGCGCGCCGACCCGATCTACAGCACTCAACATCCCGCCTTCGTGAAGTCGCCTATGTGG
CCGAGGCGGAGGATGAGTTGTCCTGTGTGAAGGGTCCGCGCTACCGCTCATGGAAGTCAGTCAGCG
GTTGGTGGCGGGGCAGCTACAACGGGCAGATCGGCTGGTTCCTCCCACTACGTTTGGAGGAGGTGGAC
GAGGCGGCTGCGGAGTCCCAAGCTCTCGAGCTCGCGCAAGGGCGGCTCGCTGAGCAATGGCCAGGCG
TCCCGGCTGTCTGATGTGTGTCAGACAGCTGTACCCCTTCAGCTTCAGTACCGCGGAGGAGCTCAACTTCGA

GAAGGGGGAGACCATGGAGGTGATTGAGAAGCCGGAGAACGACCCCGAGTGGTGGAAATGCAAAAATGC
CCGGGGCCAGGTGGGCTCGTCCCCAAAACTACGTGGTGGTCTCAGTACGGGCTGCCCTGCACCCCTG
CGCAGCCCCACAGATAAGCTACACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAGTGGTACTA
CGGGAACCTGACCGGCACCGCCGAGTGCGCCCTCAACGAGCGGGCGTGGAGGGCGACTTCTCATTT
AGGGACAGCGAGTCTCGGTAAGTGCCTGCGCCACAGCTCCGGCTGCAGGCAGTAAATGCGCCTTGCG
CGGTGGGTCTGTGTGCCGCG

232; ALL; chr2:111591678-111597436; 2; FLJ44006-BCL2L11; DIVERGENT_PROMOTER

CGACTCGGTGAAGGATGATGCCCCGAGGGTATCTCGACCTTTAACATTCCACACACCTACCTCCACGCA
CCAATCGCCGGAATCTCCAACCCGCGGGCCGCTGGGCTTTCTACCCTGCACCGCTGAGCCGCGGCCACG
GGAAGAGGCGCGCTCCCGGCGGCCAAGCTGGGAGCCAAGCTCTAACGGGTGTGGCGGGAAGTGTGGTG
GCCGCCAGCAGCTGCCACGAGCTCGCTCCACCGACGCCAGAGCTGTGGCCGGGCGGGGGCTGGCA
CCCGCTGGGCGCCACTCTCGGGGATTTTGGTGGCAAGCGGAGGTCCCGCCGAGGCTGGCGAGGTGCG
CGGCTGGCTGCTAGGAAAGAGATCCAGACGGTCCGCTGGTGGCTGGATCCCGTGCCCTTTCCCTGAAAC
CCAGCCTGGCTGACTGCAACCTCTCCCAACTTCAGTGCCGGATCCCTAGACAATCAGGGTGGGCTCCG
CGCTGCGAGCGCGCCACAGCCGGGTGCCGCCAAAGGTCTCCTGCTGTAGCGGTGACTCACATTCCAG
TGATTTAGAAAACTGTGTGTGCCGAGTGAAAGAAAAAAGCAAAACACCTTAGACAAAAGAAAA
AGCTCCACTCTTTCCGCGAGCGGAAAAAGGTTTGGTTTCAGCAGTGATGCTATTTAGTGAATCAGACGC
TCTGGGGCTCTGCAAGGAAACGCACGGACTGGGAGCAAGGAAAGTGGGAGCCTAGACTTTTGCTCTCGGCAA
AACAAGAACTCGGCTTGCTCTCCAGGCCGCGGTTTCTACGCAAGACAAGGCGCGGAAAAACATTTT
ACCATCTGACGCTGTAGTCTGTCTTTAGAAAGAGAATAGGTGAAAAGTTTAAATAAGAAATTAAGCGATGT
GGAAGTCGTTCCCGCTGCTTGACAGAGGTGGGGAGCGGGCTGGGCAATTTGGAACATAGGAGAGACCA
CGTCGGCAAAGCCTGTGGTCCGGAACAAGGGCCATGGATTTCCTATTTCTCAGATCCCGGCTGCCCGACT
TCATTTCTGTTCTTTTCAGCACAAGCCATCCCTCTCCTCCCTCCACGCTCTCTTGGCAGAGACAGAAA
GGGACACCGCTCTGCCCGCTCCAGCGCAAGGAGGTGACCTAAAACCCATGGGCCCTTCTCACACTGCG
TTCTCTGCGCTCCGGCCAGTTCGGGAGGACCTCCCG

238; ALL; chr2:156892636-156892878; 2; NR4A2; INSIDE

CGGGTTGGAGTCGACATGGGCCCTGACGAGGGCACTGATCAGACTACCGGGGGCGAAGGGGGAGAGGG
CTCCTGTGGGCTCTTCGGTTTCGAGGGCAAACGACCTCTCCGGCCTTTTAACTGTCTTGGCAACCACTGC
AAAGGAAGAGCCCTGTAGCGCCGCTTTTCCGAGCCAGGCCAGCTGCTGCCTCGGTCCCTCCCCGGGG
AAGCGCGCAGCCGCGGGGCACCAAGGCTGACGG

240; ALL; chr2:156893736-156894685; 2; NR4A2; INSIDE

TCCTAACCAATTTCAITCTGAACAGGGAAGACAGCTCCTAGCACATGCAAAATGACCCTCTTCCAACCTCCGG
TCCAGCAACTTCGGGGCGGGGCCAGCCGGTTCGCTGAATGCGAGGGGGATGCGACCTGGCCTCCCA
CTTTCTGCTTCCCTTTCTCAGACACCCGGAAGTCCCCGCGCAGCCATGGTCTCCTCGAGGGCAGCTTC
GGCGGACCCCGGAGAGCTGGGCAGTCCCGGGAGAGCTGGGGCTGGGCTACTGCACCAAGGCAGAGGGCA
CACTCCGAGCTCCCGGGCACTAGGGGCTCCCTACCTGCCTACTCCGCTCCCGCCATTGCTCACTTAAAGA
AGCCTTTGACAGCCTCACAGGTGCCACGCCGTAGTGTGGCAGGCCGGTTGTCCTCCACACACAGCGCAC
AGCCCTCGTTGGAGGGGGAGCCCCGCGACGGCGGTGAGGGCACCTGCGTGTGAGAGCAGCTGAGACGCG
TGCCCGATCTGCAGCCCGGGAAGCCCATGGACCGCGGCTTGCGATGGGGTTGGGCACAGCGAAGGTCT
GCCCGTCCACCACGTGGTGGCTGCCGCGGGCTCCGGGTTTCATGGGACGTGCAGGGGCCCTGCAAGC
GACTCTGGCAACTAGACACCGGGGTGCCAGGGGGCGATTGCTTAAGCAGAAAGGCGAGAGGCGGGAGAC
TGCGGTTTTCTCTGCTGATCATGTGCGTAGTGGCCACGTAGTTCTGGTGGAAGTTGTGGAGAGATCCC
GGGTGCTCCACATGGGGCTGTGCTGCACCTGGAAGCCCGGCTGGTGGCGCTCGGGGGCAGGAGGGCT
TGTAATAACCGACCCGAGTGCGGCATCATCTCTCAGACTGGGGGGCAGGTGGCTGTGTGTGCTGGTA
GTTGTGCATCTGAATGCTTCTACCTTAATGGAGGAC

245; ALL; chr2:171384729-171385226; 2; GAD1; INSIDE

ATACAATTACCCACACAACAAAGAGGGCCTCGGGAGAGTCGCCAGCCCTGGTAGCATATGAACCAGGCAC
CGGCGTTGGAGCTGGCCAGGGCAGGGCGGGAGGAACGCGAGGCCCTGCGCGCTTTTGTGGTGCTTTTCG
CTTGATGGATTTCTTTCTGACGCTTTCCACATTTCCCGCTCCCTTTTGGCCCTGGGGGTGGGGGTGGGG
GGTTAGCGGGCAGTTGTGTTAATTTGCCCTCCACTCCCGCGCCCTTACGGAATCCCGGTGCCCGCCAGT
CGCCGGCGCAAAATGCCAAGTACCGGTAGGAGACACAACAGAGGCGATGACCTGAATCCGACAGTGGCCT
GGTTCGCTGGAAGCTGCCAAAGCGAAGGCAAGAGAGCCCGGGACCTGTGTAAACAGCAAGCAGCAC
GTGTCCAGGCACACTGTTGCGGGCCCTTAGCTAGCTACGCATCCGCACCCAGGCTTCAAAGGCGCGC
TGGGCG

254; ALL; chr2:176737610-176738187; 2; HOXD3; INSIDE

GAAAGAGATCCGTGGGCTTCTGACCTTGGTTAGGCAAAACAGGGGGAGGCGCCGAGACCAGCTCGAGC
ACTAGCGGATTTTGAGAGAACTGACCGCAACCTCCATCGCTTCCCTCTCTTTCACTTGGATGGGCTG
ACTCTACCCGTGCGTGATTTACGACGATTGACGCGTAGTACAGCCTGGCGCCTGGTGTCCCTCCCTTC
CCAAGCCCCCTCAGCTTTTCCACTGCCACCGGCGTACAAGCAAGTGCCGAGCGGCTCCGCAAGTCCGGAC
TAGCCTCCCGGCTCCGAGGCCACACGGGCGAGCAGATTTTGGTCCCCAGCGAGGCTGGCGCGGTTCTG
CCCGCTCCGACCGCGAGCAGAGCTGCTAGCAGAAAGCAGGCGCGGTACTTTATATAACTCTGTGCTC
GCAAGGTGCAAGAGCGGAAAAAGTGGCGAGTAGGGAATCTTTGCTGCGCTGCCTCTACCGCGAGCCT
GCTTCCACTGAGAAAAGTGCCGGGCCCTTGGGAAGTGTCTTTCTTTTCACTTCTTACCGAAGCGTTACTG
CCGCGGTGGTCG

259; ALL; chr20:35582018-35583550; 20; NNAT; PROMOTER

CGGCTGGCTACCGGTGCGGGGGACCACACTCACAAACCGCATTCCGGTCTTCCCGCCCGAAATCCGCG
 CTGTGCGAGGGACCCACAAGACTGGCGGTCTAAAAGGGACCCGCTCACTTGAAAACGGGTGCGGTAGC
 CACAACCTCCGGTAGCGGTAGCGTAACCCCGTTCCGGTATCCAGCCGACAGCGCAACGGGTACAAAGA
 ACCCACTGGCTAAGGCCGACCTACCAGGGCTTGGGGGAGGGAGCGGAAGACGAGGTGGAACGACCT
 GTCAGCAGAAAACTATCCCAAGCATATTCCAACCACTTCTCCGTAGAGCTCATTCTCCGTGCATACG
 AAGGGCGCCAATCTTCCGTATCCCTCTACAGATACCGGGTGAACGCTTTTGGCGCCAAAGCGCAGT
 GCTCTGGCTCAGCTCCCTACAGTAGCGACCTCCACCGCAGATTCTCATCTCCTCGCTACCGTAAGAGAGAT
 GTAAGAATCAGACGGTTACGCGCTCAGGCACCTCATGAAGAGAGGACCTGGGCTTAAACTCATTCA
 GTATCAGGAAAAGAGCGCGGAGCAGCGGCTATTATGCCAAAGCTTCTGAAAGGGGACCCAGTITTTTG
 CTCTATGGGCGAGTAGCCCTCCCTAATTTCGGTTTTCATCCATCCCCAAGGTAGGCTTTGGAGTGGCAC
 CGGAGACTGAGCTCAAATTTGCAGGCCAGGACTGGGGAGAAGGGCGCCACACTAAGAGACCTGCACCC
 CCATTCTCGCCCTGACTCTACCCAGAGTCGTGGTCCCTCCATTTTAAAGCAAAATCCAAAAGCAAGCAC
 GGCGAATCTTCTGGAAGGGGGCTAAGATGGAACCTCAGGAGGCGGGGTCCGGTATGGAAGAGCAGATG
 GATTATTTTTTCTCTCCTGGCGAATGAGGGCGCCCCAGCCACCCCTCTCATAAACCCCCCAAGGC
 GCGCATGCGCACTTAGGTGGCGGGCGGGTACTTAAGCGCGCGCCACCGCGGTGCGGCAGTGCGCCAA
 CAGCGGACTCCGAGACCAGCGGATCTCGCAAACCTCTTTCTCGACCACCCACCTACCATTCTTGAACCA
 TGGCGCAGTGGCGGGCGCTCGCTGAACCTGCTCATCGGCTGGTACATCTTCCGCGTGCTGCTGCA
 GGTAAGTCTGACGGGTTTCGGTGGGAGAGGGT

267; ALL; chr20:60061693-60062033; 20; TAF4; INSIDE

CGTCTAATCGATGTTGGGGCGAAGGGAGAGCCACGGCGGCCCTGAGTGCAAGCACCATCTGAAACCAG
 GAGCCCATGAGGCGCGGGAGCCGAGGACCAGGACCGCCCTCGCACTGCCCTGTGACAGCTCCCGGCC
 CAGCTCTCGCCGCTCTGGATCCGTCACTAAGCAGCTCCATTAAAGTCCCGGTACGGCAGGAGCGGCAGG
 GAAACACTGGGGCACCACATCTGAACAGAGAAGATGCCACCTTGAGAAGGTACCTGGAGAAGGGAGCC
 ACGAGCGACGTTTATGCTGAGAAGCGGCATCCGTGCACCTCACTCCCGCCGTCCACGCCG

281; ALL; chr4:9756136-9756429; 4; chr4:009756149-009756196; Unknown

CGTTCGGGTGCGCGAGTTACACCTGGCTATAAGTCATCCCGTGACCTGACTAAATGCATCCCGTGCACT
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 TAAATGCGTCCCGTGCACTGACTAAATGCGTCCCGTGCACTGACTAAATGCGTCCCGTGCACTGACT
 AATGCGTCCCGTGCACTGACTAAATGCGTCCCGTGCACTGACTAAATGGTCCCGTGCACTGACTAAAT
 GCGTCCCG

284; ALL; chr4:111780013-111780343; 4; PITX2; PROMOTER

CGCGGAGAGACACAGGAGAGGGAAGGGAGTTGCGCTGAAAAGACGCAAGATACGCGCGTGCAACTCC
 CTCCCCCTTTCAGGTTTTCAGAGGTTTGCAAAACAGGGCTGAGAGGAAGGGGCTCGGGAACTCACGTTCTC
 TCGCCCCCTTCTGTCTGAGTCTCGCCCCCAGAGGCTGTTAACCCAGTCCCGGCCCGCCGAGACAC
 TGGCTGAGCTTTTGGGTCTCGCCTTGGCCAGCGCCAGTGCAGCTGAAGTGAGAGCTGGTGGGAAATGC
 AAATGGCTCTCGGAGAAATAGAAGATACAGAATGATTCTCATTCCCTCT

302; ALL; chr5:115810975-115811393; 5; SEMA6A; INSIDE

CGCGGCTGCGCGGGCTGGGCTTCCGCTTCTGCTGCAGCGTTGGGGTTGACTCTGGGGTGGGGAGGGCCG
 TCAGGTCCAGGTGGTGTCTGGTCTGCTTTAATGAGCATCTTGGCCGTGTTGCCGGGAGTGCGAGCTTGCCG
 TTGTGCATGAGTGGCGTGAGGATGGCTCCGGCTTTGGGTCTTTGGATTGAGTGCCCCAAGAGGCGCG
 TGAGCTTGGTGACGCTGCTCATGGAGCCCCGGCGGAGTGGGTGAGCTCCTTCTCTTGGCTGCACCACA
 GCCACGTCTTTGCGCGGATGATCACAGACGCAGTAGACGGTGATGCCGAGAAGACGGCCCCCATGACGA
 AAGCCAGGATGACTGCAATGGCCAAGAGGGTGACGGGAACCAGCTGGTCCGGGCCCTTTGAGGTAACCT

304; ALL; chr5:122461778-122463450; 5; chr5:122462228-122462286; Unknown

CGGCCAAGGCTGGCGGCGGCAGGTACCCGGGTGCCCGGAGGGCCACCCGCGCGCCCGCTCTGGCGCATC
 CATCAGTGCCAGCTTTCACCGTGTCTGCCAGGCGGGAAGTCCAGGTGTCAAGCTCATGCCATAAGCCT
 GACACTTGCAGGGGTCCCGTGGCTCCTCAGGGAAGCTGGGCCAAGGAGGCTGGGTTCGCGCGGGCGGG
 CGCGGAGGCCACCTTCTCGGGGCGAGGCCATCCCGCTGAGGCGCAGACACGGCGGTCTCCAGGCCCCATT
 AATAACCCGGAGGGCGCTGCGATCCGACAGCGCAGTCCGACAGGCTCTATTCCCGTGGCGCGCTGCCT
 CCTTCCAGCCCAGTTCCAGTGAGGGGATACTGGCGGCCCACTACCGCCCGCGCGGAGGGTGGGGTCCC
 TCTCGCGCAGGCTGCTTTGGAGAGTGTGGAGAGAGACAGCTTTATCTACAGCTTCAACCATTTGTATAGCA
 CAACAGAATCGCATTTAGCCTGGAGAACAGCGCTCGGGGCGAGGAGTTGTGCTTCTCTAACAATTAGGCT
 GATCGTTAAATTTGCTATTCTTTCTCCGGCGTCTAGGGAGAGCGTGACACCAAAACCTCCAGAACAGC
 ACCCGGTTCCCCACCCCGCCCACTGTCCCGCGCTGCTTACTGCTGGAGGGAGAACTGACTGCTCG
 CTTGAGGGACCCATTTCGGGCGCGCCCTTGGAGTCTCGGGCTGCGGCTCTCTCTACCGGCTGCGAG
 GCTTGTCTGCCCCGTCCCGTGGCGTTTGGGAGCGCAGTGAGGAAGCTCCGAGTCTCTGGGTGCAAGGAA
 GTGCGAATGGCACCCCGATAGACTGGCGCTTCCCCACCCCGCGCGCTTGGTGATTTTAAATCGTCTC
 CTGTGTAATTGTAAAAAGAGGAAAGCTGAATACCAGACGACAGTATAGAATCTCTTCGAGACAGCAGATT
 GGGCAAGAGACGGGCTTTTTCGCAATACAAAGGATAAACACATCTGAAACTCCAGATAGAAACCTCAG
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 AGAGATGCAGAGAGACTGAAACGGGAGGAAGAAGCCTGGAACCTGTCGGTTCCGTGGAGAGCGGACATGC
 TATCTGCGCCAGATCCGAAGCCTTTGGGGACCTAG

311; ALL; chr5:134390896-134393045; 5; PITX1; DOWNSTREAM

CACAGAAGAAAAGGCAACCCAGGCATAAAGAGGCTCTCAGCAGCCCTGCCGAACGCTCTGGCAGGC
 AAGGGCCCCATAGCACCCCTGGGCCCTCGAGGGTCACCGCAGACCCGGCCTGGGAAGAACCCGTAGAGTC
 CCGCAGCCGCGGAGGGAGGGGTTCTCGCTAAGGCGTCCCGCGGACAACGCCGAGAGGCACAGCTTAGC
 GGGTGGCAGCCGACAGGCTCGCAACGCAGGACGGTGCCTCATGGGAGCCAGGCCAGGTCGAAGAA
 TGGTGGTGGGAAGCGGGTAGGCAGACCTCGGCGGGGGCTGCCTCGGCGCTCTGCTCTACCCAAGGG
 GCCCGGTTCCCTTTCTACCCACAGTTCCCTTTCTATCCGCTCCCTCCTCAGCCAATGAAGCAGTCGGGGC
 TCAGCAGTGCCTAGCACGCTCGGACTATGGTTTAATAGACGTACATGGACAAGTCGATATAGACAGATTT
 ATTACAGTCAGTCCAACATACACAGGGACGCTGTAAACAGGGGCGCGGCCGAGAGCGGGTGTGCAAAGT
 GGGCGCAGGGCCCTGGGGCGCGCCCTTGTCTTGCCTGCGACTCTTGCACGGCGGGCGGTGAGGAG
 GGGGCTGTTCCGCCAGACAGAGGGCCACCTCCTAGCCCGGAGCGAGCAGAGGGCCTGGGCCCTGCAGCT
 AAGCTCAAGGCTGGGGTGTCTGAGATGGACCTCCCCACCTCCCGCCAGGCCCGCACTGCCCGCTGTGC
 CTCCGTGGCTTAATATAGGGCTCCGGGGCGCGGGGCCAGCAGGCTTACCAGGCGCGCCGGGGCCGTG
 TGGGCTCCACTGAGTGCCCGATCCTGGGCTGGGGCACCGTCCCCCAACCCAACGCCGCCCAACA
 CGGATCCGACTCGAGCTAAGGCGCTCTCGGCCGGCCCTGCTCGGAGAGGGCAACTTGGTTTGTACGGGT
 CGGAAATCTAGGCAAGTCCAGGCCCGCACATCCAGTCCGCAGGCCCGGCCACTCAGTCCGGATCCAG
 CGCGCGGGGACGCGGGATACGAGGTCGTCTCTCCCGCGCGCTGGGCCTCGGCGCTCGCTACCGCGCC
 GCGTGCCCTCCGCGGAGTGGGCTCGGGGGCCGTGGGAACACACACACCACCGCGCCATCCCGAGAG
 AATTGCAACTCATCATTTTTTCGCGGACCTTTCTCCGACGT

314; ALL; chr5:135442969-135443206; 5; chr5:135443148-135443192; Unknown

CGCGCGGACCGGAGGCGCACACCGGAGGGGAGGTGCCCCACCAAAATTTAAGTGCGGCGCAACATGC
 ACCACAGGTAGGGGCACTACCAGGGCAAAAAGACTTGGTGAATGCGAGGGCGGGCCTATCAAAGGTGC
 GTATGGTGTACCAGAGCAAGCGGCAACAGCTGCTCAGTGGTCCGCAACCGGGTCAAGGGACAAGAAGA
 CGATTCTGGATTGTAGGCCGCCGAGAGCG

319; ALL; chr5:174091287-174092335; 5; MSX2; DOWNSTREAM

CGGTGACTCGGAACAGAGGCGAGAAAGGATGCGGAGGACTTCTTGCTGCGTAAACAGCGCGGGCGAGAT
 TGGCACCTTGGCACCTACCAGGACTGGCGCTTCGTCCCGGTTTCCATTGTGCCCGCACCACTTTGAAAGTG
 GCGCCCGGAAACTCCGTTTCTTATGGGGCCGGGTGCGGCAACGTGGTTACAGAGGTTTACAAGCTCC
 AGCACAGAAGTGATCCAAACCGAGGGGTGGGCTCGAAGTCGGAGGCTGATTTTTCTTGCTCAGTCGCTCC
 GCCGGAGCTGAGCCGCTGGAACGACCCAAACCTACCTGAAAGCGCGTCTCTGCAGTCCCGCTGGAATCT
 CCGGCTCGAACTCCTAATCTCAGCCCGGAATCCAGCCATATTCAATTAAGATTGCGTTTTCCAAAGGCCAA
 AGCCTTTCCCGGTTTCTGTCATCAGCCGCCAGGTTGGGTCCCTAATTAGCCTGTCCACCGAGCTTCCCTCCC
 GGGCCCGCTTGGACCCCGCAGCCCCGGGCGATCTCAGCCCGGGGGGAATCCGGAGACGCCGGCTCCGG
 GTTAAGACTCTGCTCGTCCCGAGGAGGACGGGTCCGATCCAGAGTGCATCCGGAGAAAGGGCTGCA
 TCTTGCGTGGCTGGCGGTTAGACTGGAATCCGTCTGGGGACTGCGCACCATCCCCATCGCTCCAGACGC
 CGAAACAAACCTGAGGCTCGGAGAGGGGAAAGAGATTGTTACGGCTCGAACATACCGATCCCGACCTC
 ATAGTGGATGGGTTACCGAGCTGAGAACCAAGCCGAGGTCCGCGAAGCGCGGCCCTTGTCTGTG
 GGCTCCCTTCAAGCCTGCAGTCTGGGGATGGGTTCCGAGTCACCGCGGTCCGGGCCCTCGGTACGCTTG
 GTCGGGCACACAGGGCGTTTACAGAGGCAGATGACAACCTGTGGCGGCAAAAGGACTCTCCCTCACAGG
 GACCCGCAAGGCGCGCATTTGAAGATGTTAGCGTGGGGCTTTAGATATCCTTGGCTCCG

324; ALL; chr6:1549606-1560865; 6; FOXC1; PROMOTER

CGGGCTCCACGCGGGCGCGCGCTTCTCCACGGCTCTCTTGAGACCCGTTTCCAGGGGACGC
 TGTGCGGGGACAGGCGGAGCCCGCCCTTGGAGCCCGCGCGGAGAGGCGCCGCGGACAAACGCTCC
 GACGGCAGGGGCGGCTCGTAGCACGCGCAGTGCAGCGTCCGGCGCGCCAGGACGCTGCTGGCCCCGG
 GTTCCCGAGGCGCGGACCTGCCGGGTGAGGTGCCCCAGCTGAGAGCCCCAGCTGGGTCCGGCAAG
 GGGCTCCGGGCTTCCACATCGTCCCTTTTCTGCTGACGCTCGCGGGGAAGCGCGGGAAGCCTGTGAG
 GGGCGGCTGGGAGCAGACGACACAGGTACCGCGCGCGCTGCCAGGCCGACCACTCGCGAGG
 ACCAGCGGTTCCCGAGGGCTCGGCCCTCAGGTCTCGGGGAGGCCGGCTGCACCGAGCCGGGTGTG
 GCCTTGTCCCTGTCTGAGAGGTGCAAAACCCGCGCCCGCCAGGCCCGGGCTCCTGCCAGAAAGGC
 TCAGAGCTGGGGGCGGACCGCGCTTACCCGAGGAGGCCCGCGGTGCTGCCGTTGGTGCCACTCC
 CCGGCGGGGTGAGGGACGTCGGAAGGAAGTCCAGGGCGCAGGCTCCGGAAGGGAGCACTCGGAA
 GGAAGGCTGGCTGCGGCCCCCGCGCTGGGTCCGCTGCGGCGCGGGCCGAGACCTGGGAACAGCCAG
 CCACCTGCAAGGTTGCAGCCCACTCACCCCCCGCGCGGCTCCGGGCTGTCTGTGGGTCTGTCTACGGG
 GCAAAAGCCTTTCTTCCACACCCACAGCCAAGGCGCGTCCGTGAGGGGACACGCTTCTGCTCCAGCC
 CCAGGAAGGCGCTTTCGCCCTGCACTCTCCGACGCGCGGCTCCGCGCACCGCTCCGCTCCGGC
 AGACTCTGGGGCTGGGACTCGCCCACTCGCGCGCGCGCCCCACATGAGCCGAGGTTGGGAGGC
 TCGGGGGCTCTGTCTCCAGGCCGTGGAGTGGCGCGGCTCTGAGTCCGTGGGGACCTGGATGGA
 GAGAAACTGGGGCTGTTCCGCGACACATGCACATTTGTTCTTTCCGATCATCTATCCCTTTACGAATTT
 TATTTTATTCCGGATTGTTAATGCAAGACGACAGTTGAATCTCCA

339; ALL; chr7:1481682-1482268; 7; chr7:001481829-001481873; Unknown

CGGCTCGCGTGGGAAGCGGGTACGGGAGGCCAGCTTCTCCCAACAGGGTCACTGGAGAGGAGCAGA
 CGCAGCCGTCCGCCAAGACCCGGGCACGAGTCCCCAGCAGCTGTCACTGCCCAAACTAACGTGACCCCA
 CGTCCACACAGAGGTGAACAGATAAAACCAACGGCCGATCCACACAATGGCAGGCCACCCAGTGCCACAA
 CACCACGACTCTCCAGACTGTGCGAGCAGAGCACCCGCAAGCTCCCTCGGTATAAACTCAACGCAGACAA

ACCCACAGGGCCACAGGGCGGCGGAGCTGGGAAGGGGCAAGAGGGGTAGCCGGCGATGGCCATGTACA
CTGTGGCCTCCGCCCTCCCTCCCTGCCCGGCCAGGGCACCTGGGACGGCGGGGGAGCGGCAGAGTTGC
GCCCTCACCTTGACAGCGCTGCTGCTGGCAGCCCTTCGCTGTGCAGTAGGACCTCAGGCACGGGCACCC
GCAGCTCCGGCCGCTGTAGGTAGAGCTGCAGGAGAAGGTCTCGGCAGCCCTGCCAGCACGCTGGAAGA
GGTGGAGCAGGGCTCACCAGGCGGACG

340; ALL; chr7:2082782-2083345; 7; MAD1L1; INSIDE

AACACAGTTATGACACAGTGAGCCACAGCACAGTTAGCCTGCAGCACAGTGAGCCCGAGACACAGGTAT
GACACAGCGAGCACATGGCATGGTGACCTGAGACAGGGTTACGACTTGGTGAGCCCCAACATGGTGAGC
CCAAGACGTTACGACATGGTGAGCTCAGGCACAGTGAGCCTGAGATGGTTACGACACGATGAGCCCGC
AGCACGGTCAGCCTGAGACGGTTACAACATGGTGAGCCTGTGGCACGGTGAGCCAAGACAGGGTTACGAC
ATAGTGAGCCACAGCATGGTCAGCCCGAGACAGTTATGGCACAGTGAGCCCGCGGCACGGTGAGCCCGC
AGCATGGTGAGCCCGAGACGGTTATGACACAGTGAGCTCAGGCACGGTAGCCCGAGACAGAGTTACGAC
TTGGTGAGCCCGCGCATGGTGAGCCCAAGACAGAGTTACGACTTGGTGAGCCCGCGGCATGGTGAGCCC
GAGATGGTTACGACATGGTGAGCTCGCAGCACGGTGAGCCTGCCATGGCCTCAAGGGTTAAGATGTAAAC

345; ALL; chr7:2724511-2724848; 7; AMZ1; DOWNSTREAM

CTTCTCAGCAAAGGCCAACAGCTCTTTCTCGAGTCCAAGACCATCTCCCGTTCAAGGGCCCTCACCGGCT
TTGTGAGTCTGTCTCGTGGGCCTCCTTCAGTGGTCTGTGACCAGCGGAATGAATGGGACGTGTTTTGTTC
AGCCCTGACTCTTGGACGCTGGTGGCAGCCCGCGGGCGCCACTCACCTGGCACGTGGACGAAGGTGATGA
GCGCGGTGACGGCTCCCGGGGGCAGTGTGGGGTCCAGTCTGAAGCCGACGCCCTCTCGGTGAGGCTTTC
AGCAGCAGAAGGCAGTGGACTTTCACCATTTCTTCCAACACTTTCTCACGTAG

349; ALL; chr7:8449587-8450236; 7; NXPH1; INSIDE

AAACTGAGGCAACCACTTATTCGCAAGAGTAAACCCCTATGGGGAGAAGCGATTCTGCCCTCTTCCCC
CGGCGAGGAACACGGCTGGAGCCACCCAGGCGCCTTCCAGGCTAAGGCGCCTTTAGGGCGCGCAGGGGT
GAGGGAGAGGGTGGGGAGAGTCCATTTATTATGAATTTCTAAAGGCGCAGTAATTTACACGGGGAGCA
GGACAAACCATGGCTAGGCAGGGAAATCGATATATTTGCTATCGAAAAGTTCCTGCTCGCCTTTAATGCAGA
CGAATGGGGGATGCAGCCTCATTAATTTCCGTGGTTAGGCTCGCCAGCGTGGGGCCTGATGCAGCGTGAA
ATCTATCATCATTAGACCCGGGATGGAGCGCGGGGGGGAGTTTCTCTTACTTACCAAAACCGCAACAACA
AACAAACAACGACGAACAACCGGCCCTACAAACACTCATTCTCACACAACGTTGCCCTACCTCCCTCGCC
GCTTGCCCTGGCCGCTGTTGCACACTCCCCTGGGGGGCTGTCTGACGCCCTAGAGCAGACACTGCGGTCAC
TTAAAGTGCGCCAGTTCTCTCACCGCAGCGGTACACCGTTGATTTGATCCAGAAATAAGACGGATAGTA
CCGAGCGTTGCGG

354; ALL; chr7:27164708-27165039; 7; HOXA7; PROMOTER

CGCGCGCGCGTCTGTCTAGACTCAAGCGACTGAAGGGGCCAACAGAGCTGGTGTTTTAAAGTAGAACCTG
CCCAGTCCAACAGCCCGAGCAGGGAGCGATTTCCGGGATCGCGGAAGGAACGCACTCGCCAAGGGAGG
GCGGGGTGCCCTCGCCACCGGCTCATTCCTGCTCCGGTTTTCGCCGATGCGCGTCCAGGAGGTTCTGGCA
GGACGCACTGCCCTCTGCCCGGCCAAGGAGGATGCGGATACTGCCCGCAAGGTTCCGGCCTTTATGGAC
CCAAGTCAGCCAACCTGGGCCGAGTCTCGCGACACCGAAACCTCCCTTTCCG

358; ALL; chr7:27251165-27252762; 7; EVX1; INSIDE

CGCCTGTGCTCTGGACTCGCTGTGCAGGGTCCGGCTCCGAGGCGCTGGTCCGCAGTCCGAACGGAGGGA
GCGAGACCCCAAGAGCAACGGCGGCAGTGGTGGGGCGGGCTCGCAAGGCAACCTGGCTGCAGCGCCAG
TGACAGATGCGTCGTTACCGCACCGCCTTCAACCGAGAGCAGATTGCGCGGCTGGAGAAGGAATTTCTAC
CGGGAGAATACTAGTATCCAGGCCGCGGAGATGTGAGCTGGCGGCCCGCCTAAACCGCCGGAACACCAT
CAAGGTATGCGGGGTCCAGGCTGGGGAGGCGGGTGTGCACCTATTTAGCGGGAAGTAAATGCCAAGTACC
AACTCCCTGAAACGACGACGGAATCTGGGCCTGGGGTCTCCCTGCCCGGGCGTGCAGATTGACCTCG
TGACAGCTCCTAGGCAGGCATTGCTGCCATGTGGCTGACTCTGTCCCTTTCTCGTTAAATAGACAAGGGG
TGGGCGTGGGGGAAGGGGATAGAGTGCCTGTGCGGGTGACAAGGAATTTCTGGGGACACGCTCTCTGCG
GCCGACAGCAATTGAGTCCATGTCTTTCACTGCTCCTCCATACACACTGGCCTCTGGCACCCCGGG
GGCCTGGCCACCTGGGCAGAAAGGAAGGAGGGAGCGGGCTGGATCACTCCCAAAACCTCTCTCGGAGGGA
TTCCAGCTCCAGGTGGTGGTGGTGGGTGGGTCTCTACCGGCTGGTGTCTGCTTTGGCTGTCTCTGCC
TGCGAAGACTGTCCCCGAGCGGACAGACTACTGCCCTGAGCATCGGGCAAGTCCAGCTACTGAAC
CTGCTCCGCTCCTCTCCCGAGGTGTGGTTCCAGAACCAGCGCATGAAGGACAAGCGGAGCGCCTGGCCA
TGACGTGGCCGACCCGGCGGACCCCGCCTTCTACCTTACATGATGAGCCATGCGGCCGCGCGGGCGGGC
CTGCCCTACCCCTTCCCATCGCACCTGCCCTGCCCTACTACTCGCCGCTGGGCGTGGGCGCGCATCCG
CGCCCTCGCCGCGGCTCGCCCTTCCAGCGTGGCTGCGCGGCTCGACACGTTCCCGGTGCTGTGCGAG
CCCTACCCGCGGCCGAAGTGTGTGCGCCTTCCGCCACCCCGGCTCTACCCGGGCGCGCGCACGGAC
TGGGCGCCTCTGCGGCGGGCCCTGTCTGCCCTGCCCT

359; ALL; chr7:32768010-32768497; 7; chr7:032768257-032768301; Unknown

CGACTTGTCCCCGAGCCCTTGCGGACCTCCTGGTCTCATGGCGACTGTGAAATGTGGGGTGGGGAGC
ATGCGTTTCAAGCCATTTCGCGGGCAGTCCCTGCGTGTCCCCACGTTCTCCCACTCCGAGACC
CCCGCTCCGAGCTTCCCTGAGCGTGCAGTTCCAGTGAGGGCAGCCCCACGCACAGCCCCACCCCT
CCCCAACCCCTTACGCCCCGGTGCCTGTAGTCCCAAGCCACACGTCACCTTCCACCTTGGCGCAGCT
GCACGTACAGCCCCCACACGCTCCAGCCCCACTGGCGCAGAACCATCACCGCTCCGCCCTTACGCGC

TTCACCTGGGAGTGCAGCCCCACCCCGAGCGCGAGCTCCACGCAGCCTTCCACACTCTCCCCAGCGCCT
GCAGCACCCCCAGTGGCCACAGCTCTGCCAGTCGCTTCCCCCGGTGCGGCCCTGCACCACTTCG

362; ALL; chr7:55040457-55041024; 7; chr7:055040965-055041024; Unknown

CGAGCACGGCCTCGGAGGCTGAGAGGCCCTGGGAGGCAGGGCCGCTCCTGCGGGCTCCACGAGAGCCCT
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GCTGGAAACCTTCCCTGCCAGGCGCAGAAGGCCGCGCGCAAGCACGCAGCTCACAGTCACGCCACCTG
CTCTGAAACCCAGGTTTACGCGCAGGATCAGAGTCCCCCATCCCCACCCACGCAAGGAGCAGCAGATTG
ACAGCGACCCCTGAAGAAATGCAGTCGAGAGCTATTGTGAAAGGGCGCTGGCCCCGAGGCCCCCCAGCCC
TTCGCCGGGCGGCGACTGGAGGCATCTTCGGACCTCTGGGCGGCCAGCCCTCTGGCGTCTCCCCGCC
GCGCAGGACAGGCCAGTTAATCGCCTTGGTCCCAGGCCCTATTAGCGTGTATCTGCGACAGCAGGACA
CGCCTTCCCATGCCAGCCGCTTGGGGCCCGTGGCGCCCTTTTCCCTCGCAGCTGCTGCAACAAATAGCA
GTTCTTTTGAGGGAAGGAACAGTGTGGTCTCAAAGTTCATAATGAAAACTTTGAGAAAAATCATAGTTG
CTAA

364; ALL; chr7:96488158-96489591; 7; DLX5; INSIDE

CGAGCGGGACGAGCCCTGGGGCTCCACACCCGCTGGAGACTGCGGCGAGTTACACGCCATTGGGTGCGT
GGAGCTGGGACTGTGCTCCGGGGGCATCTCCCCGTTTTTTCATGATCTTCTTGATCTTGATCTTTTGTCTG
AAACCAGATTTTACCTGAGTTGGGGAACAAAGGCACACGTTACCGGGACACTCAGAGGTGCGGCCGCC
TTCGCCGGGCGGCGACTGGAGGCATCTTCGGACCTCTGGGCGGCCAGCCCTCTGGCGTCTCCCCGCC
GCTTGGCGGCTACCGCCAAGAAGCTATGCCCTTAGGCCAAACCATGGAGCTCTGCCCCAGAGGGCGCCCTG
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GGGCTACGCGCGCCTGTGGTCAGAAAAAGGAGCGAGCTCCCAACCTCCCGTCTACTCCCTTCACTCCCT
CTGCAGCTCAGAGAGGCCAGAATCTGACTGCAGCTCTTGGCGGCGCTCGAACATTCTTTATGCTTCCGTAG
GCCCCAGCTGGGTTGGAGGAGTAAAGGAATGGGACAATCCAGGAAGACTTCTACGTACAATAGCGCCC
CCACCTCGCGACCTTTCGGTGGCCGTGGCCCTGAAGCTCCGTAGGCTCAGGGCAGGACCCCTTTCAGTTTCT
CCGCTCCAGGCGGACGTTCTCAGCCTTTCTTAGCCTGAGACCACCGCGAGAACACCAGGCCCTTGTCAACC
CCGAGGAGGCTCTACATTGTTAAGAAAACAGATACTGCTCTGGGCTGCCTAGGCCGCCCTAGAAATAAC
CCTCCGCTTGCTTTCAACCCCGCAAAATTTGCCCCACAGCTCCGAGGCCCCGTACGGGGTGGGGGGCGGG
GGCGCGTTAGTGGGAGGTATCTCCAGACCGTGATGAATACCATCCCACCGTCTCAAGGCCCTGACTCAC
CGAGTTAAAGCATAGGGGCTGATGCTTTTGGCTCTGTTAGTTTCTACGGGTAAGTGTCAAAACAGCTCCAG
TCCCATCGAGACTGAACCGCGGACCAACCAGACGTG

369; ALL; chr7:155266364-155266696; 7; RBM33; INSIDE

CGATTCAAAGATGCCGGCGTCCCGCAGTGTGCGGTTTCGTGCCCTTAACCACCCGCTTCTTTGTTTCCCGCC
CCTCTGCTTTCGCAGGAGCTCTTGTGCTTGAAGTTCAGTGTAGTGGTAGCGTGGCTACTCTTGGAGGT
GGCGGCCGCTGACCGGTGTGTACTGCTTTGCCGACGGGGCTCCCGGCCCTGATGCGGTACACTCTGCG
GGGCTGCACCCGGTGGCTCTGGTTGGGGGCGAAGCTGTGTTGACTGGGAGACGTTGAAATTGAGACAT
GGAGAGATGACGGGAGTGCCTTTCTCTGGGTTTGATCTCCATCTGTTTT

371; ALL; chr7:155288454-155292175; 7; SHH; INSIDE

CCGCGTGGCCCCCGACCCGGAGCGTCGGCAGCACCTGGAGCGGTTAGGGCTACTCTGCCGCGCGCGCC
CCCGCGGTCCCGCGCGCGCTGTCCCGCGCGCGGTCCGTGCGCGCGGGCGCCAGTGCAACAGGAGCGCG
TGCGCCAGGCGGAAGGGCGCAAGGCCCGGTGCGCCAGCTGTGCTCCTCGATGACCGGTAGCACGAG
GCCAGCACCCGCTTATGAGAAATGGTGCCTGGGCCGTGAGCGCGCGCTAGGCGCGCGGCCCTCTCGC
TTAGGGTCAAGCTGTGCACAGCGCGGGCAGGAGCCGCGGTTCCCGTCAAGCTCGGCCACCAAGTACA
CGCGCTGCCCCGGCGCACGCGGCTGGCGAACAGCGCCCGAGGCCCCAGTGCGCCCCGAAGGCGGCC
CGAGCCCAGGACGCTCGGGCTCCCCGCTGGCCGAGTCTGTTGCGGCGCCACAAAGAGCAGGTGCGC
GGCGGTGAGCAGCAGGCGCTCGCGCGGCTCCCGGCTCTCGATCAGGTAGAAGCCTTTTGGCGCGCTGT
CGCGTCCAGGAAAGTGAAGAAATCGCTGTAGAGCAGCGGCCCTGCTGCTCGCGCGCCAGCACGCGGT
CCCCGGGGCTCAGGTCTTACACAGCTTGGTGGCGCCCTGCTCCAGGTGACCGTGGCCGAGCCCGGGAAG
CAGCTCCCGATTTGCGCGCCACCGAGTTCTCTCGGGGTGAGGAGAAGGGAAAGAGAGAGGACAGGGC
ATTGAGTTCGAGAGGGAGGCGCTCTCGGGCAGGAGGCGCACGCTGTTGCCGCGCTCTTAGGCCAG
GGGTGCGCAAGGCGCGGGCGGGGCGGATTGATTCCAGGCGGGTCCCGCACACACCTCCCTCCCCAACCC
CCACTGCCCCAGGGACAGGATTCCGACACATTCTTAACGACTCCTAAGTCTGGGCTGGCGGTACAGAG
GTTGGCTGGCGTTTCTTGCAGAGGCGGTTGACACTCTTTCTTCCGCTTCTCTCAACCCACCCCCAGCT
CCGACACACCCGGCTCGCGCGAATCCATCCAGAGGGGTTTGTCTGCACTTGGATTCTCAGGAAGC
CTCCTTGAAGTCCCGCGGGCGCGGGCGCACCCCTCTTCCCTCCCGCCCCGGCGGGGCGCGCGCCT
GCTGCGCACTCAGCACCCCGGCTGCGCGCGCGAAACCTGGCCCCG

390; ALL; chr8:142288380-142288718; 8; SLC45A4; DOWNSTREAM

CGCAGCGCCTCCTCGTCCCTCTCGGGCAAGGCTATCAGCCAGAGCACCTCCCCCTTTGACACTGACCGGCG
TCCCAGCCCGCCCTTGTACTGTCATCCGTCTGAGGTACAAGGTTAGAAGCCACAGAACCCGAGCTGCAG
CCTGACCCACACAAGCTGCGGGCGCAATGGCGCTTTGACAGACAAGACAGCCTGCCCGTCTGCCCTTCTTC
TCGGCTTCCCTTAAGACACAAGGTGACGACACGAGCGGTTTCAAGTGAGTGCATCTGGAATAATCTCAGT
GCAGGGCAGGGTTGAGGCCAAAGATGCTGTCAGCTGGTCCCCGCTGTGGCCAGGC

402; ALL; chrX:39749470-39754050; X; chrX:039752648-039752692; Unknown

CGAGGTATAAAGACCAACGCACGACGGGCGCGGGGCGCCGTACCTGCCTGGGTTAACAGTTCCTGCCG
CGGGGGCAGGGAGAAAGGCGCTAGAGGGGCGCGGGGTGCCGGCGGGGCGAGCCCCGGCGGGGCGAG
CCCTGGGTGCCAGGCCCTGCGCCGCACGCCACTCTCGCAGCGCTGCCGCCGGGAAAGTGCCGGCGCTGG
CTCTCCCTCCCTCCCGGAATAGCGGGCGCAGGCACGCACATCCACACACATCCAACACACACACACAC
CGCACACTCACACACCCGGGTGGCCGCGCGGGGCTCCGAGCCGCGCAGGCCTCCTTGGCAGACATCTTCC
TGTGGGAGGATTTCAAACGAGCCGTGAAAGCCAGAACTACACGGGTACAACTCCGGAATCCCTGGCCG
GCCTCGGCCTCCCTCCCCACCTCCGGCCCGGGCCCCCTCCGTTCGGCCCGTGCCAGGAGCCCCACCAAAG
GACAAAGCTCACACGCCGAAAGCGCGGGGAGATCCGGGGGCGCAGAGATGCCCCGACGGCCCTTCTACC
TTCTGACCCTGGGACCCACGGCCAAGTGCCGCGCAGCCGAGGTCGGCCTTGCTGATCTGTGGTGCCGAG
GGCGACCCGAAGCGCACCGGCTTCAGGGTGCGCCCTGGCCAGGGCTGGGGTGAGGGGTCACATAAGCCA
CCTGGCATCCGAGGGTGGCCGCTCGCCCCCTCAACGCCGCTCTCCAGGGAAGGAGGCGGCGGGGTCAC
CAGGGCGCAGCTGACAGCCCCAGGCCCGGCCAGGGCGCACCCAAAGAAGAGGGAGGCTGCTGCCTGAA
CTGGCCTGGGGCAGAGGAAAGTGGGCCCCGCGCTGTGGAAGGCCCCAGGCTGGAGCGCCGGGGACAGC
TGTCCAAGCGGCGAGGGCTAGGAGTGGCCTCGCCTAGCGCTAGCCGGCCAGGCCCTGGAGGTGCTCCGC
GCCTTCTCGGCCAAAAGCCAGCTCCGCGCGCTGGCGGAGTGGGAGGGAGGCGGCCAGGCCAGCGCCCC
GCCTTCGTGCGCCGCGGTACAGGGGCAATTACACTCCTGCTGCAGACGGTTACCAGCTCGCCCGCGCAT
CCCTCTCGGCTCCCTCTCCTCCCTCTCCTCTCCTCCCTCCCTCCTCCGCGAACTGCTGGCTCCA
TATTAGCGAGGGTGCCTGGCAGCGGACCGAGGCAACTACCCCT

TAGGCAGGAGCAGGAGGAGGAGGAAGAGGGCACCTGCTGAGATACTTCACTGGTCTGAGGGGCCCTTCTGCCC
CAGCTACGCGCTTGGGTGAGGTTGGGCTTGCAGAGCCCTGTGTAAGCCGGGGAATGCAGGCAGCATGTG
CACCCCTCTCTCGGCTCTACGAAACACTCTTAATTAGTCCGTATTCTTGCTGGAATCGAGCTTCCACGA
CCGCGACCCGACGATCCTGTGCCGCTTCTGTCTTCCGATTCTTCTCTTTCTGACGCGTTTCTCTCATTCT
GGATGGAAGCCTGTTTGTCTCCCTCAATCTTTGGCGAGGGTGGCAGGACGCCAGGCGGCCATTACGGGC
CGCGCTCCCCACGACCGATCGCTGGCAGGAGCTCCGGGGAGGGAGCAGACCCGTTACCCTCACCCC
GAACCTGAAGCAGCGAGGGGAGCAGCAGGACTGGAATGCAGCG

CGCGCTCCGCCAGCAAGACCTGGCGTCTGCAAAACACAGGCGTGAGGGGGCGTGCTTACTAATGCGCTGGTG
TTCCACGAAGGGCGGTCCCGCGAGCGGCTCCCGAGTAGGAAGGAGAGGGCTCGGCCCGCCACACACACA
CACCACAGCTGCACACGCTGTTCTCTGGGCTCTGCCTACGGTTCTCACGCTCAGCTCCGGTCTCGCGCC
TCCTTTTACGTTGTTTAGGTTTCTTTCTGACATGACTGAGGGAAGTGCGGTTTCACAGGCAGAGCTGCCTGC
GGAGAGAGTGGCAGCGCGCGCGGTTTTCACCGGGCCCGCGCTCGCTAAATTCACACCTCGCGGCGCGTC
TGCGAGCTTCCGCGCGCTGGGCTTTAGCAACAACAACCCGCTGCGGCCCTCAGAGTTCGAGGTTTGCGGA
CGTGCCCTCCTGCGCGTGCCAGTCCCTCGCCCCAGCGCTCCCCCGCCACTGTTGTCTTATTCTGGTTTG
AGGTTGTGATTTCCACATACATATTATCTGTTGTTGTTTTCAGCGTGGGGTGTGAGTCACACGGATATTTT
AATGGGAGAGTGGGGGGCTTGGGAGGCGCGCGGAGTGACAGTGTCCATCTGGCTCGTGGGGAGA
CCCCGGGCCCTCAGATGGTGCGATGTCTGAGGCTGCCCTCCTCACATTGATGGGAGCGAGGGCCTACTTG
GCTTGTCTGCCCCAAGGGGAACGTGGCCCTAGATACCGGGGAGGGCCCCGCGCAGCGCTCAACTGACTG
ACTCAGGCCCCCAGGTTAGCACAGCTGCCACAGGCTGGCGGAACTCCGGATGGGGTCTGAAAAGCCT
TTGTGGGTTGGGGGACCACACGGGTTGGGCTGATGGCGGCTGGGGGCGGGGCTCAGGGGACATTGT
CAGATAGATGACCCCAAGCGGTTGGGCTGAGGAGTCTGTTGTCAGTTGAGGGGTGTCTGGGACCGGCTGC
GCAGTGACCCCGAGCCCGCTCCGGCCCCCAGGAGTGTGAGTTTCTACGGCTGGCCAAAGAGGAGAAGCT
CGGGAGGGCCAGGAGGCCAAGCGTAACCTCGGGAAGGAGATCGAGGCTCTCCGCGCCGAGAACGAGAA
AAGATGAAAGAGGCCAACAGGATCACGGTGTGCCCTGAAGCGGGAGCTGGAGCAGGCGCGCGAGGCCGG
GTGTGCGACAAGGGCTGCGAGGCGGGCCGCTGCGCGCCAAAGTACTCGGCCAGGTATGCGGGTGGGGGA
GACTGAGCGACGACGACGGTGGGCGTAGCCGCGCTGGGCCCGGTGGCCAGTCTGCCACCGCGAA

CGAGTGCACGGCTTTGTGCTGCTCCAGGCTCACCGCGTGCOCGAAGGTCTTTGCCGCACATCTCGCAGGCA
AAGGGTCTTGGTACCGCTTGCGGCAGCTCGCGACGCTGCACCTCGAGCCGTGCGCGCTGAGAACACCTAATAGG
CGGGTGGGCGCAGAGAAGAGCCGCTGAGAGGGCCGCGGGGCGAGGCGAGCGCGGGTAGGGGAAG
CGGGCGCACGGCAGGCGAGGTGCTGAGCTCGGGAGCCTCACCTTGCTGCACTTGATGCACTTGTAGGAGC
CGCGCCGACGAGCGCGGGGTGCACAGCAGCTCCGACTCACCTTGACGCCAGCGCCCTTGTGCGCTGC
AGCCCGTGGCCACGCTCTGGGTGACAGCAAGCCCGCGCTGCGCTGGGCGCTTCATACAGTCCGCGGTGCGG
CAGACCCGAAGTCGCGGTAGAGCCCTAGGCCAGGGGCCAGGGTGGCACCGGCCCTTGGCTGCGAGCTCCC
TGGCGCCCGCGCCCGCGCCCGCGGACGCCGCTCTCGGGCGGTACAGCGCGCGCGGGTGGCCAGGCTC
CGGGCGGGTTTCGCAAGAAGGCCAGGCCAGGCCACGCTCAGGGCCCCACGCTCGGTAGCTTGC
ACCGAGTGGCCGAGGTGAGAACCCGCCAGGCGCGTCCATGAGTAGCGTTTGAAAGGACGGGGGAAGGGC
TGGGCTTCGTGTCACGCGATGGGCACATTGCATCTCTCCGAGGCTGTGCAGGCACAAGGGGAGCGTCCGGTCA
GCCTTCAGACGGCAGCGGAGCGCGGCGTGGCGTGCAGCGCTGGCGTTCGCGGAGCTCGGGGC
ACCGAGCGCTTGTAGAACACTGCGTGGCGCAGGTGCCAGGCTGCCCCAGGGTAAAAAGTGGGCCGGGGC
CTGGGGCTTCGACGCCCACTATAGGAGGCGAGCAACAGTAACACGATCATTAAAAAGCACTCGGGAGAGGAGG
TCGTAATTTCTGTGCGAGTGCAGCGAGGCGCTCGGCGTTCGAGGATCTTTTCTGCTTGGACCCGCGCA
CCTGGAGATCTACAGGAAGGGCGCATCTATAAATGCCGTAGTTGAGTGTGTTAAGGAAGGAAGCTGG
CGGCGTTTGGCCCCCTCACAGCACTCAAGGGCGGAAGGGTCCAGCGGAGGCGAGGAGCTCTCCAGTCCG
CTACATGTTCCCAATTCATTTCTTTTCTCCCGAATCCCAAGGCAAGGAGGAGGCTCCATAAATGCG
GCCCGAATACCCGAAAGGTGCTGTGTCGAATAAACCCGAAGGTATTAAAGATTCACGAAGTTAAGTCC

CGAGAGGCCCGCCACCGGCTCGGGAGCTGGGCCGGTTCGCTTTGGGAGCGGATGAGGAAGGTTAGGAGA
AGCAGCGAGATAGATCCCAATTTTACAATTCTATTTTCTTTCCGTAGGGTCTCGGCCCTCTGGGCCACGTTG
AGAGCGAACTGGGCCGAGCGGAGGACACAGAGATAAAAAGCAGCGCCGCTGTATACATAAATCCGCACC
CGCTGCCCGCCGGGTACTGCTGCTCTGCTCTCCGCTCTCTCCGAGGCTGGGCAAGTCCAAAAGTTCC
CGAAAGGGGGGCTCAAAGAGGGGGCGCTGAGTGCACGTGATTTTCG

TTCTTCCCTCTTTACTCCATTC CCTA ACTCCTGCCTCGTAGGCAGCGGTGGGGAGCCGCAGGCTGCTCCCC

GAGTCCCAACGCTACTAGGGTGTCTGTAACAGTGTATGAGGCGGCGTTGCAGTCTGGCAGGCGCTGCAGCGG
GCACCAGCTACGTTTGTCTGTGCGGCGCAGTTACCCGGACGCAAGTTAAGGGGTAGGCGCGCAGAGGCG
GTTGAGGCGGGCGGCGGCGCCCTGACCTCGGAGAGCTGCGCCGAGCAGGCGGAAAAATTTATGGTCTG
TGTAACACTTCTGTCTCAGAGCCCCGCGCACCAGAAGGATGGGGCCCTGCGAGCGCGCCCCAGGCGCGCA
GCTGGGGCGCAGGCGCCACGGCCATGTATAGTGCCACCCGACTCTGTTCTGCAGCGCTGTGGTCATAA
ACCTTCCCTTAGAGGGCGGCGTGTAAACGAAAGTCCGCGGAGAGGTGGATGCAGGCTTGCAGCGCGGA
CCCTCAGGTATAATTCTGGAACTTGCACGGAAGCCTGGGTCCCGCCATCTTCCCTGTTGTGGTGGGTAA
GAGGATAGTTTATCTGGCTGTTTGAATCCCGCGGTGGATGCAAGGTGGATTCCAGCCAGCGACGC
GCCGCGTGGCGGGAGTGCAGACAGGTACCGGTCCCGGGTGTCTGGACCGCGCGCTTCTACTGGG
CTTACTTCGGGATCTAGACTTCGGCTCCGTCTTGAAGGGCCAGATTTGATTCCGGTTCGTGAGGCG

35; SW vs SM; chr10:845627-845967; 10; LARP5; INSIDE

CGAAACCCTCGAGGAGCGACCATGACCCCGCGCTGTGAGCTGTGGCGGCCAGCGCCCTCGCCTCGA
TTGTCTGCAGCCCTGTAGTGGGCGCGAGGCACGCAAGCCGCAACTACAGCTCGCCACGGGGCACACAGA
CAGGCATGCACCACTACCCGTGCGCCGATACACTGAAGTGGTTTGAAGCCTGACAGATCGCAGAGATC
CTAATATAGCAACGACGACGTTTACGGCCACCCGCACTGACAGCCGTGATGTGATGACAGGAGGGCC
TGGGTGAAAATGCAAGACACTACTCTCAGAGAACGACGACTCCACTTGAAATTCATGT

38; SW vs SM; chr10:3150889-3151107; 10; PFKP; INSIDE

CGCGCGGCTGGGACCGCGGTGGCGTCCCTGCGGACCGCGTGGAGTTTGGGGTGTCTGACATCGTTCTCC
ACGTGGCTATTTTCAGCGTTCTCCCGGGAGTACTTGAAGAGATCGCCACACAGATCGCAGCAGC
ATCAACGCGCTGCTGATCATCGGTGGATTTCGAGGTACGTTACCGTTTCTCTCTTTCGGGTCTTGCAGGTGT
GAGCCGCG

42; SW vs SM; chr10:7489383-7495345; 10; SFMBT2; INSIDE

CGGCAACCGAGCCAGATCCAAAGAGGGGTGCGCCTCGTCTAAATTGGTTTCCACCAATGGCCTCGGATCA
GCCGCGGCTGTGCTGCGGAGCCCTCAGGACCGCGGTGGGTTGGTGCGCGGGCGCCGAACCCCAAAC
CCGCTCGGTTTCGGCAAGGTTTCAGGGAGACAAGGTAGAGAAGCTGGGGTGAGCGCAAGCTCGGCGCGC
CGATCGTCAGGGCCACGAGCCTCGCCTTGCCTTCTTGAATCCCACTTTAAAGGCCAAAGATCCT
GAAAATTCGAAACGAACTGCGAGCTGGTCTCCAGAAGTTTGAGAACGGTCTCCAGGCTTTCCAGCGT
CGTCCCGGATTTCTCGGACACCAAAACGCCATCAACACGAGCACCGGTGTCCGTGGCTATTGCCCCGA
ATGGTCCCATCCGCGTCCCGGGAACTCCCTCGGCTTTCGCGCATCCAGGTCCCGAGCCCCAGCTACTG
GTGCGCCCCGAGCCCTAGGTGCCAGAGCGGTGGTGGCGCGGGCTCCTGCCAGTCTCGGCTCCTCCCTC
CTCCCCACCAAGAAGAAAACTTGGGCCCTTCGAGAACCCTGTGGAATGTTCTTTGTAATCAATGTACATC
CGCTTCCACGGCACGGCCTCGTGCAAAATCGCGGCTTTCGGGGCTTGGAGCAAATTCGCTTGTACGCG
GCGACGTGAGGAGACAAGGGGAGGGGTTTCGCGGTGAACTGCAGCTTGCAGCACAGAGCCATTTTA
GGCTGCTCCCACTCGCGGGCCATGGGAAAGCCGCGCCCGGGAGGGCGCGCCAAACGACGCTGGA
GGAGCCACGGACGCGTCTGGCGGGCGTGTGCCATCGTTTCAGCCTCGTGCACAGGTGGGAGGGGTCA
CCTGCGCGGGCTCTCAAGCCAGTCCCGCTTGTCCCGGCCCCCCCCACTGACAGCACGGCGTCCGAGT
GACCCGTGCTAGCCTCGTTCTGCGCTCCTGCAAAACCGTTGCTGCGCTAACTACAAACCTGGCCAACTG
TCTTTGTAACCTATCATTTAAAAACGCTTCCAGGCACCTGGCGGCTGCCAGATCAGGTTTCGCGGGCCCGA
GGAGTCTCTCCACCTGCCCCCGCCAGCCCCGGGACCGTGCAGCGGCTCCGTGTGGCCCCCGCCACG
AGTTCCTCGGGCAGGAACCGCGCGACCTCTGTTTCAGCGGCGCGTCTGCCCCACGGCAGCCCT
GTGCGGAACCTGTTCCCGGCTAAGTGCCTTCCCGCATTCGGGTGGCTCTCACCCGAGCTCGCGTTT

44; SW vs SM; chr10:013553837-13554175; 10; C10orf30; INSIDE

TACAGTTGATACCCACCATCCCCATCATCGCTATTAGAATTGGGGTCAATACCCATCATCACTGTTAGACT
TGAGGCGGATACCCGTCATCACTGTTAGACTCGGGGTGATATCATCATCACTGTTGACTCGGGGTCAATA
CCCTTCATCACTGTTAGACTCGGGGTGATACCCGTCACCACTGTTAGACTCGGGGTGATACCCGTCATC
ACTGTTAGACTCGGGGTGATACCCGTCATCACTGTTAGACTCGGGGTGATACCCGTCATCACTGTTAG
CTTGGGGTGATACCCATCATCGCTTTCAGACTCGGGGTGATACCT
GTCATCG

45; SW vs SM; chr10:13556159-13556753; 10; C10orf30; INSIDE

CAACATCTGTATCGCTGTTAGATTTCGGGTCAATATCCATCATCGCTGTTAGACTCGGGGCGGACATCCG
TCATCGCTGTTAGACTCGGGGTGACACCCATCATCGCGTTGGACTCGGGGTGAACCCGTCATCGCTG
TTAGATGCGGGGTGATATCCATCATCGCTGTTAAATTTGGGGTGCATATCCGTCATCACTGTTAGATTG
GGTTCGATATTCCTCATGACTGTTAGACTCGGGGTGATATCTGTATGACTGTTAGACTCGGGGCGGATA
TCTGTATCCTGTTAGACTCGGGTCAATACCGTCATCACTGTTACACTCGGGGCGGATACCCGTCACCGC
TGTTGGACTCGGGTGCATACCCGTCACCGCTGTTGGACTCGGGTGCATACCCGTCACCGCTGTTGGACTC
GGGTGCATACCCGTCACCGCTGTTGGACTCGGGGTGCATACCCGTCATCGCTGTTGGACTCGGGTGCATAC
CGTCATCGTGTGGACTCGGTCGATATCCGTCATCACTGTTGGGCTCAGGTGCATACCCGTCATCACTG
TTGGACTCGGGTGCATACCCATCATCG

47; SW vs SM; chr10:15294510-15295293; 10; C10orf38; INSIDE

CGACAGCTTCACAGTAGGATTTATTGTGATAAAAATGACTCAAGCGATGCAAAAAGTTTCATCTGTTCCAG
AATCCGAGGGAGAAGTGAAGGTGATCGTTAGAGCATAGCGACATCAGTGGCGTTTCTAATGTCCCTGGTG
GCGGATACGCGGAGTCTCGGAAGGACATCTGGACACCACTTTTCAGCCACCTCCTTGCAGGGGCGACATC
CGCCAAAGTCATCCTTTATTCGAGTAATAACTTTAATTCCTTTTAAACATTTACACGGCAACAGGAATGC

AGTAAACGTCACGTCGGTCCCACGGCTGGGCTGCCGTTCCGTTTCTCCACGAACGGGTACGCGCTTCCA
TGAGAAAGGATATTTGGCAATTTTATATTCCACAGTCAGGTGGGTCTGCGATAGCTCATTTAATGTTAAAC
GCCATCAGGGGCTCTCCTCCGTTTCTGCCAGGGCTTTTCTTGTCTTCTCCTTGGTCATCATCATCATCGT
CTTCTCTTCTCCTGCGGACAGATCTTCTCTGCTGGGGCTGGCTGCTGGCTCCGAGGGGGCATCCGAGT
CCGTCTGGTCTCTCCTCTGCAGGCTGGGCAGCTGGCCACCCTTCTCCGACTCGCCCCCTCAACAAGC
ATCGCAGGGCACTGTCTCGGGGTACAGACCGTGGTCCCACATTGCTACCCTCTGTTCCACGTCATCC
AGGTACACGAGCTGCGTGTAGGCGGTGCTGTCTGGGCTCGAGGCTCTTCTGCTGGTCTCTTGACGG
GCG

64; SW vs SM; chr10:88112905-88117344; 10; GRID1; INSIDE

CGTGAACGCCCTCGCTCGCACCTGTGGCGCTGCCGCGGGCCCCGACCGGAGGCAGTGGCTGTGGACA
AGGGCGGCCCCGGCGTAGGCCAGGATTTCCCGCAGCCGGACCGGCCAGCTCCGCTCTTTCTGGGGGA
ACAGCGCCCCACCTCCGCGCCAGGCGGCGCGCTCCGCCCGCGCGGACAGCGAGAGAGAAACCGGC
TCCTCCAAACCTGGTGGAGGAGCGCTGCAGAGAAGCGCGGGCTGAGGCTCTGGGGGCGCGGGCGCG
AAACGCGCGCTACAGGTATGCCCCGGGAGAAGGAGACAGGTCCGGCTCCAGCCGCTGGGCGCTCCTC
ACCTCGAAGCGAGGAAACACCGGCCACTGAGATCAGGGGAGGTGCCGCCGATACAGGTACCGGGCAC
GCAGACACGCCACCCCCAAACACCGAGAAACAAAGACTGCCGAGCCACGCACGCTGCGCGGCCAGC
GCTGGGCGCACACCGCGCCCCACACAGCCCGAAGGGCGGCCACGCAACCGCAAGAACACACAGCTCCCCG
CGCTCGCAGGCTCTCCTGCGCGCCCCGAGCGCAGAGCAGTCCCGCGCGCTGCTAGGTGGGCGCGG
AAGCGCGGCCACCGCGCATGGCACCGCGCTGCCGAGGAACAGAGGGTGCCTGCGCAGCCAGCTCGT
CCCAACCCCTCCGGTGCCCACTGCTGCGACGCTCGCAGGCCGTGTCCAGTGGGCGCTGGGCACAGCGG
TCACTCACCTTCTGCACAGCCTGGATGGGTGTTGGCTCGATGACCTTGATGGAGTAGGTGATCTTCTC
GCTCTGCAGGATGTCTCGTTGAGGCTCAGGTCCGATACCGCCAACTGGAACACCCCTGCTGCTTGGCC
GCGTTCTCTCGAAGATGGCACCTGGAGGAGAGAAGGGATCAAGACCGGACTGGAAGAACCCTTCC
CGCTTCCCTTGGCCCGAGGGTCAAGGCACTCGCAGACCGATGATTGCCGGGTGCTGGGAAGTCTGA
GGATTTCAGCTTGGCGGGGTAGATTAAAGGCTCTCCGATCTCCACCTGCACAGGAATATGTTCCCTCCCC
CACCGCCCTCAGCGCACACGTGCACACAGTTGACATGAGTTACACATGCACATCCACAGGCTGCCACCA
GGTCACACAGTGTCTCAACAACCAAGGCACACATGTCTTAGCCATGCTCCACACAAAGGACTAAGCCAA
GCTGGGGTGGCCCCAGGCAGCGCCAAATCCTTGACATGGTTCCATAAATCCCATCCAGGAGCCAGGAA
G

71; SW vs SM; chr10:102986025-102986636; 10; LBX1; PROMOTER

CGGGGGGCGCCGGGCGCAGGCCGGGCATGGGGCTGAGCTTAGGCCAGGTGGAAGGTGGAAGGACCTA
GTGGGGACAGACGAAGAGACCGAGGAGCCGCGCCCGGCTAAATGGACACAGGAAAGCCTGAGTCAGG
CTTCTCATAATAATAAACTGCACGTGAATAATTCAGCAGTCGCGCGGGGCGCGGTTGCATCAGCGCGC
CGCGCGCGCGCGCGGCCAATTCGCCGCGGAGGGGAGTAGCCAAATTAAGGCACTTGAAAAGGGAGTCGG
GTGAAGATCCCCCGCACCAAGTATCCTGGATTACCCAGGTTCAGATTTCAGAGAGCCTCCCGGTCCCAA
CCCCCTCGGGCCCCATGGGTACGGGGGCGGCTGCTGGGAAGTGCTACCTCAGCTAAGCCGCTCAGGTGT
CCCGAGACTCCGGGCAAGGGAAGACAGGCGCGGAGACGGACCAGAATAAGGGATGCGGACGCTGTGACCT
GTGAAAACCCAGCATCTGCAGTGCCCGACCGGCACAGGGAACGTGGGCGCGGTGGTTCCAAGCACAGTG
AAGACGCCAGGCTCGGATCTGTGCTCAGAGCCGGATCCCTCCGGGTGCTTCG

108; SW vs SM; chr14:28317076-28317375; 14; FOXG1B; DOWNSTREAM

CGTAGCGACGACGTGGTCTTGTAGGACCAAGCATTTCTTGGCATTTCTGTGAGATTGAGATTCCAGAGCAT
CGGATGAACGGGACTTATAGCTAAGGCGTACTACCCACCCCTCCCTTCGTTCTTTACGCACGCAGCAACT
CGTCTCAGCTGCATAGGGGTAGTGACAGTGTGACTTGAATTGCTGTCCCTCGTTCCAAGCCTTTCTGT
TGAATGAACCCGAAACACTCGACAGGTGTAATAATCGTTTAAATGAGTGTGAAAAGCGTGCGACGGG
GTGACCCGACTGTCTG

126; SW vs SM; chr15:58079172-58079459; 15; FOXB1; PROMOTER

CGCTGGCGGGGGTAGGGGGTGTGGGTGGGTACGGAGTCTTTCACTGCCCGTCCGCGAGTTGGCACCAGA
GCGGAAAGTGTGTCCCTCCCCCGCTCTCTCCCTTGGGCGATTGATTTCGCCCGAGCTCAGTCGGAGTG
GCTGGAAGAGCGGGCTCAAACTCCAAAGGCAGTGTGGGAGAGTCTGAGCGGATACGTTTCCCTTGACA
TGCGCGGGTGTCTGTCTGTCCCCCACC GCCCCCCAAACCCAAACCTGCAAGTCGATGTTGTCCGGT
GACCCG

127; SW vs SM; chr15:58083339-58085812; 15; FOXB1; PROMOTER

GTGCCTAAAGTTACCTAACGATACAAACCGGATACAAACGAGAGGAAACAGAAATACCCAGCCAAAGCAAT
TTCCATGTCAAACATCATCCGCGCGCTGCTCCATCTGTGAACGTGAGTGGTCCGCTGCTCCCTCTTCCGC
GGCGGCCGCTTCTCATACCTTCACACGGCGCACACCGGCGCGCGCTCCAGCTGCTGCCAGTGGCCG
AGGCTCTTCCCCCTCGGCCAGTCTTGTAGCTGGAAGTGATTCTTATGGCCAAGGTGTCCATGTAAATAGGT
GTGAAGAAACAGAGCTGGCGGGCTCTCCCTTCTGCTCAGTCCCTCCCTCTGCAGCCCCGCTCCCC
CTCCTCTTCTCTCTCTCCAAAGGCGATTGTATATGATAGCTAAGAAAGTGGCACATTAAATGAAGCGCCG
TACAGGGGTCTTTCTGTCTCTGTACCGCTTAAACTATCAGATGGTTGAGGGAGGACATGGAGGCAGC
CACCTAGCTCAGCGGAGACGCGGAGCCACAGCAGCGCCCTCCGGAGCCCTAACACGTCGCTGCCACCAT
CCGCGCGGGGACTCCGACGCGAGCTCGGCGCGCGCGCAGGACGCTCCAGGAGCGCTCCGAGCGCGCGG
ACGGGACGCTGCGGGGCTGAGCTCAAGAGCCAGGTTGCGCGCGAGTCAACCGGACCCGGACGCTGCG
CGCGGAGTGCGGCTGAGTGCGCGCGGAGAGAGAAGCGGCGCGCAGCGGCGTCTCCCGGATGCGGACG
CGCAACTGAAGCAACTAAGGTGAGCAGCTCTCTGTTCCGTCCTGCCCTTATCTGGCCCCAGTACCG

ACTTACTTCCCGGCTATCCTCGCGCGGTTCCGCGGCTTCCCTCCCGCGCCCACTAAGCCCGCAAAGTTGC
TGGCGAAAGAGTCCGGGCGCTGGCTGATCGAGCGCGCGAGCCCAACCCCGACCCCGAAAGTCTGTACT
CGGTCTGGCTGACCCCGCGGTGTCTCTGTGCATCCATGCTACCTTTCCCTATTACCCACCCCTTCCAG
ATCCGAGCAGTCCGCGGCGCGCGGACCCAGAGCAAGAAGAGGGCGAGGAAGAAGATGCCCTGCGCCG
GCCGCAACACGTACAGCGACCAGAAGCGGCCCTACTCGTACATCTCGTGACCGCTATGGCCATCCAGAG
CTCTCCCGAGAAGATGCTGCCGCTGAGCGAGATCTACAAGTTTCATCATGGACCGCTTCCCTACTACAGG
GAGAACACGCAGCGCTGGCAAACAGTCTGCGCCACAACCTCTCCTTCAACGACTGCTTCATC

167; SW vs SM; chr17:47590175-47591465; 17; CA10; INSIDE

CGACGGGAAAACGGGGGGAAGGGGGGAGCCCGACACGGCACACACATACACTCGCACACACTTCC
GAGCGAGTGCACACTCCGACTCCCACCCGACAGCCGCGCAGGGACAGTCAACCCCAAGTCAATATCGCAG
TTTGAATTGTTCCGGCAAATCTCCCTCGGGCTCGACGGATGTGCGCCCGAGATGTGCTGACACATGTCCG
ATGCCTCGCTGCCCTTGGAGGTCTCCCGCTCGCGTGTCTTCTCTTCGCACCAGCGGGCGAAACCGCACT
AGCAGCGGCGGGGCGGCGGCGGCGGCGAGCCACCTGAAGCCACCAACTGGGCTCTTCCAGCAAAA
ACGAGACCCCGATTCTGTGCGGCCCAAGAAGACATAGACGATAGCCCGCGCGGGCTGCGCCGTGCA
ATTCCGGGCTCCCGGAGCGCGTAGCTCGCTGGCTAACCAGGCAGTCCGCGGCAAGTTGCCCTCGAAGT
CCGCCCCCTACCGGGGCGATGGTCCGAGGGTGGTGTGCTGCGCTCCGGGGCAGTTCTTCTCTGCTTCCG
GGGCGCGGGGAAGGAGCAGACACAGCAGACACAGAGAAAAGAGAGGCAGGGATTATTGCCCAAACCGC
CAGCGCGGCGAGCCTCCGCGGACCTCCCTGCTCCCGAGGTCCGCGCGCAGCCTGCAGCCTCTCAGCCG
GGTTCCGGCAGTGGCTCCAGGGCGCGAGGGGAAGGGCTGGGCCCCGGGGAGTGGGGCGCGGTGGGGG
CACACAGACTTCCAGGTCCGCGCGCCTTCTGCTCTGCTATTTCCTGAACCTCCCGACAACCCCA
GTTGCTTGGCTTCCATCGCCCGCAACTAGCGCGCTGTGAGATTTTCCGCAATACAACGCGAGGGGTGG
TTATTTCTCGCTACGGATCCCTACGCTTCCCAACTCAGAGAGAGGAGGACAGGTGGGGGCGGAGGGG
GAGGAGGAGAAGGAGGCTTGGCCAGGTGAGCGTCTCGCCCGCGCGGGCGTCCAGCGCTCAGCTCCGC
AGCCCGGCACCCGGGGGCGGAGGAGGAGGAGGCGGGGCGGGGAGGTGAGGCTGAGCGCGGCCATGAGGA
GGGAGGAGGAGGCTGGGTGTACAGCTTCAGGCCACCTTGGCCCGCGCTCGGCCCGAGTCCCTGGCA
CCGCGCTCCGCACTCCGCCCCGCGCTGGCTGCTCTGTTACCTCCAGGATTTTCGAGTTTCTCTTTAA
AAAGAACTTCGTGCTGCGGGTTGCGCGG

174; SW vs SM; chr17:67623575-67623903; 17; SOX9; PROMOTER

CGTGGGTCCGCTACCCCAAGCACTTTTGTGACGTACAGCTCCGAGGACCATCCGGGGGCTTACTCTC
GCGGAAGCCCAAAGTTGGGGTTTACCTCATGACCTTGGCCTTCCCGGGGGCGGAGGCCCTCGGGACA
GGACGCGCTGTCCCGGAGTCCGGAGCTCAGGCCAGTGGCAGTGCAGCCAGCCCCGAGACTCCCTCAGC
CGCTCCAAAACCAAAACGGAGCCCAACACGAAGCTGGGTGAAGCGTAGCTTGCAGGAGCCAGGGAGAT
GCGCTCTGCCCGACTTCCCGGTCTGTTGAGACGGAAAGGATCG

175; SW vs SM; chr17:67627870-67631593; 17; SOX9; INSIDE

CGACTCGGCTGACGTTTGTGACCCGGCCAGGAGGCAAGACCAAAACGTGAGAGCAGTAGCCCTGTTACT
GAGGAGCGTCCGCGAGGTGCGCGGTAGAGGGCGCTGGAGAATGACTTGTGAGAGCTCAGGTGATGTGG
CGCGGGGCGGCTCGAGAGCGCGGCTCTGCGTGCCACGGCGCGCTGCCAAGCTTCCGCGGGAC
TTAGCTTTGCTTTCCATTGACTCCCTTTGCAAAAGCGCAGCAGAATCCTGACCAGCCGACCCAGCCCCGCG
GAACCCGAGCATGTAATCTATTATATGATTATTACGGAGGAACAGCGGGCGTTGAGTCAACCAAAACATT
TGCTTCAAAAGACTATTCTAAGCACTTTGCAAGCAGGAGGCTCGCTCCAGGCGGCTAAACTCGGCTAC
GCATTAAGAAGCGGCTGCTTTTGAATACTGCAAAACCCAGCTAAGTCCCGGCTGCGCGGAGAGAGAGT
GAAAAGAAATGTGCGAGGTGGGGGTAGATCCTAGTCTAGACACACACACTTGGCGGCACACACACACA
CACACACAAGATTCCGCGGAGAGGCACTAAAATTCTGGCATTCCGAGAGTACGACAACTACACACTT
GGAAGTCCCGGGTCCCCGCCCTTCCCGCAGCACCCCGCGCCCCCAACCTACCGTCCGCGCTTTGGCT
GCGATCCCCCTCCCTCTCTCCCTCCCGCTCTGTCACCCAGCCAGTGCCACAATCCTCTCCCTCCCCA
AAATCGGGTCCAATCGCTGCCTGCCAACCTGGGACTGCTGTGCTGTGATTGGCGGGTGGCTTAAGGTG
AGCGGAGATTTTATTAAAGAGACCTGGGCTGGGAGTTGGAGAGCCGAAAGCGGAGCTCGAAACTGACT
GGAACCTTCAAGTGGCGCGGAGACTCGCCAGTTTCAACCCGAAACTTTTCTTTCAGGAGGAGAAGAGAA
GGGGTGCAAGCGCCCCACTTTTGTCTTTTCTCCCTCCTCTCTCTCAATTCCGCTCCCCCACTT
GGACCGGCGAGCTGTGAAGTGGCCACCCCGCGCTTCTAAGTGTGCGCGCGGTAGCCGCGCACGCGC
CAGCTTCCCGGGAGCGCTTGTCTCCGCATCCGGGCAGCCGAGGGGAGAGGAGCCCGCGCTCGAGTCC
CCGAGCCCGCGGGCTTCTCGCTTTTCCCGGCCACAGCCCCCTGCCCGGGCGCGGTATGAATCTCTCT
GGACCCCTCATGAAGATGACGACGAGCAGGAGAAGGGCTGTCCGCGCGCCCCAGCCCCAC

199; SW vs SM; chr19:42586101-42586705; 19; ZNF569; DOWNSTREAM

CGATTGGGGCTCAGCCTTAGTCTTCCAGCTGGACCCCTGGGATGGTGGCGGGCTGTGGCTCTGGGAAGT
ATCTTGGCCTGCACCGGTTTACATCATTTGGAGCACAGGCCTCGCCCTCCGAAGTAGAGGCCAGAGCC
CTTCGCGCGAGCGTTTCCCGCTTTCCCTGTCTCAAGTCAATTGCCAGAGGCACTCGGGCGGCTTCT
GCCGTGCTGGAGCTGCGGGCCCGGTGTTCCAGGGTGAACGAGCAGTGCAGGCGGTGGTGTGTTGTA
TCCGGGATAACAGGTAGGGCGGCTGCATGCTTATAGAGGCCAGCCTGTGCCGACCGGAGCTGTAGGAC
GGTCTGTGTCTGGGGTGTCTATGGGTATTCCGCTGCGCTTCCCGGTGCGCGGTCCGAGCCTACTCACGA
GAGCGTGTGTGTCTTCTCTCTGCTTGTGATGTTGCATCTGTGTGGCTGGAATAGCTTGTGTTGTG
GGGGCCCGCGCTGACCTGTGTGTGCGTTACTGTGTGTCTCAGGCAGGATAGTGACGGGCGGTGTGAC
TGTGACGCCATCATAGGTTGGTGAGATGGCGTGACCGG

204; SW vs SM; chr19:57082579-57083180; 19; ZNF577; INSIDE

CAGCAGACCCCTTTTAAAGTACGCATGTGATAAGCAATGAACACGAACTGCCCAGAGCAGTCTCCAACACT
 GACACGATTTCGCTTCCCCACCACGACGCCCTAGCGCTACTGTGCAACGAAGACCTCCAAGCACTGGTTCC
 AATGCGGAGACCATGGGCTCCCAGACTCTGGGAACCTCAAACACGACTGCGAAACGAACTCCGAGCGAGGA
 CTCCTCCGAGAGCTCCCCGCAACACGGACCTCACGCGCTAGCGAACAACAGAAAAAAGCGCGCTCTC
 CCTGCCCCCTGAACATTTCCAGAAAGCCACGACAGACCGATGACCTGTCTCCACTGCTGGAGGCGAG
 TCAGGGACCCGAAGTCTCTAAACACTCGCCTCTACCCGCCGCCCGCGAAGCCACACACTGCAGACGCG
 ACACTCGCAAGTTTCGGGGATGGCGGCCGGCGAGGGCATACTGCGTCTTTCCGGAGACACGGAATACGGC
 ACCAGCCGTCCTTTATGATGCAATATGTCTGCGCCAGGGGACGCTTGCTGGGAGCAGCCATTTTCAACC
 CTACTGCCGTAGAGCAGGCGGAGTCCCTCTTTTCGCG

233; SW vs SM; chr2:119329502-119332035; 2; EN1; PROMOTER

CGAGGAGGCTGCAGGGACGCGCATGGAAGAGCCGCTGCGTGGGAGGGTTTGGCGGGGGACATCGCGCC
 CCTAGGGGTGACCCCACTGGGTCCCGTGTGCTCTCCGCGGAGCCGGCGGAGCCTTGTCTCTGCACCCGG
 CGCGCAGCGGCCCTTAAACAGTGAACCGTGAGGCGCTCTAAGCCGAAGGGCTGGAATTTGGGTTTCT
 CGGGTTTTATTTAGACATTTCGGCAACAAGCCCGAGCTCCCCCGCGCACCGCTTCCAGTCCCTTTCTT
 TCCATAGAGCGACCGAAGCCGCGGTGGCGCAGGGAGCCGAGTCTGATGAGCTCGCGGGCGGCTGAAGG
 CCGGCTTCCCTGTGGGGAACGCGCCACCTGTGCGCGCCAGTGAGAACTGCGTCTGTGCGGCCCTCGGG
 GTATTTCGGGGCTGCGGGGAGATGTGTGCCTGAAGCCCTCGCTTGGCGTGGGACGCTCCGGCCTCTTTCCCT
 GGCAATTGACCCCTGAGGCGGGAGAGACAACGGAATTTCCACAAAGGGATCCTTCTCGGGATCTCCCCAC
 CTCAGACAGCTAAAGCTGGAGGAAAAGCCCTCCGGGGGTGGGGGTGCGGGTTTGCCTTGGATTCC
 GAAAGCAGAAAATACCGAGCCACACAGGACGGGGCGCGCGTGGTAGTCGGGGCTACGTTCTACTCC
 CTCTACCTCCCCCGCGCTGTGTGACCTGGGCGGAACCCGCTGCTCTCTGGGCCTCAGTGTCTTATTCG
 TAACTGAGGGCGTTGAGAGATTGGTCTCTCCCACTCTGACCTTGAAGCTGATACTGAATCTGAGCAG
 CGTCTGTAGACACCTGTGCCTTGCCTTCTATTTCTAGCCTTGAATAAATCCTGGACTTTTATGTGCCATTTA
 TATCCTAATCTCATATATATTATGTATAACTGCTGCCATATTGTTTCTCAATTGTCTAGGTTTTCATTG
 GATGGGGTTAGGATGGTCCAAATTATCCCGATAAGTGCCCATTAACCTTAAACCTTTTAAAAAATGAAACC
 AGTAAACCTTCAATTCATTGTCAGTGTGGACACTGCTGGAGAGCACCATGTGCTGGGTCCCGGAGGACA
 CAAGGAGGGGCTTAGAGACATGCGGGAGGCTTAGATGAGAAGACAGCACCCGGGCGAGCGGTCACTGTTA
 GAGAGAGGACCCGTAAGAAGGGCCGAGCCTACAGGGAGAGCGAAGACTGAGCCAACGACGACCTGAGC
 CCTGGGGTGGGGGTGGAGCGTGGCTCCTAACCCAAATCTCCTGCCAGGCAGTGTCCGAC

264; SW vs SM; chr20:54633629-54640196; 20; TFAP2C; PROMOTER

ACCATGAGCTTCCAGTTCCTACGGGTGAGAAAAGAGGTGTCTGTGTGGAGGGCAGGTGCGACCCCGGGG
 GCTAGCAGAGAGGAGAGGCTGCGGGAGGACTCGCTGCGAAGGGCGAGGGGTGGCGCTGGTGGGACGGG
 CGCTTGGGGCCGTGACGGGTGGCTCCTGGGTGTCTGCCCGGGCTGCCTGTGCGCCAGTACTGCGCGAGGA
 AGACGGGTCCGCGCAGCGTCTGGCAACAGTGGCCTGCTCCACGCTGGAGGCGACCAAGTTCTGAGTTAA
 AGGCGCCGGGCTTAGCGGGAGTGTATGGCGACCCAGAACACGAGCGGAGAGGAGAAAGGCTGCGGAGACG
 AGGCTACCGCCTTAGTCTCCTCGGGCCTGCGCTCCGAGCGGTAGGGTGCGTACGGATGGGCTCCGGGATGT
 TAGTGGAGAGGTGACAGGAGTCTACCATCCACGGCCAAGCGCTGAGGCCTCCGCGGGCGGGGCTCC
 CCCGGGGCAGGGCAGGGGAGAGTCAGGCATGTCTCTAACCGGCTCCCTAGTAGAACCCGCTAGGAAAG
 TGGCCTTCAACCCTAGGACACCTTTGTGGCTTTCAGGTAGTTGGGCGACTAAAAATTCACCTTTGCTGCGT
 GAAATGGGACAGGTGGTTGTGTCAGGTAGAGACTGTGCCACGAAGTCTCGTTTGGCGGGCCGGGACTGAC
 TGGACCCCGGGCCCTCCTCGGAAGCTTGGGAACCTGTGAGCCCTCAGCTCCTCGCCCTCACTTTGCCTGT
 TTGAAAAAAGGAGTTGTTTGGAGAGAAGAGTTAAGGCTCAAAGGTTCTAAACGAAGAGCATGCGGCTGA
 CGCGGAGCGCAAAGAAGCGAGCAGTGAATCTGGTGGGACTGAGACCAGAGGCGTCTGTATGCGG
 CGGCGCTTTCGCGCCCTATTAAAGCAATCTGTTATTACGATAATCATTTTGTAAATTTGAGATGGCTG
 TGACTTGATGTCTGTGCTGCCCGAGGGCATGCCCTTACTGGACATAGATACTTCAGGCTGCCCTTTGACGC
 CAGTGTGCGTCCAGTGGGTGCCAGTGCCGGAAGGGAGGGTGGCGGGCGTGAATGCCCCCTCCTCCTGG
 GTTGCCGCGAGGCCCGGCTTTCCACCTTGTGATCCTGGCGGGTCTGCCACTTACTGAGGTCCCCTACCG
 GCGCTCACGTTCTCCCGAGAGGCGGGACAAACGTCGGCGCGCTGCCGCGGACTCTGCCAAAGCGCTCGG
 GGGCCTCCATCTTCTGCTCGGGAGTCCCTCCCTGGGGCGGGAAGAGGAGTCCGAGATCTGCCGAATCT

280; SW vs SM; chr3:148619483-148620015; 3; ZIC1; DOWNSTREAM

GAGTGCCTAAAGGGAAATTTTGCATTGGTGGATTTATTGAAAGCATGGAACAGTCTTCGGGGGTAGGT
 GTAGGGGTGCAACAGCGAGACTTCCCCACAACACCTCCACCGAAGGCTGGGTGCTGCGGTTTGAAGGAC
 CCTCCCGCCACCCCGCAGCTTGGCGGGGCGCTTTCCAAATCGTCCGCGCAGGCTCTGGCGGGCAGGGC
 GAGATGTGCGCATGCGCGGCTGTGGCCCCAGGTTCCACGTGCTGATGAATATGCATGAGACTCCCCCG
 CCTCGCGGGCTAGGAGAGAACCAAGCAGAGGCTCCGGCCTGTGAAAGTCCGTGGCTAGGCTCCCAAAATA
 GTGCGCGGGGTAGCTGCACTGTTGTTTCAAACCGCTGCTTAAAGTGAGTTGAGGAGTCCGCGGAGCC
 GACAGCAGAGGGTAGAGCAACCTGGGCTGTGCCATTGAACGCGAGTTGAGCGGGCCTGTACAGGGCC
 TCTCCGCGAGGGCGGGGGGTGCATGGTGTCTGAGCCCCAG

289; SW vs SM; chr4:134288613-134289892; 4; PCDH10; PROMOTER

CGCGTTGCCCCCTGCGCCTCCGGAAGGGGCACTCACAGCTGGTCAAGCGCGTCCCTTCGGAACCTCGGGGAGG
 CTCGTTGGGGCTTACACAGAGCTAAGCCCTGGGCCAGGAGGATGGATGCAAGTCACTGCTGTGCAAA
 CGTGTTCGCAGATACCCGACGCGTGCACACTCGGGCCCCCTCGTGTGCACGGGCCCTGCCACACCCCCG
 CCCGCTTCGCGCGCCGCCCCACTGTCTCATCCCGCGGCTGACCCAGGATTGGCAGAAATCAGTGGTC
 TAATCTAGCATGTGGTAAAGGGATCGATCTCCAATTGCCAAAAAATAAGAAATAGCCGGTGTTC

AGCCGCTGCGTGGCACTTGGCCGCACAAGGCGCAGGGATATCAGAGGCGCTTTGACGCGCTTGGCGGTG
CTGTGTGCCGGATGCCCCAGAGCCCGCGTTAGGATGCGGGCTTGTAGGAAGCGGCTCAAATCAACTCCT
CAGTCACTGATGAACCGCTCACGGCTCGAAGCTAGGTCTCGAGTGAGTTAATCTACTTGGTAAGTATTT
TGTGAATATGTATTTGGGAGGAAAAGACAGTCGAACGCGCTGCCCCGTCTGTAAGCGCGTCATCCCC
ACATCCTTTAGCGTGAAATTCCTCCGCTTTTATAGGAGTCACTCCACCCCTACTCCGTATGCTTCGCGCTT
TCCTCACGGCCCCGTACAGCCCCCTCACCTTTAGATTGACACATGCCATATAATACTCACTTTTAAATGC
CCTGCCAGTCTCTTAGGGTCCCTTAATTAGGTAACCTTGCCAATTAGTGGGCCCTGCGCTACTTTTTCC
CTTCTCGATGATTTATTCATGATGCGTATTAGGGAAAAATACCTTAAAGGAAAAAGAAATGTTAGCATCAT
TGGAAATCCCGCTCCTAGGAGAGGATATCGCAGCTGTGCTATTATGTTTCGATTTGCTGATGCAACAG
GGGAACCTCTCTATTCCTCCCCATTACCTGCGGCTGGGGACTGGGAACCTTCCGCGGCATTTGTCGCCAGC
CAGCGCTCGGGACCTGCGGGGCTGTTCTCGCTCTCACACTCACACTCACCCCGCGCGCGGGCGAGAGT
TCTGTCCCGCCCCCGCGGTGCGCGCTGACGTGTCTGTTTGGCGGCCAGTTTGGCCAATCATCGGCAGC
TCGGTGGGTGCTCTCTGCGGATTGTTGGCAGAATGAGGCGCTGCGCAAAAACGGAGAAGCCGAG
CGCTCG

290; SW vs SM; chr4:134291113-134293078; 4; PCDH10; INSIDE

CGGAGCCAGACCTGACGGTGGAAATCTCTGAGAGCGCCACGCCAGGCACTCGCTTCCCTTGGAGAGCGC
ATTGACCCAGACGTGGGCACCAACTCCTTGGCGGACTACGAGATCACCCCAACAGTACTTCTCCCTGGA
CGTGCAGACCCAGGGGATGGCAACCGATTTCGTGAGCTGGTGTGGAGAAGCCACTGGACCGAGAGCA
GCAAGCGGTGCACCGCTACGTGCTGACCGCGGTGGACGGAGAGCTGGGGGAGGAGTAGGAGAAGGAG
GGGAGGTGGCGGGGAGCAGGCTGCCCGCCAGCAGCAGCGCACCGGCACGGCCACTACCATCCG
AGTGTCTGGACTCCAATGACAATGTGCCCGCTTTCGACCAACCCGTCTACACTGTGTCCCTACCAGAGAACT
CTCCCCAGGCACTCTCGTGATCCAGCTCAACGCCACCGCCCCGACGAGGGCCAGAACCGGTGAGGTCTGTG
TACTCCTTCAGCAGCCACATTTCCGCCCGGCGCGGGAGCTTTTCGGAATCTCGCGCGCACTGGCAGAC
TGGAGGTAAGCGCGGAGTTGGAGTGAAGAGAGAGCCAGTGTACCAAGTGTACGTGCAAGCCAGACCTG
GGCCCCAACGCCGTGCTGCGCACTGCAAGGTGTAGTGGAGTACTGGATGCTAATGACAACGCCCGCAG
AGATCAGCTTCAGCACCGTGAAGGAAGCGGTGACTGAGGGCGCGCGCGCCCGCACTGTGGTGGCCCTTTT
CAGCGTGACTGACCGCGACCCAGAGGAGAATGGGCAGGTGCAGTGCAGCTACTGGGAGACGTGCTTTTC
CGCTCAAGTCTCTCTTAAGAATTACTACACCATCGTTACCGAAGCCCCCTGGACCGAGAGGCGGGGG
ACTCCTACACCTGACTGTAGTGCTCGGGACCGGGGCGAGCCTGGCTCTCCACCAGTAAGTCGATCCAG
GTACAAGTGTGCGATGTGAACGACAACGCCCGCGGTTTCAGCCAGCCGGTCTACGACGTGTATGTGACTG
AAAACAACGTGCTTGGCGCTACATCTACGCGGTGAGCGCCACCGACCGGGATGAGGGCGCCAACGCCCA
CTTGCTACTCTATCTCGAGTGCCAGATCCAGGGCATGAGCGCTTCTACCTACGTTTCTATCAACTCTGA
GAACGGCTACTTGTACGCCCTGCGCTCTCTGACTATGAGCAGCTGAAGGACTTCAAGTTTTCAGGTGGAA
GCCCCGGACGCTGGCAGCCCCACCGCTGGCTGGTAACGCCACTGTCAACATCCTCATAGTGGATC

309; SW vs SM; chr5:133887842-133891327; 5; PHF15; PROMOTER

CGAGAGAAGGTGAGCTCGGCGGGCGCAGCGGCTTGGGTGGGTGTGGCCCCGCGCTCCGGGAACAGACCC
AAGGCCCCGCCACCGCGGCTAGCAGCCGACAGCCCGCCCGCTGCGGAGCGCAGGCCTTCTTCAGAA
ACTGCGAGGATCCGAGCGTACTGTTGTGCACCACAAGGTCAAGTTCGGGAAGTGGAGCGCGGAGGAG
GGGCGAGGAGGCGAAGGTGGGGAGAGGGGCGCCCCGCTTCTCGCCATGTGCCAGCCTTTTGAAGTTA
CCCTCGGTTTAACTTTTCGGGGTAATGGGAAGGAAGAGCAAGGAGGAAGGGGTGCGCCCGGGGCAAAA
TCCTGCTGGGGCCAGGATGTGCAACCACCCACCCGCTCATCACTGCTTCTCCACCCCGGAAAT
GCGGGGCAGCGCTAGGCGCCAGGAGGCACCCGGGAGGGGGAGGGGGCGACGAGCCCAATGGGGACCT
CTCTACCGACCGCCCTCTTTCTTGAGGTGCGCTACAATTTCAAGTTCCCGCGCCCGGAATGTTAGTTT
CCATTGGAGTGGGTGCGGGGAGGAGGGCGCGCCCTCCCCAAGACTCGCGTTCGCCCTCCACCCCT
TCTGCCAGCACTTCTGCTCACTTCTGGTGTGCAAAAACGCCACGCAATTTATTCGATTTCGATTTTAAAA
CCAGCGATTTCAGAAAGCAGGGCTAGGGCGAGGGTCTCCAGCGCTGGAGCCCCGGGGGGCGGGTGTCTC
AGTGCAAACTCCGTTCCCTCGCGAGTGTCCCTCCAGGCTGTTATTTGCAAAAGAAACGTCTTTTTCAGCA
GGGAGAAATGGCAAAATTTAAGTACGTCAATTAATATGGCGCCAAAAGATTTTTTAAGTATAAGCTCGCTT
TTTTTTTTTTTAAAGGTTGCGGGGGGCGCGCCCGGCTTGGGCGCGTAGGGGGCGGGGTGTGAGCAGAA
AGTGTGAGTGAAGACTGGAGGGGCGGGGTATGTGTGCTGCTGAAAGTGTGAGCAGACCTGATGGG
ACTTGCACGGGGCGACCGCGCTCGGGCCCGGCTGGGGACAGGGCGGGCTAGGGGCGCCCCAGAGT
CATGGGGAGTCCGGGCGCAGGGTGCACGAGGCGTGGTGGTGGGGCTGCGAGGGAGGGCACCCTTCCCC
CACGGGGCGCAACGCTACTTGAATCCCGCGCGAGCCAAACAACTGGGCGGGGGTGGGGGGGCG
GCGAGGGGGTGTGCGGAGCGGAGATCGAGTGAATAAGAAAAAACTGGCTACTCCCCCTCCCTCGCTCC

328; SW vs SM; chr6:5080084-5080849; 6; LYRM4; INSIDE

ATCCCTATTCCTTCTCCTTCTCCTTGGTAACGGCACTCCTAGGGCTGTGGAGGGTGGCGTTCACTCC
TGGGACTGTGGAGGGTGGGATCACTCCCGGACTGTGGAGGGTGGCGATCGCTCCGGGGCTGTGGAGG
GTGCGGATCGCTCCCGGGGCTGTGGAGGGTGGCGATCGCTCCCGGGGCTGTGGAGGGTGGCGATCGCTC
CCGGGACTGTGGAGGGTGGCGTTCACTCCCGGACTGTGGAGGGTGGCGATCGCTCCCGGACTGTGGA
GGTCCGGATCGCTCCGGGGCTGTGGAGGGTGGCGTTCTCTCCCGGGCTGTGGAGGGTGGCGATCGCT
CCCGGGGCTGTGGAGGGTGGCGTTCACTCCCGGGGCTGTGGAGGGTGGCGTTCACTCCCGGACTGTGG
AGGGTCCGGATCCCTCGGGCTGTGGAGGGTGGCGTTCACTCCCGGACTGTGGAGGGTGGCGATCGC
TCCCGGACTGTGGAGGGTGGCGATCGCTCCCGGGCTGTGGAGGGTGGCGTTCTCCCGGGGCTGTG
GAGGGTGGCGTTCACTCCCGGGGCTGTGGAGGGTGGCGTTCACTCCCGGACTGTGGAGGGTGGCGATG
CTCTGGGGCTGTGGAGGGTGGCGTTCACTCCCGGACTGTGGAGGGTGGCGATCGCTCTGGGGCTGT
GGAGGGTGGCGATCGCTCCAGGTGTGATTTTCAATGGAATGGAACCTGGCTCCCTAGGTGCTGTTCATTTCT

379; SW vs SM; chr8:65653638-65653908; 8; BHLHB5; PROMOTER

CGAACGCCGGGGAGGGACGGTGGGAGGGGTGCGGTGAGCGAGGGGCTGCCCTGCATGTAAACAGCCTC
 GGGGTCCCAGACGAGACAAGTGGGACCGCTCAAGCCTGCAGAACCCCGGTCTCGGTCCAGGCACAAGA
 GCCTCCCGTAGCCCGCCTGATCTTTCTCAGTCTTTAGGTTCCAGGACATCCAAAGGAGCGTAGGTAACCG
 ACGTCTACGTAGTATTTCTGTCCCGGAAGACTGGATCTCAGGGAATTATTATGGAAGATA

386; SW vs SM; chr8:72916429-72917309; 8; MSC; INSIDE

CGGGGCAAGGGCGCGTTCCCTATCGCAGGATCACTTGCTATGGTAAGCCGCCACCCTGCGCGCTCCTCC
 GCGCGGGGAAGAACCTGCGCGGCAGGACGTGGTGTGGAGTTGGGGCGCCCGGAGCGGGAGTGGGGAG
 ACCTGATGCAGAGAGTCTGGAGTCGGAGCTGGGGGTGCTGCAGGTAGGAGCAGGAGCGGGGCGGAGAGG
 GAGGCCCGAAGAAGACCCACACAGGTTGGCGCAGCGGGGCTTGGGGAGGCTTCAGCCAGAAAGTGGAG
 AGGTTGACAGACGCCGCTGATTAGAAAAAGCCGGAGCTTGGGAAGGAGACGGGATTGAAGAAGCCA
 CCGGCAGGGAGGCCGAACGGCCAGAGCTCTCCGGTAAACCCGCTGCGGTGATCTGGCAAGTGTG
 TCTCCACCTAGCCCTGCGAGCAGCGGCTTCTCCCGCCCGTTGAAGGGCGCTGTGCTGGAGTACGAACC
 CGGCCAGAGAAGCCACTCGCCCTTCTTTGTCACTTAAACCCCTGTCCCGACGCGGATCTCACGTCTAGAC
 CTCTGTCTTTAAAGCGGATGTAGAGCGCGTTCTAACCCTTCCCTAACCATTGTGTACCGCGAAAGCGGG
 GCTGTGTGAACCGTCCCGCACGTGTGCGATGAATCTGGCTCCGCTGAGAACGGATCCGTGGGCTGTCTG
 GCGCGGGCTGGGGCAGCAGCCGAGAGTTAGTCTACAGAGCTAGGGCCCGAGGGTGGACCTGCGTCCGCG
 TCTCGTCACGAAAGGAAGCTCTTTGGAGAGGCAAAACGTGGTCCGCCAGATCCGGCCAGCTGTAGCCG
 TGGGCGCTGTGCAGTGACAGCCACCCGCCACCTGTACG

400; SW vs SM; chrX:2845926-2846236; X; ARSD; INSIDE

TTTCTCATCAGGATACAGTTCCAGCGTCGCACAAACCCGAAGGAGGAGTACCAAGAGATGAAAAACAGGC
 AGCCACGCCGCCATGCCGGTGAAGTCTCTCGCGGAGACAGAGAAGAAACCGCAGGCTGCCCGGCAGC
 CAGGGTGAGAATCCCAGCGCCAGGAAGTGGGTGTAACCCAGAGCTGCGCCCTCAGGGCGGCGTCCACT
 TCGGGGGCCTGCCTGGGTACAGTCCGTTGTGAGCGTGAAGGGCATGCCGTAGAAATAGTCAAATCCGT
 GGTTCAGGGGGTGTGGCAGTGATCCCGCG

Table 5. CpG islands potentially involved in progression and death of disease. Provided for each are: ID; Comparison; Coordinates of selected regions containing relevant CpG islands based on Homo sapiens full genome as provided by UCSC (hg18, Mar. 2006); Chromosome; GeneName; Location relative to gene Sequence.

406; DOD/alive; chr2:115635091-115637285; 2; DPP10; PROMOTER

AAAAAAGAAATGAGTATCAGAGTCTTATCATCATTACAGTTCTTATGGTTTAAACCGACCTTTAGGAGTTTC
CACCGACGTGACCCAAGCAGCTGGTAGGAGAATCTGGGCTGGATTGGAAGGCGCGCTACAGGACGCCC
GCTGCCCGGATCGGAAGGCGCAGCACCTCAGGCCACAATCTCAGACACGCCCTCGGGTCCCCGACAGGTG
TTGCCCCCTCCCACGGGGCTCCGGGACCCCGGTCCCCGGGCTGCCCTGCTTCTGGGGCGCTGGAGC
GCGCGCAGTGGCGGAGCTGAGCCACCCAGTGCTTCGCACGGGCGCGCTCCGCTTCTCCGGTTTATGCGG
AAGCCTGCGGGGGCGGGTAACCGCGGAAGCGGCGCGCGTGGCGCGCGGGTTGGGGGCTCTCGCG
CCGCTCCGGGCTCTCCCCCCCCCGGCTGCGGTTGCCGAAGAGAGCGCGGAGCGCGCGCCCGGCTGCTC
CACCTGGCGCGCTGAGCACCGCGCGGGGAGCCCCGGGGCGGGCGGTGGGGGCGCGGACTGCGGGA
AGAAGGCACGAGGCGTCCGCGCAGCTCGGTCAGGGGCGGGGCCCCGCGCTCGCGCTGCACTAATTT
GCGCTTGGTCTCGCTCCCGCGCGGCTCGCTGCGCTTTGGGTGGCGGGGGCGGGGAGAGCGGGGAG
TCAGAGGTCTGCGGTGGCGGAGGGAGCCCTACGACGGGAGCCCGCCGCTGCGCTCTCTTCC
CCTCCCCCGCCCTCCGCTCCCCCACCCTGCTCCCTCCGCGGATTCCGGGAGGACGGGCGCCCGTGACCT
GCGAACGCTGCCAAGTGACGCTCCCGGAGTCTGAAGCGCCCGGAGGAAGCGAGCGCCAGCGCGGGCGG
CCGCGGATGACGGCCGCGAAGCAGGAGCGCGCAGCCACCCCGGGGCCAGGGCGAGCCAGCGCGAGCC
GGCGGACAGGTGAGAGCGGCAGCGCGGCCAGGCCCTCCCGGAGGGGTGGCTCCAGTGCGCGCTCCG
CCGCGCTCCCGCTTCCAGGCTGGGCTCCCGCGCCTCCCTCTTCTCACCTCCCGCGCCCGCCAGTTTC
CAGGCTCTCTGCTTCTCCACGGACTCTGCGGGAAGTTAGAGCCTCTGCTGCGCTCCGGGGCCCGCGAG
AGGATGCGCAAGGTGGAGAGCCCGGGGA

407; DOD/alive; chr3:62330280-62330608; 3; FEZF2; INSIDE

AAAATTGGTGCAATTTAGGAAGGAAATGCTATAAACGCCCTAATTCCTTCTCGTTCTTTGGGGTTGCTGAGCT
GACCTCGCCGCGAGGGGAGAGGGGAAAAAACCGCCTAATGATTCTGTTATTAGTTATATATGTAT
ATATTCGCTGTTGCTGTACAGGAGGATTTACATGGCTGTATAAGATGGCTAGGGGCGCCGCGCTCTTC
TGGGCGCTCACGGTGACAGGCTGGGGTTAAAACTGGCTGCCCCAGGAGAAGCGAGGCGCTGGAATTA
ATACGTTTCGGCGCACTGATTTAAATAAGTTTCTGAATATACAAA

408; DOD/alive; chr3:62331767-62332398; 3; FEZF2; INSIDE

AGAGCTTCCCCCTACACCAGGCACAACCCGATTCTAAAGAAATGCTGCGCCCGCGCTGCAGATTTGCGCT
TCTCTCTCCAGATCCCTCTTTGCTTCTGCGAGCCAGCCGCGACCCGAGTCTGAGTGAGGTGAGAAAGA
GAAGCCCTCGCTGCGACGTTACCTTTTGGTGAAAGCCTTTGCCGCAAAATTCGACAGACGAAGGGCTTG
TAGCCCGCTGGATGCGGATATGCGTGTGAGCGTGAGCTGCGGTGAACGCTTTGCCGCACTGGTTGC
ATTTATGTGGCTTTTCTAGGAAAGGGCGAGTGACAGTAAGGAGAGGCCACCTCGGGAACACCTGGAA
GGGACATCCCCCACCCTCAACCTAGAGGGTAAGGGATAATCTTTGGCCATCGTATCCCGGTG
TTATCACTAAGATTCTGGGGCTTGGCGCGGGCTAGGCCGACCCGGGGCACCTACCTGGGTGTGATA
ATTTTGTGCTGACAGAGCGTGCTGGCTGGCGAAAGCCTTTGCCGCACTTTGACACAGAAAGGTCTGG
CTCCGGTGTGGACCGCATCTGCGCGCTGAGATTATAGTGAGCGTTAAACACCTATGAAAGACATGG

409; DOD/alive; chr20:22514762-22515148 20; chr20:22514762-22515148; Unknown

ATCTTTTGTGCTGAAATGCAGATGTTTGGACACTTCATAAAGAGGGCATTAAAGCCCGCGAGTGAG
CGCCAGGGCGGGATTCTCCACAAATTCAGGTCTGTATCTCCGCGGAAGCCGTGCTATCGGTCCCCGA
GTGCTGAAGGCTCCACAGGGGCGAGGCCAGCCCGGTGCGCCAGGGAAGGAGCTTATGTTGTGTACGG
CTACGTAGTGAACGTGGAGGTGTGCGCAGCGGAGTCAGAGGGGCTAGATCCCCAGCATTTCCACGGGGT
CCACCTAGCGGTGGATGGAGCACTTCATCACTCCACCGAGGGCAGGGAAGAGGAGTAAGCATTGGA
GCTCAAAGATGAGCAATTTTCAAAGCTTTCTCC

410; DOD/alive; chr20:22510737-22514165; 20; FOXA2; PROMOTER

CGGGTGGTTGAAGGCGTAGTGGTGTTCGGCTTCAGGTGGGCTCAGGCGGCAGGCCGGGTGGTGGGG
CGGGCCAGCAGGTGGGCGCGGCTGCTGCTGCTGCCCGGAGAGGGCGCCGGCTCTGGGGCTCAGC
GCCGAGCCGCGTCCCTTCAGCTCTCCAGGCCCTTCCGCTTGTGCTCTGGACAGGGGAGGCGCTCG
AGTGAGGCGACTCGGTGCCCCGCGAGTCTCGGAGCGCGCCCGCGGCTCCCCGAGTTGAGCCTGTG
AGGCTGGGCTCCGCGCGCGCTTCTTCCGCTGCCGCGCGGCTGCGGCTCTCTAGCGCCAGCTGC
TTCTCGCACTTGAAGCGCTTCTGGCGCGCAGGTAGCAGCGCTTCTCGAACATCTTCCCGAGTCAGGT
GCAGGCTCCAGAAGGAGCCCTTCCCGGCTTGTGCGGCGAGCGGGCACCTTCAGAAACAGTCTGTAA
GGAGAGCGAGTGGCGGATGGAGTTCTGCCAGCGCTGCTGGTTCTGCCGCTAGAGGGGAAGAGGTCCAT
GATCACTGGTAGATCTCGCTCAGCGTCAGCATCTTGTGGGGCTCTGCTGGATGGCTGTGAGC
GAGATGTACGAGTAGGCGCTTTGCGTGGCTGTAGCTGCGCTGTAGGTCTTGGGGTCCGGGCGCGGCT
CAGGCCCGCTGCCCTACATGGGGCTCATGGAGTTTCATGTTGGCTAGGGGGCAGGCCCGCCATGGCC
CCGGCGGCTGCCCGGAGCGGGCTCAGGCTGGGACTCAAGTGCGGCCATGCCCGCACCGCGGCG
CCCCGGCGAGCCGCCATGCCCGCATGGCGCCCGCGGGGACATCCCGCCAGGGACGGGCTCA

TGCCAGCGCCACGTACGACGACATGTTTCATGGAGCCCGGCTCATGTTGCCCCGAGCCGCTGCCCATGGC
GGCCGCCGACATGCCATGTACGTGTTTCATGCCGTTTCATCCCCAGGCCGGCGTTTCATGTTGCTCACGGAGG
AGTAGCCCTGCGGACAGAGCCCGGGAGGGAGGCGACAGCGTTAGCACCGCGGCTGGAGGGTGCCAGA
CCTCCCACCCACCGCCAGGCCTCCGCGTCCGGGGAGGCCTCCGGGGGCCCTTTCCTCCCGATGGCCCA
GTCTCCGGAATCCGACTCTGTTTCATT

411; DOD/alive; chr8:57520625-57522095; 8; PENK; PROMOTER

ACAGAGGACTTCTCGGGGTTCCCGAATTTCCAGGGTTAAACAAACTTGGTTTGTGCGGCGACACCGCTA
CCCTTACCGGTCCCCAGATAGTCGCGGATCCCCGAAGCTAAGAGCCAGGGCAGGACTCAGTCAGTGTTC
AGGAACAGCTGAGACACCCAGGTACACACGGGCTCGCGCCGCTGCGGCTCCGACCCGCTGCGAACCGCC
ATACGCGCCCGCGGTTGGGCCGAGGCAGTCCGCGTACTGTTGCGGAAACTCTGTCTACAAGGTGCGCA
ACACTCGCCGCGCGCAACACCACAGGAAGTTGATGTCGCGCGGGCGCACTAGCGGTAGCTGCACGTGCG
CGCAATCCTGGCTGCATTCCGCCCGCACGGTCCGACGAGCCCGGGGCCGAGCAACAGCAGCCAAGTGC
AAAGTGTCAAGAACCGCGCCATGGACTGCGAGGAGAGAGGGACGCGTGTCTCGGCTGCTTGGGCGCAG
AACGGGGTCCCTCGGCAGGACCTCGCCGCGACAGCCTCAGCAGGGGATCGTCGAGCAAAAGCCCGCAG
GAATGCTCCTTTCTGGGGCCCCCGCTCCCGGCCGACAGCTTTTAGGTAGACGTGGAGGCGACTCAGATC
GCCTGCGCGTTCCCGGTGGCGCGGTCCGCCCAACGCGAGGCTGCCTGGGGCACCCCGGCTTTTCTCTG
GGCTCCGCGGCCAGGCAAGATTCCGAGAGAACGCCGACAGCAGGGGCGAGAGAGCGGGAGCGG
GGGAGGCGAGGACATTGACTGGGGTCAAAAGAAAGAACAGGGAACGCTGTGGGGAAACCCATGCAATGA
AATGTGAAGGAAAGAGGGCGGGCAGACGTCCCCAAACCCGCTCAGCAAAAGACAAGCTTCGGGCAAATTC
ACTCAGTTGACGCTGTTCCGATGGAGCAGGCCAATTGAAAAGCCGGTTTCAACACGACTCTAGAGGG
AAGAGAAGAAGGCAGTGTGAGGAGGGCGGGCTCGGGGAGAAGCGGGCCCGGTTGTGCTGGCGGACGT
AGGGCTCACCGTCCGCGTCTCAGCGTCTCTCGGGGTACCGGGCAGGCTGCGGGCTCTGAGCGCC
TGCTCGCGTCCCGGGGCTTAACGGCTGCTGGAGCCACTTTATAATTACCCAAACCGAAGGAGGGCGG
CGCGCCCAATCGCGCGGGGCTGCAGCT

412; DOD/alive; chr17:24303411-24303889; 17; PHF12-SEZ6; DIVERGENT_PROMOTER

GATCTGCTCTCAAGAGGAAGCCTAAAGTGGAGAGTTTGTAACTCTGACAACGCCAGCTACCTGCGTACC
CCGACTCCAACTCCAGTTTGCAACGCCAAAGGGTCTAAAGGGCGAAGCGGGCGAATTCATCTCTGGGA
GCAAGAATCGCGATAGCTCTGATGGAATGTGGGAAGTGTAGTTCATGTGCGTGGCATGCACTCTATGGT
AGGATAGACCCGGGAAGAGTCAATTTGCCGCCAGGAAGGGATACITTTGAGAGCGTCACTGCTGATGC
CGGATTTGTAGTCTGAGGCCCGCTCGCATTCTGGCGGGGATTATGCTCCTTTTCAGGGCGCCGCT
CTCCCTTGGTATGCGCTCAGAGATGGGCGGTGGTTATTGCTGCTGATGGTGGATGAAGCAGTGGA
AAAGAGAATTGTATCGCTTGACTAGGAGTACACTAGGGGTTTAGTTGGAATTGTGCTTC

413; DOD/alive; chr1:149638545-149639227; 1; PSMB4; PROMOTER

TAGGATTACTGCATGTTTCACTACGACCTCATCAACATGGCTGCTGGAAGTCTCTACAGGAAAAAGAAAG
AAATGACACTGAAGGATCACTTCCGCTTCCGTTGGCGCAAGCGCTTTTCATTTTTCGCTACCGTGACTAAG
ATCGAAGCGTTTTCGGGTCGCGCTCCGCACTTTGGGGCGGGGGTCCGGCCCCAGGACAGTTTACCGCA
TTCCGTCCTCCACTCCGATTCTTTCATGGATCCGGCGTCTGCACTTTACAGAGTCAACTACCGGACCCAG
TAAGTTCTCGGCGCTTCGTTTTCGCTAGCGGGAGGGACCGTGGGGCTGGTGTGCGGGCTGGTTTTCGAG
GCCCGGAAGGTGAGGCGGGGACCCCGGGGGCGCGCAAGCGGAGGGGAGCTCAGGGCGCGGAGTCCCT
GGAGAATGCAGAATAATTGGAAGGAATTATAGAAAATCAGAAGCGCAGTACTGCGCGGAAAGAGGGCGC
AGTCCATCCCCCTCTCAGCTCCACCGTTCTCACTTTTAGGAACCCCATGGTGACCGGGACCTCAGTCC
TCGCGGTTAAGTTTCAGGGCGGAGTGGTGATTGCCGCGACATGCTGGGATCTACGGCTCCCTGGCTCG
TTTCGCAACACTCTCGCATTTATGCGAGTCAACAACAGTACCATGCT

414; DOD/alive; chr21:36990008-36995832; 21; SIM2; PROMOTER

TCCTTAGTGACAAGGTCTCTGATCTCCTGCTGCCACTGCAATAGCCTCTCCATCCCGCGGGGAACGGCCG
GAGTTCTTCCCTTGATCTCTCCGAGTCCGGCTTCCGCTGGGGATGGATCGCAGGTAGCGCCGCGCGGGCC
TGGGGAAGAACAGTTGCGGAGCATCTGAAGCGGAAAATCCAAGCAGATGTGAGCGCATCCGGGCCCGCC
TCGTTCTCTTGGGGCTGAATTTCTTCCAGATAAGTTTCTTAATGGAACATTTCTAAGAGGTGGGGTACG
AGGCGGCTTGCTCGCACGGCAGTGGGACAGACTGCGGGTGGGGACGTACTGAGAGGTCCCGGACCTCAAT
GCGTCCGACCCGTCTCCACACCGCCCTTTTCAGCCCCAGTCTCCTTTCATTCCTACTCTTCAGGCTCC
TTTGGGGCCACTGGGTGAACCGCCATTAGAACGGTGCCCTCGGACTCGGGGTCGTGCGCTCCATCTCTGCT
CTCCCCCTGGGGCCCGGAGGCTGGTCCGGGCTTTCTGAGCTGGGCGTTCCGCTTTTAGGCCCAATACCT
GGACCAGGAATTTCTTCTCCCCGCCGAGAGGGAAAGACATAGGAGGTGTCCAATCTGCGGTCAACCGC
CGATGCTCTGACACTCTAGTGAGCACCTGCCCGTACTTTTCCATTCCAACAGAGCTTCCAGCTTCATAC
TAATATCCACATACGGCTGTGGGTATTAGCTCTAAGTGTCTTTTCCGAGGGCCGAGGCTCCCGCTC
CAGCAGGGAGAGCTCCGGGACGGCCCCACCAAGGGTTGGGTTCTTCTTCAATTTCCACAGAGGCATC
CCTGTCTTCTACTCTGGGAAACCTCGAGGTGCGGTGCCGTGTACTTCTGGTACTTTGCGTGGTGCCATC
AGGGACCCAGAGCCACAGCTGCGTGTGTGTGGATGTGTGTGTGTGTGCGCGCGCGCGGTGTACG
GCGAAGGATGTCTTGGGGGAGCGAGTACACAACGCTGTGCTTGGGCACTGCTGGGCGAGGCTTGGG
CTGAGGATCTCACCCACGATCTTCCAGTCTTCAAACCGGCATTGCTCTGCCTCCCGTAGCGCGCT
TCGAACCTGCCTCGCGGACAGTGAACAGAGGCTGCCCTGGGAAGATAAGTGGCTTTTCCCGTAAATCC
GGGAATTTGCCTTG

415; DOD/alive; chr1:232106869-232108183; 1; SLC35F3; PROMOTER

AAGTACTGAACTGGGAGCGGCAGGCTTTGAGTCAAAAGAGAAGGCTGGAGAGCGCTCCGCTGCCCA

AGGCTTCCAGGCGGAGCGCGGGCGCGAGGTGCGGGCTCCGGGGCGGAGCGCACGCCCCGAGGCGGGGAA
 GTGGGCGAGCGCCCCCGCTGGCCCCGTGTCGCCCCGACCCGACGCTCCCCGCCCCGACCAGTGCCT
 CGAGAGCGCACAGCTGGGAGGGCTCTCCCGGTGCGGGCGAGACTCACGCTGCGGTGTGCTAGGGCGGC
 GCGGACGGTGACGGGCTGGGGCGCGCGTGCCTCGGCTGCGGGTCTGCGGGCGAGCGCGCGGGCC
 GGCTTGGAGTCAACGGGCTGAACCGCGCGCTGCATCGTCCGCGACGCGCGGAGGCGCTCGGGTACA
 GACCGCGCGGGCGCGCACAAAGCGGCCCGGGCGGGCGCGCGCGAGACCTCGGTGGCAGCGCACT
 CCAGTCTTCCAGGCTAGCGGCTGCAGGGAGCTCCGGCCCGCGGCCCTCCGCTCAAGTCTGGGAGCTG
 CCGGTCCCACTCTGTCTTTGCTATGGGGATTTCGAGAGTTTCCAGCGCGCACCCAGGGGCAAGAGCAT
 TGCCGTGTGAGTAGCGCCCCGCGTGGGTGAGCGAGCCGGCGGGCGGAGCGCGAGCGCGCGGGTAG
 CCTTTGAGCTGGGACACTGGGCAGTCTGAGGCTCGGGGAAGGCGCGCGCGGTGGAGCTGCTCG
 GGAAGTTTCAGTCATTCTTTCCCTCGCCACTCGCCCCAACCCGCACTGCCCGAGAGCCAGGATAGGGC
 ACTGGGGACAGCTGCCCGGGGAAGTGGGTGAGTGGCGCGGGAAGGGAGGAGCGCGGGCTCTGCCCG
 CGCTCGCCCCCGAGGGCCCCCGCGCGCTCTTGTCTCTGCGCTGGGATCTGCTCCTACGAATCCCT
 CCTCTCTGTCCATGCTCCCTGCCACCCACCTGCGCGTGGCGCGCTGCGACCGCAGTGGCATGAGGAGGT
 CACCGGACGTGAGCCCCGAGAGCTGTCCGACATCAGCCCCAGTCCGGCAGCTCAAGTACTTGGTGGT
 GGACGAGGCGATTAAAGGAGGATCTGAAATGCTCGCGCTCCGTGGAGGATCTCCAGCGGGCGCGTGGG
 CTCACGTCCATCAGGAGCGGATCCTGCGCATC

416; DOD/alive; chr6:21704622-21705099; 6; SOX4; INSIDE

TGCATCACCACTTGGTTTGTTTTATTTTGTCTCTTGGTCAAGAAAGGAGGGGAGAAACCCAGCGCACCCC
 TCCCCCTTTTAAACGCGTGATGAAGACAGAAGGCTCCGGGTGACGAATTTGCCGATGGCAGATG
 TTTTGGGGAACGCCGGGACTGAGAGACTCCACGCAAGCGAATTCCTGTTTGGGGCTTTTCTTCTCCCT
 CTTTTCCCTTCCCCCTCTGCAGCCGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGG
 CGCTAGGAAATGACCCGGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGGA
 CACGAACTGGAAGGGGTTTACCGGTCAAATGAAATGGATTTCACGTTGGGGAGCTGGCGCGCGCGC
 TGCTGGGCTCCGCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCAGAC

417; p-np; chr1:160220156-160220709; 1; OLFML2B; INSIDE

TTGGGGTTGTAGTCTATCTGGGTCTATAGGAATACTCATTTCTGAACAGCAGCCTGGGGACGATCTGTGT
 GTTGTGTGGGTGTGAAAGCGTAGGAGATGTTGGCATTCCGCTGTTGTAGCTATACGGCATACAGCA
 CCGCACAGATGACGAAGCAGTTGCCGTAGAAATTCCTCGGAGCGCCGTGCGCCATGTGGTCTCTCTG
 TGTGCTCAGGTCCGCGGCATTGAGCTTGTCTACGACAATGACCTCCTGGCTGAAGCCCTCATCGTCCAGG
 GCCGGGTAGATGAGCCATGGCCATTCTCGTCCACAGCAAAAGTCCACGTCTGAGTGGCCCTGCCATCGCCA
 GGGGCTGGCTCCTCGTAGGCCACGTGATGAGCATGGCCAGGCAGCCAGTAGCGCTGCTTACAGTCTG
 TACTTGTATGATGTTGCGGGTGAAGGCGCGATTGTAGTAGAAGGCGCCATTATACACAGTGGCTGTGCG
 GATCCAGCTGTACGGGAGCTTGTAGGAATTGCTCCAGCGACCTGCAGGTGGGGAGAAAAAC

418; p-np; chr3:129688131-129694023; 3; GATA2; INSIDE

TCACAGGCCAGCTGGAAGTGGGCAGAAACCTGTGGGTCCAGACCTCCCAATCGGCCGCTGCTCCCA
 CCTCTCCCGCCCAATTTTTCAGCAGCTCGATTCTGCGGATCCTACATCCGGGAAGAAGCAGACGGGCC
 CTCCTCCCTCCCTCGCCTGGCGCGCGCGCGCTGGGTTCTCATCACCAGGGGCCAGTGCCTACCTGCG
 CGGGCTGTAGGAGACCGCGCGCCGCGCGTGAAGCGGGTTGGCATAGTAGGGGTTGCCCTGCGAGTCCA
 GGTGATTGAAGAAGACGTCCCTCGTCTGGAGGCAGCAGCTGCGCGGGTTCCATGTAGTTGTGCGCCAGG
 CCGGGTGGTGTGAGTGGGGTGTGCGCATTCAGCACGGCGGGTGGCCATCCAGCGCGCTGCTCG
 GGCGCCACCTCCATGGCCGGCGCGCGGCTCAGGGTCTGGGTGCAGACGGCACGGCCCTGCGCGAGGA
 AGGGGAGTGAAGCGTGGCGCAGCGCTGACACCCCCAAAGTCCACACGAGGTGTCCCGCACGCC
 ACGGAGCCCCAGCCAGATCCGCGGAGAAAGAGCACCAAGTCCCGGTGGGAGGAAAGCCCAAGGCTCAA
 AACGAAAGGAAGGCGGGGAGGGGTTTCAGCCACGCACACTCACGTGGTGACCCGCGGCTCCAGAATCAC
 ACACCGTGACATGGGGTACGCGCGGGGACGGGTCCCGACACCAAGTGAACCCCAACAAACGCACAGAG
 CAGCACTTCAGTCAGACACTCACACTGAGCCCCCGCGCGGTAGACAAACAATGAACACAGACTCAAAA
 GTTGGAGACAGGCGCCCGGCCACCCAGTGTGGCACTTGATCCAGCGACACCCACACACCCACACTTGGC
 GCCAGATACACATACTGATCTCAACCCCGAAACATGCACACGACGCCCCCTGAGCGCAGTACTAAGCGG
 CACAATCAGGACCTTCAACAAAGCACACCAAGCAGTCGCCCCGAGCCTGGCCCCCGCCCTAAGTCCCC
 CCAGAGTCCCTCAAAGCTAGGAGCGCCCCAGGCCCGCGCTCTCAAACCCAACTTACACACGC
 AGCCGTGGGGAGGGGAGGACTCGGCTCTGAGAGTGAAGGAGTTCGGCGGGAGCCCCGAGGGCGACG
 GGCCAGGGACAGCACGTCCGAGGCTG

419; p-np; chr6:26312699-26313302; 6; HIST1H4E; INSIDE

GTCTGATCTGTGAAGGGTAGGGCCAGCAGGCAGCACCAAGTTCCCGTATGCGCGTTTTCAGTCTTCATTT
 AGGTCCGAATTCGGGCATATAAGAATACTACCGTCCGTTGTTTTCAGATTTTGGGCTATTTTCGTGGT
 GTGTTGGTCTGTGTTGTCGCGGCAAGGGCGAAAGGGAGTGGGTAAAGGAGGCGCTAAGCGTCACCGT
 AAGGTCTCGGAGATAACATCCAGGGCATTACCAAGCCTGCCATCCGGCGCTTGTCTGCGCGGGGTG
 TCAAGCGCATTTCTGGTTTCATCTACGAGGAGACTCGCGGGTTCTGAAGGTGTTTCTGGAAGGCTGATTC
 GTGATGCTGTGACTTACACGGAGCAGGCCAAACGCAAGACAGTGACAGCGATGGATGTGCTTACGCGCT
 GAAGAGACAGGACGCACCTTTTACGGCTTCGGCGGCTAATGCTACCGTTAAACGACTCAGCATCTCGAC
 TTCCCAAAATCAAAGGCCCTTTTTCAGGGCCGCGCCACAGTTTTCGCAAAAGAGCTCATGACTTGTAGACGA
 TTGGTTGGTCTCTTTATAAGTTAATTGTTCTCTGTCAA

Table 6. Primers and probes for MEIS1 MS-SnapShot.

BSP Primers (MEIS1)						
Fwd. 5'						
GGGTTTTTAGAGGTTAGGGGAA 3'						
Rev. 5'						
CAACTAAATAACCAAACCTCTCCTC						
3'						
MEIS1 A/B SNAPSHOT Probes						
Probe	Sequence (5'-> 3')	Size (bp)	Strand	UM	MT	μM*
MEIS1 A	T21 GGAGAGGGGGGTTATGATGTTAGG	45	sense	Υ	C	0,2
MEIS1 B	T14 GTTTGTTTGGTTTATAGAGAA	34	sense	Υ	C	0,2

Table 7A. Differentially labeled CGIs between subgroups relative to blood

CGI	Gene Name	Probe location	Subgroup
chr01:2072175-2072389	PRKCZ	chr01:002072146-002072190	NMI-mt vs Ref
chr01:2106293-2106715	PRKCZ	chr01:002106497-002106541	MI vs Ref
	PRKCZ	chr01:002106664-002106715	NMI-wt vs Ref
chr01:47672249-47672972	FOXD2	chr01:047671905-047671953	NMI-wt vs Ref
	FOXD2	chr01:047672191-047672235	NMI-mt vs Ref
	FOXD2	chr01:047682633-047682689	MI vs Ref
chr1:63554983-63563059	FOXD3	chr01:063559476-063559520	NMI-mt vs Ref
	FOXD3	chr01:063559476-063559520	NMI-wt vs Ref
chr01:68288825-68289104	DIRAS3	chr01:068289060-068289104	NMI-wt vs MI
	DIRAS3	chr01:068290072-068290116	NMI-wt vs Ref
chr01:71284766-71286392	PTGER3	chr01:071284980-071285024	NMI-wt vs Ref
chr1:90955098-90955445	BARHL2	chr01:090955137-090955181	NMI-mt vs Ref
chr01:119333484-119333719	TBX15	chr01:119333484-119333528	NMI-wt vs MI
	TBX15	chr01:119333569-119333613	NMI-wt vs Ref
chr1:163590111-163590435	LMX1A	chr01:163590167-163590226	NMI-wt vs Ref
chr1:173258989-173259419	MRPS14	chr01:173259418-173259462	NMI-mt vs MI
chr01:178464743-178471598	LHX4	chr01:178470479-178470532	NMI-wt vs Ref
	LHX4	chr01:178470597-178470641	NMI-wt vs MI
	LHX4	chr01:178470597-178470641	NMI-wt vs NMI-mt
chr1:196153712-196154414	LHX9	chr01:196154203-196154247	NMI-wt vs Ref
chr1:219117072-219117487	HLX1	chr01:219117515-219117568	NMI-mt vs Ref
	HLX1	chr01:219121301-219121352	MI vs Ref
	HLX1	chr01:219134113-219134157	NMI-wt vs Ref
chr1:241719037-241719368	SDCCAG8	chr01:241719439-241719492	NMI-wt vs Ref
chr02:19424445-19425131	OSR1	chr02:019415391-019415435	NMI-mt vs Ref
	OSR1	chr02:019424965-	NMI-wt vs Ref

		019425009	
chr02-45249374-45251726	SIX3	chr02:045013420-045013464	NMI-wt vs Ref
	SIX3	chr02:045015982-045016033	MI vs Ref
	SIX3	chr02:045015982-045016033	NMI-mt vs Ref
	SIX2	chr02:045085251-045085298	NMI-wt vs Ref
chr2:54536404-54537878	SPTBN1	chr02:054536311-054536361	NMI-wt vs Ref
chr02-63134470-63134933	OTX1	chr02:063134470-063134515	MI vs Ref
	OTX1	chr02:063134470-063134515	NMI-mt vs Ref
	OTX1	chr02:063134803-063134847	NMI-wt vs Ref
chr02-66525936-66527222	MEIS1	chr02:066525898-066525942	MI vs Ref
	MEIS1	chr02:066526023-066526067	NMI-mt vs Ref
	MEIS1	chr02:066526791-066526835	NMI-wt vs Ref
chr02-70984709-70985764	VAX2	chr02:070985519-070985563	MI vs Ref
	VAX2	chr02:070985519-070985563	NMI-wt vs Ref
chr02-72224630-72228512	CYP26B1	chr02:072227412-072227461	NMI-wt vs Ref
	CYP26B1	chr02:072227537-072227583	NMI-wt vs MI
chr2:73004709-73005568	EMX1	chr02:073004783-073004827	NMI-wt vs Ref
chr2:85213468-85216104	TCF7L1	chr02:085215511-085215555	NMI-wt vs Ref
	TCF7L1	chr02:085216153-085216212	NMI-mt vs Ref
chr02-105864220-105865009	NCK2	chr02:105864372-105864417	NMI-wt vs Ref
	NCK2	chr02:105864443-105864487	NMI-mt vs Ref
	NCK2	chr02:105864906-105864950	MI vs Ref
chr02-111591678-111597436	FLJ44006-BCL2L11	chr02:111592037-111592081	NMI-mt vs Ref
	FLJ44006-BCL2L11	chr02:111593125-111593170	NMI-wt vs Ref
chr02-115635091-115637285	DPP10	chr02:115636612-115636656	NMI-wt vs Ref
chr2:119329502-119332035	EN1	chr02:119330694-119330738	NMI-wt vs Ref
chr02-156892636-156892878	NR4A2	chr02:156892639-156892683	MI vs Ref
chr02-156893736-156894685	NR4A2	chr02:156894489-156894533	NMI-mt vs Ref
	NR4A2	chr02:156894576-156894620	NMI-wt vs Ref

chr02:171384729-171385226	GAD1	chr02:171384729-171384773	MI vs Ref
	GAD1	chr02:171385019-171385063	NMI-mt vs Ref
	GAD1	chr02:171385019-171385063	NMI-wt vs Ref
chr2:172653235-172653630	MAP1D	chr02:172653288-172653332	NMI-wt vs Ref
chr2:174907710-174910885	FLJ46347	chr02:174910857-174910905	NMI-wt vs Ref
chr2:176652334-176656692	EVX2	chr02:176655532-176655591	NMI-mt vs Ref
	EVX2	chr02:176656139-176656183	NMI-wt vs Ref
	EVX2	chr02:176656517-176656563	MI vs Ref
chr2:176720618-176720921	hsa-mir-10b	chr02:176720535-176720594	NMI-mt vs Ref
	hsa-mir-10b	chr02:176720535-176720594	NMI-wt vs Ref
chr02:176737610-176738187	HOXD3	chr02:176737609-176737653	NMI-mt vs Ref
	HOXD3	chr02:176737609-176737653	NMI-mt vs MI
	HOXD3	chr02:176738050-176738094	NMI-wt vs Ref
	CENTG2	chr02:236438664-236438711	NMI-wt vs Ref
chr3:11721578-11721824	VGLL4	chr03:011721492-011721547	NMI-wt vs Ref
chr3:12983649-12984210	IQSEC1	chr03:012983600-012983644	NMI-wt vs Ref
chr3:25680561-25681574	TOP2B	chr03:025681366-025681410	NMI-wt vs Ref
chr03:129688131-129694023	GATA2	chr03:129692644-129692688	MI vs Ref
	GATA2	chr03:129698463-129698509	NMI-wt vs Ref
chr03:148591199-148594390	ZIC4	chr03:148592447-148592499	NMI-wt vs Ref
chr3:148613030-148613264	ZIC1	chr03:148613058-148613102	NMI-mt vs Ref
	ZIC1	chr03:148619483-148619541	NMI-wt vs Ref
chr4:4910534-4911092	MSX1	chr04:004910620-004910670	MI vs Ref
	MSX1	chr04:004910620-004910670	NMI-mt vs Ref
	MSX1	chr04:004910620-004910670	NMI-wt vs Ref
chr4:30330303-30333940	PCDH7	chr04:030333744-030333788	NMI-mt vs Ref
	PCDH7	chr04:030333834-030333878	NMI-wt vs Ref
chr4:41678680-41678940	WDR21B	chr04:041678597-041678646	NMI-wt vs Ref
chr4:85636684-85639823	NKX6-1	chr04:085637474-085637518	NMI-wt vs Ref

chr4:94974810-94975333	ATOH1	chr04:094974874-094974918	NMI-wt vs Ref
chr04:111780013-111780343	PITX2	chr04:111780048-111780092	NMI-mt vs Ref
	PITX2	chr04:111780288-111780343	NMI-wt vs Ref
	PCDH10	chr04:134291474-134291518	NMI-wt vs Ref
	NR3C2	chr04:149586403-149586447	NMI-wt vs Ref
	TRIM2	chr04:154436244-154436288	NMI-wt vs Ref
chr04:155881084-155881434	LRAT	chr04:155881084-155881128	NMI-wt vs Ref
	LRAT	chr04:155881330-155881378	NMI-wt vs MI
	HAND2	chr04:174687934-174687985	NMI-wt vs Ref
chr4:184255825-184258373	FLJ30277	chr04:184255924-184255968	NMI-wt vs Ref
chr5:360287-360592	PDCD6	chr05:000360593-000360637	NMI-wt vs Ref
chr5:1161803-1162051	SLC12A7	chr05:001162056-001162100	NMI-wt vs Ref
chr5:3647468-3656054	IRX1	chr05:003654466-003654525	NMI-wt vs Ref
chr5:5192442-5193941	ADAMTS16	chr05:005192514-005192558	NMI-wt vs Ref
chr5:6790705-6791004	POLS	chr05:006790682-006790728	NMI-wt vs Ref
chr5:54554812-54555385	UNG2	chr05:054555175-054555219	NMI-wt vs Ref
	UNG2	chr05:054555391-054555442	NMI-mt vs Ref
chr5:114542616-114544119	TRIM36	chr05:114542773-114542817	NMI-wt vs Ref
chr05:115810975-115811393	SEMA6A	chr05:115811349-115811393	NMI-wt vs Ref
chr5:127899858-127900162	FBN2	chr05:127900012-127900056	NMI-wt vs MI
	FBN2	chr05:127900012-127900056	NMI-wt vs NMI-mt
	FBN2	chr05:127900101-127900154	NMI-wt vs Ref
chr05:134390896-134393045	PITX1	chr05:134390896-134390940	MI vs Ref
	PITX1	chr05:134390896-134390940	NMI-wt vs Ref
	PITX1	chr05:134391093-134391137	NMI-mt vs Ref
	TRPC7	chr05:135720277-135720321	NMI-wt vs Ref
chr05:140724146-140724826	PCDHGA5	chr05:140724562-140724606	NMI-wt vs Ref
chr5:140780945-140781256	PCDHGA11	chr05:140781192-140781236	NMI-wt vs Ref
	PCDHGA12	chr05:140791316-140791360	NMI-mt vs Ref

	PCDHGA12	chr05:140791441-140791494	NMI-wt vs Ref
chr5:141235749-141238152	PCDH1	chr05:141237048-141237094	NMI-wt vs Ref
chr05:174091287-174092335	MSX2	chr05:174091297-174091341	NMI-wt vs Ref
	MSX2	chr05:174091410-174091454	MI vs Ref
	MSX2	chr05:174091473-174091517	NMI-mt vs Ref
chr6:1326743-1330210	FOXF2	chr06:001329813-001329866	NMI-mt vs Ref
	FOXF2	chr06:001329813-001329866	NMI-wt vs Ref
chr06:1549606-1560865	FOXC1	chr06:001551371-001551415	NMI-mt vs Ref
	FOXC1	chr06:001551429-001551473	NMI-wt vs Ref
	FOXC1	chr06:001551500-001551559	MI vs Ref
chr6:5947471-5950124	NRN1	chr06:005947569-005947613	NMI-wt vs Ref
chr6:10498025-10498551	TFAP2A	chr06:010498473-010498517	MI vs Ref
	TFAP2A	chr06:010498473-010498517	NMI-wt vs Ref
	TFAP2A	chr06:010498811-010498870	NMI-mt vs Ref
chr6:22677564-22678684	HDGFL1	chr06:022677587-022677632	MI vs Ref
	HDGFL1	chr06:022677587-022677632	NMI-mt vs Ref
	HDGFL1	chr06:022677587-022677632	NMI-wt vs Ref
chr6:25834434-25834701	HIST1H2AA	chr06:025834650-025834695	NMI-wt vs Ref
	HIST1H2BA	chr06:025840937-025840981	NMI-wt vs Ref
chr6:41176454-41177326	NFYA	chr06:041177112-041177165	NMI-wt vs Ref
chr6:50895246-50896050	TFAP2B	chr06:050896068-050896112	NMI-wt vs Ref
chr6:75968300-75968853	COL12A1	chr06:075968669-075968713	NMI-wt vs Ref
chr06:101023927-101024343	SIM1	chr06:101024299-101024343	NMI-mt vs Ref
	SIM1	chr06:101024299-101024343	NMI-wt vs Ref
chr6:101953488-101953856	GRIK2	chr06:101953514-101953560	NMI-mt vs Ref
	GRIK2	chr06:101953514-101953560	NMI-wt vs Ref
chr6:108592365-108597232	NR2E1	chr06:108595517-108595561	NMI-wt vs Ref
chr6:126122028-126122524	HEY2	chr06:126122132-126122176	NMI-wt vs Ref
chr6:166499964-166503413	T	chr06:166502963-166503011	NMI-wt vs Ref

chr6:169801163-169801511	WDR27	chr06:169801059-169801108	NMI-wt vs Ref
chr7:1029023-1029492	hsa-mir-339	chr07:001029489-001029533	NMI-wt vs Ref
chr07:2082782-2083345	MAD1L1	chr07:002083155-002083200	MI vs Ref
	MAD1L1	chr07:002083155-002083200	NMI-wt vs Ref
	MAD1L1	chr07:002121288-002121332	NMI-mt vs Ref
chr07:2724511-2724848	AMZ1	chr07:002724511-002724555	MI vs Ref
	AMZ1	chr07:002724511-002724555	NMI-wt vs Ref
	AMZ1	chr07:002724629-002724673	NMI-mt vs Ref
chr07:8449587-8450236	NXPH1	chr07:008449587-008449636	NMI-mt vs Ref
	NXPH1	chr07:008449587-008449636	NMI-wt vs Ref
	NXPH1	chr07:008450192-008450240	MI vs Ref
chr7:19113449-19113833	TWIST1	chr07:019113860-019113907	NMI-wt vs Ref
chr7:27149139-27152087	HOXA5	chr07:027150566-027150625	MI vs Ref
	HOXA5	chr07:027151311-027151355	NMI-mt vs Ref
chr07:27164708-27165039	HOXA7	chr07:027164869-027164913	MI vs Ref
	HOXA7	chr07:027164869-027164913	NMI-mt vs Ref
	HOXA7	chr07:027164944-027164988	NMI-wt vs Ref
chr7:27170441-27172987	HOXA9	chr07:027170467-027170515	NMI-mt vs Ref
	HOXA9	chr07:027170467-027170515	NMI-wt vs Ref
	HOXA9	chr07:027170998-027171042	MI vs Ref
chr7:27198331-27199622	HOXA11	chr07:027198283-027198327	NMI-wt vs Ref
chr07:27219187-27220360	EVX1	chr07:027245650-027245694	NMI-wt vs Ref
chr07:27251165-27252762	EVX1	chr07:027251482-027251527	MI vs Ref
chr7:35263447-35264743	TBX20	chr07:035263668-035263712	NMI-wt vs Ref
chr7:96469320-96469736	DLX6	chr07:096469212-096469266	NMI-mt vs Ref
	DLX6	chr07:096469526-096469572	MI vs Ref
	DLX6	chr07:096469776-096469827	NMI-wt vs Ref
chr07:96488158-96489591	DLX5	chr07:096489129-096489173	NMI-mt vs Ref
	DLX5	chr07:096489475-096489520	MI vs Ref

	DLX5	chr07:096489536-096489591	NMI-wt vs Ref
chr7:119702299-119702721	KCND2	chr07:119702676-119702723	NMI-wt vs Ref
chr07:121727243-121727884	FEZF1	chr07:121727241-121727285	NMI-wt vs MI
	FEZF1	chr07:121727336-121727380	NMI-wt vs Ref
chr07:155288454-155292175	SHH	chr07:155291537-155291581	MI vs Ref
	SHH	chr07:155291593-155291637	NMI-mt vs Ref
	SHH	chr07:155291751-155291795	NMI-wt vs Ref
chr7:158509937-158510390	VIPR2	chr07:158509989-158510033	NMI-wt vs Ref
chr08:9798161-9799053	hsa-mir-124a-1	chr08:009798455-009798508	NMI-wt vs NMI-mt
	hsa-mir-124a-1	chr08:009798593-009798644	NMI-wt vs Ref
	hsa-mir-124a-1	chr08:009800023-009800077	NMI-wt vs MI
chr8:10624024-10624296	SOX7	chr08:010624244-010624300	NMI-mt vs Ref
	SOX7	chr08:010624319-010624366	NMI-wt vs Ref
chr8:11597006-11600365	GATA4	chr08:011599544-011599588	NMI-wt vs Ref
chr8:25955253-25955609	EBF2	chr08:025955446-025955495	NMI-mt vs Ref
	EBF2	chr08:025955446-025955495	NMI-wt vs Ref
chr8:55532724-55535078	SOX17	chr08:055533948-055533992	NMI-wt vs Ref
chr08:65661156-65662687	BHLHB5	chr08:065661235-065661282	NMI-wt vs MI
	BHLHB5	chr08:065662258-065662302	NMI-wt vs Ref
chr8:72916429-72917309	MSC	chr08:072917197-072917241	MI vs Ref
	MSC	chr08:072917336-072917380	NMI-wt vs Ref
chr8:140700279-140700514	KCNK9	chr08:140700520-140700564	NMI-wt vs Ref
chr08:142288380-142288718	SLC45A4	chr08:142288398-142288442	NMI-mt vs Ref
	SLC45A4	chr08:142288610-142288657	MI vs Ref
	SLC45A4	chr08:142288610-142288657	NMI-wt vs Ref
chr8:145014900-145015187	EPPK1	chr08:145015195-145015240	NMI-wt vs Ref
chr9:959530-963276	DMRT3	chr09:000959621-000959665	NMI-wt vs Ref
chr9:21979774-21980108	CDKN2A	chr09:021979951-021979995	NMI-wt vs Ref
chr9:23812413-23812667	ELAVL2	chr09:023812373-023812424	NMI-wt vs Ref

chr9:37024136-37028341	PAX5	chr09:037024964-037025008	NMI-wt vs Ref
chr9:101621613-101627382	NR4A3	chr09:101627386-101627439	NMI-wt vs Ref
chr10:7489383-7495345	SFMBT2	chr10:007491431-007491476	NMI-wt vs Ref
	SFMBT2	chr10:007491576-007491626	NMI-wt vs NMI-mt
chr10:13556172-13556753	C10orf30	chr10:013556159-013556211	NMI-wt vs Ref
chr10:15294605-15294858	C10orf38	chr10:015294592-015294641	NMI-wt vs Ref
chr10:21828640-21829645	C10orf114	chr10:021828885-021828929	NMI-wt vs Ref
	C10orf114	chr10:021828954-021828998	NMI-mt vs Ref
	C10orf114	chr10:021829373-021829417	MI vs Ref
chr10:76825135-76839606	ZNF503	chr10:076834917-076834976	NMI-wt vs Ref
	ZNF503	chr10:076837381-076837425	NMI-mt vs Ref
chr10:88112905-88117344	GRID1	chr10:088115612-088115656	NMI-wt vs Ref
chr10:94441310-94441717	HHEX	chr10:094441395-094441439	NMI-mt vs Ref
	HHEX	chr10:094441744-094441795	NMI-wt vs Ref
chr10:99068802-99071038	FRAT1	chr10:099070245-099070298	NMI-wt vs Ref
	FRAT1	chr10:099070376-099070420	NMI-mt vs Ref
chr10:101277153-101277910	NKX2-3	chr10:101277900-101277957	NMI-wt vs Ref
chr10:102974173-102980053	LBX1	chr10:102975940-102975999	NMI-wt vs Ref
	LBX1	chr10:102976227-102976273	NMI-wt vs MI
	LBX1	chr10:102976227-102976273	NMI-wt vs NMI-mt
chr10:106389558-106392802	SORCS3	chr10:106392567-106392611	NMI-wt vs Ref
chr10:124891898-124892607	HMX2	chr10:124892023-124892067	NMI-wt vs Ref
chr10:128863581-128864054	FLJ45557	chr10:128864100-128864145	NMI-wt vs Ref
chr11:22319439-22319953	SLC17A6	chr11:022319657-022319701	NMI-wt vs Ref
chr11:31776637-31777992	PAX6	chr11:031776609-031776653	NMI-wt vs Ref
chr11:68274244-68274755	MTL5	chr11:068274304-068274348	NMI-mt vs Ref
chr11:117983446-117987106	PHLDB1	chr11:117984800-117984844	NMI-wt vs Ref
chr12:1844001-1845219	CACNA2D4	chr12:001844114-001844158	NMI-wt vs Ref
chr12:40253533-40253742	PDZRN4	chr12:040253480-040253529	NMI-wt vs Ref

chr12:52726910-52727810	HOXC4	chr12:052727781-052727833	NMI-mt vs Ref
	HOXC4	chr12:052727781-052727833	NMI-wt vs Ref
chr12:79634857-79635257	MYF5	chr12:079634813-079634857	NMI-wt vs Ref
chr12:94776044-94776377	SNRPF	chr12:094776044-094776094	NMI-wt vs Ref
chr12:95164929-95165298	ELK3	chr12:095165171-095165220	NMI-wt vs Ref
chr12:113657930-113659205	TBX5	chr12:113325125-113325174	NMI-wt vs Ref
chr12:113609113-113609535	TBX3	chr12:113609153-113609207	MI vs Ref
	TBX3	chr12:113609259-113609303	MI vs NMI-wt
chr13:34950488-34951119	MAB21L1	chr13:034950488-034950532	MI vs Ref
	MAB21L1	chr13:034950709-034950765	NMI-wt vs Ref
	MAB21L1	chr13:034950955-034950999	NMI-mt vs Ref
chr13:35817738-35819004	SPG20	chr13:035817882-035817927	NMI-mt vs MI
chr13:57101588-57102323	PCDH17	chr13:057101685-057101729	NMI-wt vs Ref
	PCDH17	chr13:057105585-057105629	NMI-mt vs Ref
chr13:94152191-94153185	SOX21	chr13:094152286-094152330	MI vs Ref
	SOX21	chr13:094152463-094152507	NMI-mt vs Ref
	SOX21	chr13:094152463-094152507	NMI-wt vs Ref
chr13:105943410-105943788	EFNB2	chr13:105943362-105943406	NMI-mt vs Ref
	EFNB2	chr13:105943488-105943532	NMI-wt vs Ref
chr13:111763361-111764235	SOX1	chr13:111764262-111764315	NMI-wt vs Ref
chr13:112249708-112249928	TUBGCP3	chr13:112249984-112250030	NMI-wt vs Ref
chr14:19992581-19993863	APEX1	chr14:019993551-019993604	NMI-mt vs MI
chr14:23710894-23712060	REC8L1	chr14:023711936-023711980	NMI-mt vs Ref
chr14:28317076-28317375	FOXG1B	chr14:028317289-028317343	NMI-wt vs Ref
chr14:33338698-33340189	NPAS3	chr14:033339869-033339913	NMI-wt vs Ref
chr14:36122289-36122589	NKX2-8	chr14:036122225-036122274	MI vs Ref
	NKX2-8	chr14:036123184-036123232	NMI-wt vs Ref
chr14:36205192-36206099	PAX9	chr14:036196442-036196486	NMI-mt vs Ref
	PAX9	chr14:036205602-036205647	MI vs Ref

	PAX9	chr14:036206112-036206171	NMI-wt vs Ref
chr14:37137198-37138958	FOXA1	chr14:037137114-037137159	NMI-wt vs Ref
	FOXA1	chr14:037137543-037137587	NMI-mt vs Ref
chr14:56347822-56348040	OTX2	chr14:056347712-056347756	NMI-wt vs Ref
chr14:60045486-60047933	SIX6	chr14:060046995-060047041	NMI-wt vs Ref
chr14:60173732-60174416	SIX1	chr14:060173710-060173754	NMI-mt vs Ref
	SIX1	chr14:060179528-060179574	NMI-wt vs Ref
chr14:98781593-98783184	BCL11B	chr14:098782637-098782681	NMI-mt vs Ref
chr15:50867751-50870991	ONECUT1	chr15:050870481-050870525	NMI-wt vs Ref
chr15:58083428-58085812	FOXB1	chr15:058084349-058084393	NMI-wt vs Ref
chr15:62984853-62985116	ANKDD1A	chr15:062984784-062984834	NMI-wt vs Ref
chr15:65902540-65909629	LBXCOR1	chr15:065908791-065908850	NMI-wt vs Ref
chr15:72206924-72210097	ISLR2	chr15:072206870-072206914	NMI-wt vs Ref
chr15:74414579-74414893	ISL2	chr15:074414745-074414789	NMI-wt vs Ref
chr15:88158407-88159577	ANPEP	chr15:088158433-088158477	NMI-wt vs Ref
chr15:94688798-94689131	NR2F2	chr15:094688839-094688885	NMI-wt vs Ref
	NR2F2	chr15:094688901-094688949	MI vs Ref
	NR2F2	chr15:094689087-094689131	NMI-mt vs Ref
chr16:727072-727328	NARFL	chr16:000727383-000727427	NMI-wt vs Ref
	CBLN1	chr16:047869472-047869516	NMI-wt vs Ref
chr16:52873104-52882105	IRX3	chr16:052879704-052879750	NMI-mt vs Ref
	IRX3	chr16:052879918-052879974	NMI-wt vs Ref
	IRX3	chr16:052880382-052880426	MI vs Ref
	IRX5	chr16:053528320-053528364	NMI-wt vs Ref
chr16:66071900-66072846	ATP6V0D1	chr16:066071973-066072017	NMI-mt vs MI
chr16:85098883-85102729	FOXF1	chr16:085098933-085098977	NMI-wt vs Ref
	CNTNAP1	chr17:038089272-038089316	NMI-mt vs Ref
	CNTNAP1	chr17:038089272-038089316	NMI-wt vs Ref
chr17:44074280-44075233	HOXB5	chr17:044026017-044026069	MI vs Ref

	HOXB5	chr17:044026017-044026069	NMI-wt vs Ref
	hsa-mir-196a-1	chr17:044074404-044074448	NMI-wt vs Ref
	hsa-mir-196a-1	chr17:044074457-044074501	NMI-mt vs Ref
chr17:58865328-58865618	CYB561	chr17:058865281-058865326	MI vs Ref
	CYB561	chr17:058865281-058865326	NMI-wt vs Ref
	CYB561	chr17:058865512-058865556	NMI-mt vs Ref
chr17:67627870-67631593	SOX9	chr17:067630891-067630945	NMI-wt vs Ref
chr17:71582000-71585125	GALR2	chr17:071583191-071583235	NMI-mt vs MI
chr17:75531280-75531546	TBC1D16	chr17:075531439-075531483	NMI-wt vs Ref
chr17:75936057-75936582	C17orf27	chr17:075936313-075936368	MI vs Ref
	C17orf27	chr17:075936313-075936368	NMI-wt vs Ref
chr17:76404186-76404427	KIAA1303	chr17:076404103-076404162	MI vs Ref
	KIAA1303	chr17:076404103-076404162	NMI-wt vs Ref
chr17:77537903-77538626	ASPSCR1	chr17:077538538-077538583	NMI-wt vs Ref
chr18:894579-899574	ADCYAP1	chr18:000899042-000899087	NMI-wt vs Ref
chr18:5186244-5187389	ONECUT2	chr18:053259508-053259552	NMI-mt vs Ref
	ONECUT2	chr18:053259508-053259552	NMI-wt vs Ref
chr18:68359955-68362770	CBLN2	chr18:068361299-068361343	NMI-wt vs MI
chr18:74837994-74842232	SALL3	chr18:074838538-074838582	NMI-wt vs Ref
chr18:75565313-75565933	CTDP1	chr18:075565319-075565363	NMI-wt vs Ref
chr19:898548-898981	ARID3A	chr19:000898650-000898694	NMI-wt vs Ref
chr19:4059891-4060207	MAP2K2	chr19:004059891-004059935	NMI-wt vs Ref
	MAP2K2	chr19:004060122-004060166	MI vs Ref
	MAP2K2	chr19:004060122-004060166	NMI-mt vs Ref
chr19:9131907-9132918	ZNF317	chr19:009132692-009132736	NMI-wt vs Ref
chr19:12985960-12986259	NFIX	chr19:012986040-012986084	NMI-wt vs Ref
chr19:42586165-42586705	ZNF569	chr19:042586544-042586592	NMI-wt vs Ref
chr19:55553586-55553895	NAPSA	chr19:055553837-055553881	NMI-wt vs Ref
chr19:57082654-57083180	ZNF577	chr19:057082979-057083023	NMI-wt vs Ref

chr19:60283718-60285792	EPS8L1	chr19:060285492-060285536	NMI-mt vs Ref
chr19:60907042-60907388	EPN1	chr19:060907107-060907151	NMI-mt vs Ref
	EPN1	chr19:060907320-060907364	NMI-wt vs Ref
chr19:62043096-62043807	PEG3	chr19:062043010-062043054	NMI-wt vs Ref
chr19:63321122-63322053	ZNF329	chr19:063321824-063321868	NMI-wt vs Ref
chr19:63420090-63420541	ZNF274	chr19:063420437-063420481	NMI-wt vs Ref
chr19:63784504-63785085	MGC2752	chr19:063784639-063784683	NMI-wt vs Ref
	MGC2752	chr19:063784804-063784848	MI vs Ref
	MGC2752	chr19:063784804-063784848	NMI-mt vs Ref
chr20:9444472-9444893	C20orf103	chr20:009444951-009444998	NMI-wt vs Ref
chr20:21433933-21444714	NKX2-2	chr20:021439947-021439991	NMI-wt vs Ref
chr20:22505518-22507240	FOXA2	chr20:022505822-022505866	NMI-wt vs MI
chr20:22510737-22514165	FOXA2	chr20:022505888-022505938	NMI-wt vs Ref
chr20:22514762-22515148	FOXA2	chr20:022507864-022507908	NMI-wt vs NMI-mt
chr20:23294035-23294650	GZF1	chr20:023294489-023294536	NMI-wt vs Ref
chr20:25011839-25013525	VSX1	chr20:025011908-025011952	NMI-wt vs Ref
chr20:35582018-35583550	NNAT	chr20:035582918-035582969	NMI-mt vs Ref
	NNAT	chr20:035582918-035582969	NMI-wt vs Ref
chr20:36785545-36790786	SLC32A1	chr20:036787891-036787941	NMI-wt vs Ref
chr20:38749965-38753401	MAFB	chr20:038753128-038753174	NMI-mt vs Ref
	MAFB	chr20:038753269-038753318	NMI-wt vs Ref
chr20:49542203-49542863	NFATC2	chr20:049542266-049542311	NMI-wt vs Ref
chr20:54012011-54014085	CBLN4	chr20:054013134-054013178	NMI-wt vs Ref
chr20:54411932-54412178	CSTF1	chr20:054412143-054412187	NMI-wt vs Ref
chr20:55680656-55681057	TMEPAI	chr20:055680906-055680952	NMI-wt vs Ref
chr20:56860125-56860442	GNAS	chr20:056860480-056860524	NMI-wt vs Ref
chr20:60061693-60062033	TAF4	chr20:060015181-060015225	MI vs Ref
	TAF4	chr20:060062094-060062139	NMI-wt vs Ref
chr20:62371744-62371958	PCMTD2	chr20:062371900-062371944	NMI-wt vs Ref

chr21:33316999-33322115	OLIG2	chr21:033318624-033318681	NMI-wt vs Ref
chr21:36990008-36995832	SIM2	chr21:036991619-036991663	NMI-wt vs Ref
	SIM2	chr21:036999107-036999151	MI vs Ref
chr21:43350621-43351134	HSF2BP	chr21:043902052-043902096	MI vs Ref
	HSF2BP	chr21:043902052-043902096	NMI-mt vs Ref
chr21:45511336-45511549	POFUT2	chr21:045511551-045511595	NMI-wt vs Ref
chr21:46892946-46893236	PRMT2	chr21:046893181-046893225	NMI-wt vs Ref
chr22:18453364-18453931	DGCR8	chr22:018453720-018453764	NMI-wt vs Ref

Table 7B. Sequences of differentially labeled CGIs between bladder cancer subgroups relative to blood

CGI: 561 range=chr1:63554983-63563059
 CGGGCAGGCCCAAGCTGCGATGTGGAGAATTCGATGTCCGAGCGACCTCCTCGGAGGAGTGGGTTCGAGTTAAATATAACCGCGCAATGGAATGGCGCTAAAAATAAGGCAGCAGCTGGCCTGTCCACAGCCCTGTCCCGGAGGGGCGGGGGGGCCAGTGGTCTTGGGCAGGAAGGCCGCGTCCGGCCAGGGGCGAGAAGGCTGCGGCGTCCGCAGCAGGGCTGGAAGGCCTGGGAGGCCGCGCTCTGTGGGCCCGGGGCTCCATTCCGGCTGGGTGCGGGGCTGGACGGGACTGTCCAGAGGCATCCGAAAGCCAGGCCAACTTGCCTGGACGTAACAAGACGGAAGGGCTGGGCGCTGAGGTCTGTCCAGCCCGGCCCGCCAGAGGGAGCTGAGCGCCAGAGGAGGACAAGCCGAACCCCTTCAGGAGGCCGGGCGTCTCCGGAGACCGAAGCGCCGGAGGACCCGAGGAGGTCTGCCCGCGCGCTGCTCTGGAGACTCCCGGGGGGTGGCGCTCGGCCCTTCCGCTCCCTTCCCAACAAGTCCCTTCCCGCGCGCGCCACAGGCCCTGCCCCCTCCCGCTCAGCGCCCCAACCGTCAAGCCAGCAATTGAAACGTTTCCAAAACGGTCTATTTATTGCTCCCAATAAATCGATCGGCGGTGATTAAAGAATCGATGTGGCTGGGTGGGCGAGTCCGTTGAGGGGAGGGATGGGGGCTTTTCGCCCGCGCTGCGAGGAGGCCGAGGGCGGGCGCGGGCTGAGGGAGGCGTTCGCCCGCGGCCACACCCGAGGACCCGACACCTGGGCTGGCAGGCCCGCGCAGGCAGCGTTCCCTCCGGCGGAGAGGGGCGCGCGCCCGCGCTGCTTTCCTCGGCCCTCTCGCCTTTCTCGCGCGCGGGGAGGCTGTGGCCGCCAGTGGCTGCGGAGCTGCTCAGAGGCTTTTGTGCTCCTCGGCCGCTGAATGGGGATTTTGTAAAGCGGGACAGATAAAAATGAGCAGCATCATATTGTTTGACAGAATGATCTCGCATGATGAAGTGTGGCTCCGAAGGGGTGAAAATGGTGAATTCCTAAAAACCCAGCCCTGGGCTCCTCTCGAGCTGCCGGTAGCCTGGAGGGACCCAGCGGACAGCCGGCCTGGCCGATCGCTCCAAACGGTGTGAGAAAGACTCCGGCTTTCAATGCCAAGTCATTTTAAAGCCCCGATCCTGTCCAGGACCTTTCTCCTCGTGGATGAAAAGAACAATTTTCGAGAGAAAGGCTCGTTTTTATTAAATCCGACATGCTGCTGATAACTCCATGCTAATGTGAAATAATTAACATAATAGCCATAATTAAAGCACGCTAACAAATGCCATAAATTTATCACACAATTTTACTAGCTTTCTGCCCTTAACGCTCTCTCATCGTTAATTAACGTTGTTGCCTTTTACAGAATGGATGTTTATATATTTTCCAATATAAATAAATTCGAAACCATCCTCTCTCTCTCTCTTCTCTCTCTCTCTCTTTTGGTCTCTCGCCATTACAGGCACGCTTGGCGTGGACCTGAGTGGCAGACATCTTGAAAATAAATGAAGTTTGGAGATGCAATCCAAACAAGAACATTAAAATAGCCTCTTTTTTCCACCCCGAAGAGATCCGGAGAGGTATACAAGGGGTAGTGGTGGGTAGAGAGTTGAAAATCCCCGCTTTGGGAAATGGAAGTAATCTGGGTGGGTGGGGCCTTGGGTACCACCTCTGCCCTTTCCACCTTCCCTGGTGGCGGCCATCCAGACAAAAGAGCCGGTAATAGTTTAAACAATCTATGAAGATTTCAAGAAGCAGCAGACTTTGATTGTTGGGGCGCGGGGTGTTGGGGAGAAAGGAGGGGAATTTTCTAATAGTCCCACCCACGTTTGTCTCCTCTTGGACAAAAGAGTAATCTTGGTGGGGGACGCGCCCTTCTACTCCGCGGAACCTGGTCCCAACTCCCCGATTGTAAAGAAAGTGCACCCCGCGCGGGCATGATGATTCTATCTCACATCGCGCCAACGACTATTCAAGCCACTGGCACTGTCTCTGACTTAAAGAGGAGAGAAAGAGGCATATGGGTTCACTTGGGCTGGTGGGGGTAGGTGGGCAATTCCCGCTTCCGCACTCTAACCGTGCCCTCCTCCAGTGTGACCACTAAGAACCACAAATGTAATTAATTTCCCTTTCTCCATCATAAATTTTCTATCCATTTCTTCCCCCATCCCCCACTGGACGCACACATAAATCTCCCCCTCCCCGAGAGCTCTCAATTTCTTCTCTATCGATCCGGACTCCATTCTTCTTGGCTCTGTGCTAGAACCTTAGATCCCCCACTCCCCGCACCCCTCATTTCCACCGCGTCCAGGTGGCTTCCCAGCGGGGTACCATGTACTCTGCCGCTCCAGAGGAACCGAAGGGGTTTCATTCCATTCTCCTTTGGTTGAAACATTTCAAACATTTGACAGGTGAGGCAGCTGGCTGCCATCTTCTTTTTTAAATCTCTCCTGGGAAGTTGCTTGTGAGACTCAAAGAGTCACTCAAACTCATAATTGCGTGTGTGTCTACTCATTCTCCCTCTATCTCTCCAATAACCCCTTTGAGACTCAGAACTTTTTATCCACATACACCCTTTATCACATTTTCTTCCCCCACTACATGTGTCTCACTTTCTCTCTGTATCTGTCTCGCTTCTTCCGTCTCTGTCTACAGCTTGGCGGTAACGACGACCTGTGAGCTTTTAGCTGCAAACTGCAACTACGCGGCAACAATTTATTTAGCCCGACATCTAGCCGGTCTCCGGCAGGACCCCTGCACCCGCTCGGGATCGGACCCCTTCCGCTGGGGCGGCTCTCGCTCAAGGCCAGCAGGAACCTTCTGTGCGCTCCCCGGCCGCCGCTTCCGCTCCTTCCCCGCCCGGAGGTGTGTCAGGCGCTATGGTCCGCTTGGAGGAGAAAGCCGGCGGCCGCTTCTGAGCCGAGAGCGGCCGCGGAAAAATCCTCTGCTCCGCTGGAAATCGATATTAGGCCGGCGCGGGCGGGGACGTGGGGCCGCGAGCCAGTAGGTGTGTCACGCTCATCATTTAGCTAATCGAGTCGAAAAGTTTCTGTAAGGGCCGACCCAGCATCAGATGGTAACACTGATTGAACAAGAGATTAGCACAAATAGATCTCTAACCAGGGGAAGCGTTGCTTTTACGCTACGCGCCGTAATTAATGGTATGAATCAATTAATTGACTTTTATTGTGTCGAAGGAAAAAAGCGCAACAATGGAACCGCAGCTGGGAGTTGTTGCTCTCCACCCCTTCCCCAGGGAGTTCCAAGGAGACACCGGGGAATGGACGGATCAGGCTGGGCCGTGGCAGAGGGAGGGTAGGAGGCAGCGACCAAGCAGCTGGAGGGAGTCCAGAGAGCTAGCCTCTGCGGACGGCGGAATCGAAATTAGGCTCATTGGAGACTACTTTCAGACCCGTGAGGGGAGCCCTGTAGCCACCATCTCCGGCGCGCATCCACACATACTAGTCCACGCGGGCCAGCCACCAAGGCCGCGGCGAGGGCCAGCGCTGCGCCCCGGGCCCCCTGCCTTTAGGGGTGGGCAACCCAGCAGAGCAAAGGAGGTTCTGAATGTGTAAATTTCCGCTTTTTTAGCTTTTTTTTTTTTTTTTTTGGACCTTCCGA

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CGI: 58 range=chr1:196153712-196154414
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[illegible]

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CGI: 173 range=chr2:119329502-119332035

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CGI: 295 range=chr2:174907710-174910885

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Table 8. PcG target genes methylated in all bladder tumors or specific subgroups.

All	NMI-wt only	NMI-mt only	MI only	NMI-mt and NMI-wt	MI and NMI-wt	MI and NMI-mt
DLX5	ADCYAP1	BARHL2	TBX3	CNTNAP1	EVX1	HOXA5
DLX6	ATOH1	BCL11B		EBF2	GATA2	
FOXD2	BHLHB5			FOXA1	HOXB5	
GAD1	C20orf103			FOXD3	MSC	
HLX1	CACNA2D4			HHEX	NKX2-8	
HOXA7	CBLN1			HOXC4	SIM2	
HOXA9	CBLN4			HOXD3	VAX2	
IRX3	CDKN2A			MAFB		
MAB21L1	COL12A1			ONECUT2		
MEIS1	COL27A1			OSR1		
MSX1	CYP26B1			PCDH17		
MSX2	DMRT3			PCDH7		
NR2F2	DPP10			PITX2		
NXPH1	ELAVL2			SIM1		
OTX1	EMX1			SIX1		
PAX9	EN1			SOX7		
PITX1	FBN2			UNG2		
PRKCZ	FEZF1			ZIC1		
SHH	FLJ46347			ZNF503		
SIX3	FOXA2					
SOX21	FOXB1					
TFAP2A	FOXF1					
	FOXG1B					
	GATA4					
	GNAS					
	GRID1					
	GZF1					
	HAND2					
	HEY2					
	HMX2					
	HOXA11					
	IRX1					
	IRX5					
	ISL2					
	ISLR2					
	KCNK9					
	LBX1					
	LBXCOR1					
	LHX4					
	LHX9					
	LMX1A					
	LRAT					
	MAP1D					
	NFIX					
	NKX2-2					
	NKX2-3					
	NKX6-1					
	NPAS3					
	NR2E1					
	NR3C2					
	NR4A3					
	NRN1					

TABLE 8 Continued

All	NMI-wt only	NMI-mt only	MI only	NMI-mt and NMI-wt	MI and NMI-wt	MI and NMI-mt
	OIG2					
	ONECUT1					
	OTX2					
	PAX5					
	PAX6					
	PCDH1					
	PCDH10					
	PHLDB1					
	PTGER3					
	SEMA6A					
	SFMBT2					
	SIX2					
	SIX6					
	SLC32A1					
	SNRPF					
	SORCS3					
	SOX17					
	SOX9					
	T					
	TBX15					
	TBX20					
	TBX5					
	TFAP2B					
	TRIM2					
	TRIM36					
	TWIST1					
	VIPR2					
	VSX1					
	ZIC4					

TABLE 9. CpG islands (CGIs) methylated in blood but not in bladder cancer. Provided for each are: ID no.; Coordinates of selected regions containing relevant CpG islands based on Homo sapiens full genome as provided by UCSC (hg18, Mar. 2006); GeneName; Location of the probe used; the Fold Change; and the sequence of the CGIs.

No	CGI	Gene Name	CGI probe location	FC
1	chr19:53930240-53930625	RASIP1	chr19:053930330-053930374	2.66
2	chr7:72883371-72883981	CLDN4	chr7:072883457-072883501	2.64
3	chr22:26522794-26528592	MN1	chr22:026525238-026525282	2.21
4	chr7:5614184-5614510	FSCN1	chr7:005614143-005614190	2.15
5	chr16:66239477-66241425	RLTPR	chr16:066241103-066241147	1.93
6	chr5:551112-551430	SLC9A3	chr5:000551380-000551424	1.86
7	chr19:6426223-6426998	DENND1C	chr19:006427051-006427102	1.82
8	chr3:32836146-32836433	TRIM71	chr3:032836466-032836511	1.78
9	chrX:129301145-129301626	SLC25A14	chrX:129301313-129301357	1.76
10	chr9:124027565-124030907	LHX6	chr9:124029663-124029718	1.74
11	chr10:129424401-129427356	FLJ46831	chr10:129426989-129427033	1.71
12	chr1:3147370-3148160	PRDM16	chr1:003147944-003147988	1.65
13	chrX:128941527-128945710	BCORL1	chrX:128944842-128944886	1.64
14	chr17:7584523-7585036	DNAH2	chr17:007584859-007584908	1.63
15	chr1:27548507-27550603	SYTL1	chr1:027550188-027550232	1.6
16	chr19:10304689-10307022	ICAM3	chr19:010306004-010306051	1.56
17	chrX:129132628-129134108	AIFM1- RAB33A	chrX:129133196-129133244	1.55
18	chr21:45648960-45650662	COL18A1	chr21:045663489-045663539	1.53
19	chr10:134864694-134865392	KNDC1	chr10:134865054-134865098	1.48
20	chr9:129556229-129557670	SH2D3C	chr9:129556146-129556190	1.48
21	chrX:47305347-47306043	ARAF	chrX:047305953-047305997	1.45

Sequence of the CGIs of

1 chr19:53930240-53930625

CGTGGGGGCTGGGGCGGGCGGTTACCTGGGCGTCTGGTAGCCCTGGAGCAGCAGGAAGTAGGGGCGGTTGCTG
GGGGCCTGGATGAGGCACTGAGTCAAACTGATCGAAGTCCCCGGGGTCTGCAGTTCCGATTTGGGCGTCCGGCTGCC
CCTGGGGCCATGCTAAGTGCCCTGCTGTCTCCGCTCCTGCTGCCGCCGCCGCCGCCCTGAAGGCTAAGCTCCGAC
ACGCTGCGCCGCAAAGACAAGTTTCTGAGCGCTCCTTGCCCTCCAGACCCAGCTGGGGCCCCGTATCCGGTCCCC
GGGCCAGGACTGGCCAGCGCTGCCCCACCGACGCCGCCCGGGAGCGGTTCTTCTGTGGCCGCCACGAAGGGGG
GCCGGTGCCCTGGC

2 chr7:72883371-72883981

CGAAGCTTAAGTCCGTCCCCAGCGCTTGAATCCTACGGCCCCACAGCCGGATCCCCTCAGCCTTCCAGGTCCT
CAACTCCCGTGGACGCTGAACAATGGCCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGGCCGTCTGGGCTG
GCTGGCCGCTATGCTGTGCTGCGCGCTGCCATGTGGCGCGTGACGGCCTTCATCGGCACCAACATTGTCACCTC
GCAGACCATCTGGGAGGCCTATGGATGAACTGCGTGGTGCAGAGCACGGGCCAGATGCAGTGCAAGGTGTACG
ACTCGCTGCTGGCACTGCCCGCAGGACCTGCAGGGCGGCCGCCCTCCTCATCATCAGCATCATCGTGGCTGCTC
TGGGCGTGTGCTGTCCGTGGTGGGGGGCAAGTGTACCAACTGCCTGGAGGATGAAAGCGCCAAAGGCCAAGACC
ATGATCGTGGCGGGCGTGGTGTTCCTGTGTGGCCGGCCTTATGCTGATAGTGCCGTGTCTGGACGGCCCAAC
ATCATCCAAGACTTCTACAATCCGCTGGTGGCCTCCGGGCAGAAAGCGGGAGATGGGTGCCTCGCTCTACGTGGG
TGGGCGCCCTCCG

3 chr22:26522794-26528592

CGCCAACGCTTGTCTGTCCTCCGCGCTGTCCACCAGGGGCTTGTTCAGCGGGCATGTACCAGGCAGCGCTGTGCTC
 TGCCATCAGCGAGTCCAGGTCAATGGTGCTCATGGCGCTCTTGACCGCTCGGAGCAGCAGCTGCCAGCTCGCT
 GTCGCCATTCTGCGCCCTGAGGCCCCGACGGCGCACTACCCCTTCTTGCCACCTTCAGCCCCAGAGCTGGTC
 CTCGGAGATGCTGAACCTGCTGCTCTGTAGCTGGATCTGCGCCTGAAGGATCTCCAGGGGGTGGATCTCGTCGGG
 TGGCGGGGCGCCGCTGCTGCTCTCGGGTGGGACCTGCTCCAGGCCCGAGTGCCCGGATGCCCGGGGCCCC
 CACCGCCCGCTAGCTGTACAGGGTTCGAGGTAGAGTTAGACATGATGCCAGGCCGAGGGCGGGCGGGGCGCC
 TTCGGTCCGTGTTCCCGGGCGCTACCCACGGGGAGGGAGTTTGGGCGAGCCGGTACCAGGGGACTCCTGCTC
 GCTTAACTAGTGCCTGGGGTTGTACAGAGCTGGACGACACCTCGTCTCATTGGCGTAGCTCGTGCTCACTCG
 TCCGAGGCCAACTACCCACGTTTGGCGAACTACTGTCCGACTTGGCCCCCGCTCCAGGGACCCAATGAGGTCC
 GGCTGATCCCCAGGAGCAACTCAGCCCCCTTCCCCAGGATGGCGACGTGAGCGCCTTTTCGTGGGGCGTCGGT
 GCCCGCGCGTCTCGCTGCGGAGCTTCCCCGACGGCTCGCCTGACGCTTGTCTGCCCTGACCCCA
 GGTGGCCCCCGCTGTCCGGAGCCGCGGACTACTGTCAAAGAAGGTGCCAGGGCTCAGCTGACCTGACCTCTT
 TTTCTGCGACCCCGTCCCGCGCCGCCGCCCGGAGACCGGCTTGCGCTCATTCCCGACGTGGATTCCAGGGTG
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 ACTGGTCCCGGACGGGCTCCGGGTCTGGGGCCCCAGGAGCAGTCCCTCTCTGGGAAGTAATCCGAGCCCGGGT
 TGCCGGCCACTGCGCGCCGCTCGGTCTCGTTCTGGCTCAGTTTCTCTTGGCCTCTGGCGGGTCTCTTGTGTGAA
 GGTACGTTGAGGTTGGGGGCCCGAGGCTGGCGATCATGTTCTGGCAAGCGGTGGAGAGCGCAGCCAGGCAGC
 TCTGGCCGAACAGGTTGTCTTGGAGCTGGGCTTGTGTAAGGAGCCAGCGAGAGCGCGCCCAATTTACTGGCCG
 AGGTGCGCTGCTGGGCTGGAAATCAGGCTGCGGCGGCTAGGCACCCCGCCACCGCCGCCACCAGAGCTGCCA
 CCGCCCCCTCCCGCGCTGGGGGGCGAGTTACAGCCTGGACCGCTGTGGCGGCTGGACTGCCGGCCGGTGCACC
 AAACGGAAAGCCCGCTGGCCCCCGAGCCAGACGTAGCAAAAGTCCGGCGCGGGGGCGCGCGCTCCGAAAGCAG
 CGCTGGGGAGCCCCACGCCCGCCCGGGCGACTGCAGCTGACCCAGGCTCCAGACTGCCCCGAACTGCAGG
 CCGGCTGAAGGCAGCGCGCGGACGCTGGCCCTCTCCGGGCATCTCATCGGCTCTGACAGGGGCCCGGAACAG
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 GAGCCGCCATCTACGGGGCAGCAGGTTCTCCGGGCGCGGATGCGGACCTGAGAACCACCGGCTCTCTTGGCG
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 CCAGCTTGGGCTGGCGCAGCCGCTGCTGCTGATTCCGCGACGCCATCTGCTTAATCATGAGGGCCGCGTTTGGC
 GCTGCTGCTGCTGCTGCTGTTGCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
 CTGCTGTTGACGGGACTGGTGGTCCGGGCGCGGATGCTGACGGGGCGGCCCGAAGGGAAGCTGTCGGGCACAG
 GCGGTGGAACCTCGCCGGGTAGGCTGGGTAGGCGGAAGGCTGATTATCCAGAGCGGCTGCTGTGCTGCTGCTG
 CTGCGCTTCCAGGAAGCGCAGCGGTCCACTCCCGGCTGCCCGGAAAGTCAAGCGCGGCTCTTGGCCACGTTT
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 CAGGCGGACCAATTTTGTGCGACTAGAAGCCCGGCTGGCGGCGCGGCTGCTGCTGTTGGCGGCTGCTGCGG
 GGCTGCTGAGGGGGTGGCGGGGCTGCTGGGGAGGCTGCATTAACGGGTGCCCTGGAGCCCACTGAGGGCTC
 CAGACCCACAGGCATCTTCTGGCCCCACTGAACCTCTCAAAGAACACACCATGCTGCTGCTGCTGCTGCTGGG
 CTGCTGCTGCTGCTGCGGCTGCTGCTGCGGTGGCTGGGCGTGCAATTTGGACAAGCCACCATGCCCGCAGCTT
 GGGATGGCCGAGCGCCCGGGAAGCGCCCCAGAACCTGGCGACCCGCTGCATAATGAGCGGCTGCCCTT
 CGGACTCAGAGGGCGAAAACATGTCAAAATGTCCCGAGGGCGCTCGCCCGGTAATTGTATTCCAGCGAGTCGA
 CGGCTCTTGGTTCTGACCCCTCCGTGGCTCCAGACTGTGGGAATCGGAGCCGCTGAGGAGCGGAGGCGGTG
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 GCAGGCACAGGCCCCGGGTCCGGGCCACCGAAGTTGCCCCAAAGTGGGGTGATGCTGGTGGGATGATGA
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 GTGCAACTCCGAGTGGCGCGCGCGTGAAGCGTATGGGCTCATGTTTCATGCCCAAGATCGGGGGTTGCCCA
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 CCAGCCCAACATACCTTGGCGGGGGCAGAGGGGATCAATAGGGCATGACAGCCGCTCTCCCGCGCGCGCT
 CCGGCCAGCTACTCGTTCCAGCCAGGATTGGGGCTCCGGGACGCTCAGCACCGCGGGGCTCAGCGCGCACC
 TCCACCCCGCTGATGTGAGGACGGGGGGCGGGTATTAGTCTCTCTCTGAAGCTCCGATTCTGCCCGGGAG
 GGCCTCTCATCTTGCAGGCGCGGGGCTCTAGGAGCGTGTGGGGGGCCATGCCCGGGCGGTTGTCA
 CAGCGCGGCTGGTCTGCGGGGAGGGACGAAGCCCGGATGAACGGAGACAAAAGTTAAGTGGGGGAAT
 GGGAGGGGAAGGGGTGGGAGAGCAGAGCATCACTTCTCAAGTCCGATTGGGTCTGCTGGGAGCCCTCAG
 GACCGCGCCGACGCTCCCGAGTCCGTGGCAGAGCTGCTAAGGGCAGGGGAGGGAGACCCCTCAAAGCGCG
 GCTGGCGCGGGCAGCGACAGAGCGTCCCTCCCCCGCGCCCGGAGTCCCGCGCGCCCGCAGCGCGGAGCCT
 CACCGACAGCATCCGCTCGCAACAATCCCGTAGGCTCCGGCGAGCGGCTGCTGCTTCTCAGCGGCTCGAGG
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 GCGGGGGCTGAGCGCGAGGCTCGGGGAAAGCGCGCTCTCTGCTCGGCAGCGGCTGCGCTGCGGCTCGGCG
 GCAGCTTCCGCGCCACGTCCGCGCGCTGCGCTTCTGTTCTCCCGCTTGGGTGCTGAGTTCTGAGTCTCC
 GCGCACCGTTGCAGGCGCGGGAGGGCAGCGAGAGGAGGTTGGGTGCTCCAAGGCTCCGTTCCCTGCTCC
 GCGCTGAGGTGCTTCCGAGATCCCTCTCGGACCTGAGGGAGGGGGCGTACGCGGGTCCGGGGGCCACGCGGG
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 GGGTCTGCGCACCCCTCTCCGACTAGCGGGGGCTCTGCGTGGGGCTTCCGAGGCTCTCGGCTCCCTCTC
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TTTGCACCAATCAGCGCCGCCAAGTTCCGGGCTCGGGGCGGGGCTCGCTCTTAAGGTGGTCCGGGGTCTGGCT
 GCCGAAGCCCCGCCACGAACCCGCACTACCCAGCTCTGGGGTCCCTCGGCCCGCTCTCTCGGGGTCCGGC
 GTCAGTGCCTGGGGGCGGCCCGGCTCCGGGCGCATCGAGCTGGAGAGGGTGCAGGCGGAGGAGAATGGC
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 CGGGTGGGCAGGGGCGGGGAGGTGGGCGGTGAGCGGTACGGGGCGCTCAGACAATGAGGTGCCAGGCAAAAG
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 GGGTTCGGGTCTCACCGGCGGGCGTGGCTCCAAGGAGTACAGTCACTCAGCCACTTTATGGGGGAGACAT
 CGGTTGAGCCAGTAACCGGAGCGACTTGCAGGCGGCTGGGAACCCGAGAAGACACGCACGAAGAGGGCGCA
 CCGCGGGGCGCACACCTTGCCCTGGGCCACCGGTCCAAGACCCAGACCTCTGCGGGTGCG

4 chr7:5614184-5614510

CGCTACACAGTGGCCGAGATTCCCGAGGCTGCAGCCAATGAGCAGCATAGTCCGATGGGGGAGGCTGGAAGGG
 CCGTTACGAGATCTCTCGGAGGAATCGGTAGGAGCTGCCCAACTGAAAGGGACGGGGGAATAACCCGGGGCG
 AGGACCTGCCAGGCCCTGCCCTCTGGCGGAAGCCAGGCCAGGGGCGGGGGCATCTCTGGGCTCCAGGTG
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 GGCAGTGCAGGACCGGAGACTCTGGGGCG

5 chr16:66239477-66241425

CGTCTAACGTACTGTCTTCTGAATCTCGCAGGCACCGACACTGCCCTGGACACTGTGAGGGGGTGTCCGTG
 GGGGGATGGATGACCGGCAGGGCGGACTGGAGGGGGGACGGGGAGGGCTCGGTCCCCCGCGGGTGTAGCCA
 ACAGCCTCCCCCGCAGCTCTTCGCAGCGGTATCCCGAGGCTGCTGCACCAAGCCTTACCCACCTCGACGCTTCGA
 GGAACGTCTTCTCCCGCACGTAAGGGGGACCTGTCCGGGGCGGGGAGGCTGTGGAAGCCGCTCTTGGCGG
 CCGAGGCCACCTTCCCACTTCCCCAGCAAGTCCCGCGCGCGCGCGCGCTGCAGCTCTTCCCTCAGCGCG
 CGCGGACGCTGCGGCACCTGGGCTGGCGGGCTGCAAGCTGCCGCCGACGCGCTCAGGTCAAGTGTGCGACCCC
 GGCCACGCCCGCGGGCGCTCCACCTTGGCTGGCTTCCCGCTTCCCGCTCTGCTTCTGTGCTTCCACA
 ACTTCCCGCAGATCTTGGCCCTGCCCTCTTCTTCTCGCACCTGGAGCCCTGTCCAGCTTCCCGCACCCCGGTG
 AACGTCCTTCCAGAGCCCTTTTGATGGCTCGCGCTCAACACGCACCTCCCGACCTGCACCTGACCTCAG
 CGCTTGGAGGTGAGCGCGCGCCCGCAGAAGAGACCACACATTGGGAGAGGCGCTGGGAGGCGGAAGGGCAGG
 GCCGTGGGGCGCTGCCCTTCCCACTCGCGGCTAAGTGGGTCCCACTTCCACCTTCCACCTCCACATACAG
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 GATAACGGTGAGGCTGCAGGAGAGCCCATCTCGCATCATCCACTCGATTCCCAATCCCCACCTACCTTGCAC
 TTGCGCTCTGCGTGACCCGAGTCAACCCAGGCTTCGGCTCAGACATGGTGAATCTGGTGTGGCCATCGGGAG
 AAGCCGCTCCCTGAGACATGTGCGCTTGAAGGAACCTTCAACGTCCGGTGAAGTGAGCCCCACCCCTACTCTCT
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 CAGCGGGCAGGGGCGCGCTGAGAGGAGGGCACCGGGCTAAGGGGAGCGGACTGAATGAGCGGAGCAATGG
 AGCAGGCTGACGAGGCGAATGGACTAGGCCGAGGGTTGGGTGGGCGCTGGGAAGCTCCGTCCCCGACTGAAGC
 CAGGCCCGCCAGGTCTGTGTCTGGGACCGGAACACACATCTGCTTTGGGTCTGTGTGGAGCGCAGCG
 GCTGGAGCAGAACACAGCCTGAAGGCCATGCCTCTGCCACTGAACGACGTGGCCAGGCGCAGCGCAGCCGCC
 CGGAATGACAGCAGTGCAGTCCATCAGGTGGGCGTCCCTCTTCCCTTGCCTTCTCTGCACGGTAACTCCGT
 CCTCG

6 chr5:551112-551430

CGGATGCCGGCTCTGCTCGGCCACCGCCCTCTCTCAAGGATGCTGTTTTGCTCTGGTGGCTCTATCTTAT
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 CCGCTGCTACTTCGGGGCCACGTCTCGGTCCGACGCTGAGGGGTGCTGCCAACCGTGTCTTCTGTGAACGTCC
 TCACGATGAACGCCCGGTTCCACTTCCACCTTGGAGCTGCTGCTTCCGTGACTACATTCGGGCCATTTCCGTG
 GTGTGAGGTACGGCG

7 chr19:6426223-6426998

CGTTACATTGCGATTCAATTCAGGAACCCACGAGACCTCTCCCGCAGCGTCCCGCTGCTACCGGGCTGCAGACG
 AGTGGCTCGCGGTACCCCCGAAGAGCAGGGCGCTGGGCTTTGAGGAAGAGACGGGACACCCCTTCCCGGGGGC
 CAGGGCGACCTTCTGAGCCGAGCCTCAGCAGGGACACCTGAAGCACAAGGGAGTGGCCCTGAGTGGGAGGT
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 AGGTAGGGCATGGCGCGCTGCGGACCGAGGGGACGGGGTCAATGACGACCGCCCCAGGGCCTGCCACAGG
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CGGTGGAGTCAGGGCCTGGACCCTCTAGCGCG

8 chr3:32836146-32836433

CGTGAATCGCCGTTCTGTGGGCCCACGGCTGCACCCCGAGATAGAAGCGGAATAAAGGGACGACGTTACCTTCAC
CAGCCTGAGTCTCTTTGGGCCGCGCCCGCTGCCCGACTCCAAGCCCTACAGGAACCGGTTTCCCTGGTTAGGAG
GTATCCACCCGGCTCAACCAGGGTCTCGACTTCCTTGAAAGGACCAAGGCAGCGGTACGCTGCTGGAACGCCG
AGTGCAAAGGCTTTTAGGGCTACATTGCAACCCTCGGGCTCGATTTTCCGCTTTTGGGCTGTG

9 chrX:129301145-129301626

CGTTGCCGCTTTTCTGTACTGAGCGCGCAGGGCACTACGCCCACTCCCTTTGACCCACTCCTCAAGCCCTGA
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CCTCTTTTCCCTCTGCGCGAGCAGTTAACTGGGGAAGCTACCAAATTTCTACGCTTAGCTGCCCTGCCTCCACCT
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CCGCTCTTTATTTCCGCGCTTTGTTTTAGTTTGGAAAGGGCGGAGTTGAAATGGTTCGCCCGCGGTTGCCGAA
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10 chr9:124027565-124030907

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GCAGCTGGAGCAGATGTTCTTGCCTGCAGACGCGACGGAGGAGGCGGCGAGAGGGCGGTGAGCAGACAGATGGCG
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CATCACCTGGGGAGGGGGGGAGGGAACGACGCGGGCGGCGGCTGCTGAACCTGGCTCCGACAGCCTGAGCCCA
CGGCTTCCCGCGCCTGTTATATAAACCGGCGCGCAACAATGAGTCTAACTTTGTAGTGGGCATTTAAAGCCCTT
CCCCACAAAAGCGGTGTCTCTCTAATGAAGCAATTTGAATTTGGATTGGATTTTTCCTCTCTCTCCCTCTCCCT
TGCACTTAACCCGTGCTCTTGAAGTAATCGCTTAGTTCCCTTGAATCCAAGCCTCTGAGGGGGGAAGAAAAACA
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AAAATCGAATTTTCTCTCTTCCACCGCCCCCCCCACCCACTCCCTTCTCTGCTCCCTTCTCTCTCGGCAAAA
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11 chr10:129424401-129427356

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12 chr1:3147370-3148160

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13 chrX:128941527-128945710

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 CCGCTGCC

16 chr19:10304689-10307022

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 GGGGTACG

17 chrX:129132628-129134108

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GTGGAGCCCTCAAGGGGGGTTGGGGCCCCGGTTCCGTCCGGGGGAGATGGCGCAGCCATCTCGGCCATGGGA
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18 chr21:45648960-45650662

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19 chr10:134864694-134865392

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GCAGCAGCTGAGGTGGCGAGGACAGACGGCCAGCTGGCGGGGCTCAGACGTGAGGCACTGACCCGACTGG
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20 chr9:129556229-129557670

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21 chrX:47305347-47306043

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AATGTCAGGATTCTCGCCTCT

Table 10. Hypermethylated genes and CGIs in bladder cancer.

Symbol	CGI	Fold Change
MEIS1	chr2:66525936-66527140	4.76
NR2F2	chr15:94688798-94689034	2.93
SOX21	chr13:94152191-94153185	2.8
MAB21L1	chr13:34950554-34951119	2.68
OTX1	chr2:63134539-63134851	2.67
MGC2752	chr19:63784504-63785085	2.64
IRX3	chr16:52873104-52882105	2.63
PAX9	chr14:36205265-36206099	2.62
FOXC1	chr6:1549606-1560865	2.5
DLX5	chr7:96488158-96489487, chr7:96489900-96490182	2.45
NR4A2	chr2:156892636-156892878, chr2:156893804-156894601	2.45
CNTNAP1	chr17:38089258-38089793	2.35
FOXF2	chr6:1338049-1339169	2.35
HHEX	chr10:94441310-94441717	2.33
PRKCZ	chr1:2072175-2072389, chr1:2106293-2106661	2.31
HOXA7	chr7:27164708-27165039	2.27
MSX2	chr5:174091287-174092335	2.26
SLC45A4	chr8:142288380-142288627	2.22
FLJ44006-BCL2L11	chr2:111591678-111597436	2.21
MAP2K2	chr19:4059920-4060207	2.2
SHH	chr7:155288454-155292175	2.19
chr13:	chr13:49605587-49606020	2.19
MAD1L1	chr7:2082894-2083307	2.18
hsa-mir-196a-1	chr17:44074360-44075233	2.17
NXPH1	chr7:8449658-8450236	2.17
chr18:	chr18:5186244-5187389	2.12
C10ORF114	chr10:21828640-21829594	2.1
SIX3	chr2:45014932-45016562, chr2:45013398-45013616	2.08
TFAP2A	chr6:10530308-10530634, chr6:10498025-10498551	2.08
ISL2	chr15:74414579-74414893, chr15:74419318-74422570	2.05
VAX2	chr2:70984709-70985764	2.04
AMZ1	chr7:2724531-2724783	2.01
CYB561	chr17:58865386-58865618	1.99

HOXD3	chr2:176737660-176738187	1.97
SIM1	chr6:101003802-101004342, chr6:101002495-101002783	1.95
EFNB2	chr13:105943410-105943788	1.91
GAD1	chr2:171384799-171385226	1.91
MSX1	chr4:4915358-4915735, chr4:4910534-4911092	1.9
FOXA1	chr14:37137198-37138958	1.88
HDGFL1	chr6:22677564-22678684	1.85
chr13:	chr13:49595986-49600287	1.84
chr16:	chr16:87372445-87372706	1.84
EVX1	chr7:27251165-27252762	1.83
UNG2 (CCNO)	chr5:54554812-54555385	1.83
ONECUT2	chr18:53254153-53259851	1.81
HSF2BP	chr21:43902100-43904249	1.8
chr1:	chr1:119350668-119352843	1.8
FOXD3	chr1:63554983-63563059	1.79
FOXA2	chr20:22514822-22515055, chr20:22510737-22514104, chr20:22505518-22507240	1.77
GRIK2	chr6:101953488-101953856	1.77
chr2:	chr2:45249374-45251690	1.77
SIX1	chr14:60178708-60179539	1.76
HOXA9	chr7:27170441-27172987	1.75
FOXD2	chr1:47671713-47671985, chr1:47682300-47683607, chr1:47672249-47672972	1.73
NKX2-8	chr14:36122886-36123441	1.72
ZNF274	chr19:63420090-63420541	1.72
TAF4	chr20:60061693-60062033	1.71
SIX2	chr2:45085286-45086054	1.7
chr8:	chr8:145909302-145910517	1.7
PCDH7	chr4:30330303-30333940	1.69
PITX2	chr4:111774415-111774953	1.68
TCF7L1	chr2:85213468-85216104	1.68
chr6:	chr6:10492952-10493478	1.68
SOX7	chr8:10624024-10624296	1.66
HOXC4	chr12:52726910-52727810	1.65
PITX1	chr5:134390992-134393045	1.65
PCDHGA12	chr5:140790679-140792801	1.64
chr6:	chr6:170422815-170423038	1.64
EPN1	chr19:60907042-60907388	1.63
DLX6	chr7:96469320-96469736	1.62
hsa-mir-10b	chr2:176723195-176723460, chr2:176720618-176720921	1.62
SIM2	chr21:36990064-36995761	1.61

CACNA2D4	chr12:1844001-1845219	1.6
HOXA5	chr7:27149139-27152087	1.6
NCK2	chr2:105864220-105865009	1.6
OSR1	chr2:19424445-19425131	1.58
C17orf27 (RNF213)	chr17:75936057-75936582	1.57
chr6:	chr6:169051743-169052507	1.56
EVX2	chr2:176652334-176656692	1.53
ZNF503	chr10:76825135-76839606	1.52
chr5:	chr5:92931996-92934631	1.52
KIAA1303	chr17:76404186-76404427, chr17:76390187-76390410	1.48

Table 11. Genomic distribution of methylated probes in bladder cancer.

Probe location	% on array	% in bladder cancer
divergent promoter	2.5	2.4
downstream	3.9	4.0
inside	52.4	52.3
promoter	26.0	25.9
intergenic	15.3	15.3

Table 12A. Overview of the CGIs differentially methylated between tumor and control urine.

Symbol	CGI	Fold Change
HOXA9	chr7:27170441-27172987	16.53
PENK	chr8:57520681-57521969	14.69
PCDH7	chr4:30330303-30333940	12.00
KCNA1	chr12:4888847-4891432	11.89
HLX1	chr1:219134071-219134808	10.46
POU4F2	chr4:147778656-147781351, chr4:147777682-147778033	10.17
LHX4	chr1:178464743-178471598	9.79
FOXD2	chr1:47682300-47683607, chr1:47672249-47672972	9.67
LBX1	chr10:102986025-102986636	9.44
chr11:115956893-115956940	chr11:115955870-115957122	9.03
LMX1A	chr1:163590111-163590435	8.86
BHLHB5	chr8:65662303-65662699, chr8:65661156-65661382	8.61
OTX1	chr2:63134539-63134851	8.22
GAD2	chr10:26544390-26547440	8.02
EVX2	chr2:176652334-176656692	8.02
FLJ44006-BCL2L11	chr2:111591678-111597436	7.89
ONECUT2	chr18:53254153-53259851	7.75
ZIC1	chr3:148619591-148620015	7.33
FOXA1	chr14:37137198-37138958	7.24
DSC3	chr18:26875488-26877115	7.19
SIM2	chr21:36990064-36995761	6.78
MEIS1	chr2:66525936-66527140	6.74
FEZF1	chr7:121727243-121727884	6.62
ZNF503	chr10:76825135-76839606	6.57
SLC35F3	chr1:232106922-232108080	6.34
FEZF2	chr3:62331811-62332352	6.26
NR4A2	chr2:156893804-156894601	6.20
EN1	chr2:119329502-119332035	5.59
PCDH10	chr4:134291113-134293078	5.53
OSR1	chr2:19424445-19425131	5.23
ZIC4	chr3:148591199-148594390	5.00
CBLN1	chr16:47868915-47869809	4.92
HMX2	chr10:124891898-124892607	4.89
FOXB1	chr15:58083428-58085812,	4.76

	chr15:58079172-58079459	
chr19:057648585-057648629	chr19:57648469-57649057	4.58
DPP10	chr2:115635208-115637235	4.55
chr7:032768257-032768301	chr7:32768010-32768497	4.48
C10orf114	chr10:21828640-21829594	4.44
FOXD3	chr1:63554983-63563059	4.39
chr5:092933638-092933682	chr5:92931996-92934631	4.25
TCF7L1	chr2:85213468-85216104	4.21
VAX2	chr2:70984709-70985764	3.99
CBLN2	chr18:68359955-68362770	3.97
PCDHGA12	chr5:140790679-140792801	3.94
chr21:037857850-037857894	chr21:37857725-37858416	3.89
HOXA7	chr7:27164708-27165039	3.79
GRIK2	chr6:101953488-101953856	3.77
NKX2-8	chr14:36122886-36123441	3.65
SOX9	chr17:67627870-67631593	3.64
chr18:005186349-005186393	chr18:5186244-5187389	3.50
SOX21	chr13:94152191-94153185	3.43
SNRPF	chr12:94776152-94776377	3.39
MSC	chr8:72916429-72917309	3.18
PITX1	chr5:134390992-134393045	3.05
SOX7	chr8:10624024-10624296	2.99
chr2:042182832-042182879	chr2:42182944-42183157	2.97
TBX15	chr1:119333515-119333719	2.96
SIM1	chr6:101003802-101004342	2.91
PFKFB1-APEX2	chrX:55043085-55043710	2.89
GATA2	chr3:129688183-129694961	2.86
chr5:122462228-122462286	chr5:122461778-122463450	2.82
GPR103	chr4:122521018-122521740	2.81
SIX2	chr2:45085286-45086054	2.80
SFMBT2	chr10:7489383-7495345	2.79
NXPH1	chr7:8449658-8450236	2.73
CA10	chr17:47590175-47591465	2.71
CNTNAP5	chr2:124498723-124499725	2.66
ZNF274	chr19:63420090-63420541	2.62
HOXD3	chr2:176737660-176738187	2.61
PITX2	chr4:111774415-111774953	2.55

OLIG2	chr21:33316999-33322115	2.54
FOXA2	chr20:22505518-22507240, chr20:22510737-22514104	2.53
DBC1	chr9:121170908-121172035	2.49
PAX2	chr10:102497473-102499636	2.45
MAB21L1	chr13:34950554-34951119	2.35
CYP26B1	chr2:72224630-72228512	2.31
CBLN4	chr20:54012011-54014085	2.26
GAD1	chr2:171384799-171385226	2.25
HHEX	chr10:94441310-94441717	2.22
chr9:013268499- 013268548	chr9:13268313-13269805	2.20
FOXF2	chr6:1338049-1339169	2.17
DLX5	chr7:96489900-96490182	2.08
TBX3	chr12:113589232-113589931	2.04
MEIS2	chr15:35174679-35174906	2.04
PTGER3	chr1:71284813-71286392	2.04

Table 12B. Overview of CGIs associated with progression of NMI-BC.

Symbol	CGI	FC
GPR103	chr4:122520930-122520974	1.81
chr2:042182832-042182879	chr2:042182832-042182879	1.96
KCNA1	chr12:004890074-004890118	2.01
HLX1	chr1:219134113-219134157	2.14
DBC1	chr9:121171898-121171944	2.59
GPR103	chr4:122521031-122521075	4.17
TBX3	chr12:113609259-113609303	2.76
GATA2	chr3:129693434-129693486	2.20
TBX2	chr17:056833879-056833928	2.15
TBX2	chr17:056835246-056835290	2.10
ZNF577	chr19:057082979-057083023	2.08
MSC	chr8:072916695-072916739	1.82

EXAMPLES

Example 1

The CpG island hypermethylations as indicated in the Tables 1-5 are the result of comparative studies using well characterized patient samples. Both tumor samples and controls were analyzed. The DNA was extracted directly from the tumor and control tissue. DNA samples were analyzed using a CpG island microarray comprising 200.000 CpG islands (Agilent Technologies Inc.). The results obtained are indicated in the various Tables 1-5 as listed herein.

Example 2

Materials & Methods

Patient samples, ethics statement and DNA isolation

Samples from 44 fresh frozen bladder cancer tissues were collected, representing 29 non-muscle invasive tumors (19 with FGFR3 mutation (NMI-mt) and 10 without (NMI-wt)) and 15 muscle-invasive tumors (MI). Tumor tissue of patients was obtained from the Department of Urology of the Erasmus MC, Rotterdam. The medical-ethical committee of the Erasmus MC Rotterdam approved the project. All patients gave written informed consent. For validation, 90 formalin-fixed, paraffin-embedded (FFPE) bladder cancer samples (27 Ta NMI-mt, 13 Ta NMI-wt, 10 T1-mt, 14 T1-wt, 26 MI) were collected from the Department of Pathology. Usage of these samples was performed according to standards presented in “The Code for Proper Secondary Use of Human Tissues in The Netherlands”. Tumor samples were included only if at least 80% of the sample consisted of cancer cells, as verified by H&E staining. DNA from tumor tissue was isolated with the DNeasy Tissue kit (Qiagen, Hilden, Germany), according to the instructions of the manufacturer. Commercially available normal human genomic blood DNA (Promega, Madison, WI, USA) was used as a reference in the genome wide analysis and the GGMA. DNA isolated from cells present in

normal urine of four healthy persons of more than 50 years old was used as reference DNA in the GGMA validation assay.

Differential Methylation Hybridization (DMH) and Data Analysis

DNA amplicons were prepared for hybridization according to the DMH (differential methylation hybridization) protocol described by Yan et al [Yan et al. 2002.) *Methods Mol Biol* 200: 87-100]. Briefly, 0.5 µg of genomic DNA was digested with the four base (T^ATAA) restriction enzyme MseI, which restricted genomic DNA into fragments less than 250 bp in length, while leaving the GC-rich CGIs relatively intact. Subsequently, the sticky ends of the fragments were ligated to linker primers. Samples were then digested with the methylation-sensitive restriction enzymes HpaII and BstUI to increase the genome coverage and to ensure complete digestion. Reference samples were treated in the same way to generate amplicons. PCR reactions (20 cycles) were performed using the purified, digested, linker ligated DNA as template to generate final target amplicons, followed by coupling to fluorescent dyes (Cy3 in case of human genomic reference DNA and Cy5 in case of tumor samples) before hybridizing to the Agilent 244K CpG island microarray. The pooled amplicons were co-hybridized on the array. Using this approach, genomic DNA fragments containing unmethylated CpG sites in one sample (e.g. the human genomic reference DNA) were degraded by restriction digestion and not amplified. However, corresponding DNA fragments in the other sample (the bladder tumor) that contain methylated restriction sites were protected from digestion and subsequently amplified by PCR. Differentially methylated sequences were identified by comparing hybridization signals between fluorescently labeled tumor (Cy5) and reference (Cy3) amplicons.

All microarray data generated are compliant with current MIAME standards according to Brazma et al [Brazma 2009. *Scientific World J* 9:420; Brazma et al. 2001. *Nat Genet* 29:365]. Normalization, preprocessing of raw data and statistical analysis were done using Bioconductor packages in an R programming environment. Raw hybridization

signals were normalized by applying the within-array global “lowess” normalization method [Yang et al. 2002. *Nucleic Acids Res* 30: e15], which assumes that the bulk of the probes on the array are not differentially expressed. The normalization also includes a pre-processing step, as a result of which the normalized intensities were log2-transformed. The log2-transformed intensities were then subjected to further statistical testing to determine which loci were differentially methylated. The linear model “limma” was applied [Smyth 2004. *Stat Appl Genet Mol Biol* 3: Article3]. We performed the following comparisons: All tumors vs. Blood, NMI-mt vs. NMI-wt, NMI-mt vs. MI, and NMI-wt vs. MI, to find genes that have different methylation profiles across the groups compared. These comparisons are analogous to a classical two sample t-test analysis.

The p-value threshold was calculated using the Benjamini and Hochberg method [Benjamini et al. 2001. *Behav Brain Res* 125: 279]. The loci corresponding to p-values less than 0.05 and a log fold change of either greater than 0.5 or less than -0.5 with more than 2 probes representing the same CGI were classified as differentially methylated. We left chromosome Y probes out of the subsequent analyses.

Illumina custom Golden Gate Methylation assay and statistical analysis

We designed a custom Golden Gate Methylation assay interrogating 384 CpG containing probes representing 238 CGIs, 184 genes, and 46 intergenic regions. The selection of the probes was based on the differentially methylated loci in the genome-wide analysis. Probes were included to detect methylation in all bladder subgroups, but also probes that appeared to be specific for a certain subgroup compared to others, and some probes specific for progression or death of disease. The methylation assay is an adaptation from the Illumina high-throughput SNP genotyping assay described by Fan et al. [Fan et al. 2003. *Cold Spring Harb Symp Quant Biol* 68: 69]. In short, non-methylated cytosines (C) were converted to uracil (U) by treatment with bisulfite. Sodium

bisulfite modification of genomic DNA was carried out using the EZ DNA Methylation Gold Kit (Zymo Research Corp, Orange, CA, USA) according to the manufacturer's protocol, using 0.8 µg of FFPE DNA. The conversion efficiency was monitored by PCR with universal BS specific primers provided with the kit. Arrays were run at Service XS, Leiden, the Netherlands according to the manufacturer's protocol and as described by Bibikova et al. [Bibikova et al. 2006. *Genome Res* 16: 383].

Data were analyzed with Illumina's BeadStudio Methylation module software. All array data points were represented by fluorescent signals from both methylated (M) and unmethylated (U) alleles. The average methylation value β was derived from approximately 30 replicate methylation measurements for each locus. The methylation level was given by $\beta = (\max(M, 0)) / (|U| + |M| + 100)$. The β -value ($0 \leq \beta \leq 1$) reflects the methylation level of each CpG site where 1 represents fully methylated and 0 represents unmethylated. At each locus for each sample, the detection p-value was defined as $1 - p$ -value computed from the background model characterizing the chance that the signal was distinguishable from negative controls. Using this as a metric for quality control for sample performance, 6 FFPE samples (6 %) were dropped from the analysis, because they either had very low overall signal intensities or > 25% of loci failed. The significant differences were assessed by comparing the average β value per locus per group. Significant loci were selected on the basis of an average β value ratio larger than 1.4 and a difference between the average β value ($\Delta\beta$) larger than 0.3.

Validation of methylation of individual CGIs

We used the MS-SNAPSHOT method described in [Gonzalvo and Liang 2007. *Nat Protoc* 2: 1931; Lurkin et al. 2010. *PLoS One* 5: e8802] to investigate methylation in urine DNA quantitatively. The method involves the bisulfite conversion of genomic DNA and the subsequent amplification of interested genomic region. This is followed by the methylation specific single nucleotide primer extension with CpG specific probes and finally the

fragments are visualized on a ABI sequencer. To test the method, methylation of MEIS1 gene was investigated using normal, patient urine samples along with bladder cancer cell lines. *In vitro* methylated DNA was used as a positive control. A list of primers and probes used is given in Table 6.

Results

A genome wide methylation profile for bladder cancer

To investigate global DNA methylation in bladder cancers, we analyzed 44 bladder tumors on Agilent 244K human CpG island microarrays using differential methylation hybridization. We found that 729 different probes were significantly more methylated in bladder tumors compared to blood with a log fold change greater than 0.5 and a p value of < 0.05 . To select the most hypermethylated CGIs, we used as an additional criterion that 3 or more CpG dinucleotides should be highly methylated in a specific CGI. This selection generated a list of 82 CGIs representing 71 genes and 11 CGIs not directly associated with a gene according to the Agilent information file. These are shown in Table 10. The gene showing the highest degree of methylation was MEIS1 with a log fold change of 4.8 for the most highly methylated probe and an average log fold change of 2.2 across the 10 probes that were present on the array for this CGI (Figure 1). We observed that for most of the significantly methylated CGIs, the adjacent CpG dinucleotides within a CGI were co-methylated. In contrast, CGIs neighboring a methylated island were usually not methylated.

Methylation of intronic CGIs is associated with reduced gene expression

The 244k array contains probes for CGIs as displayed in the UCSC genome browser (<http://genome.ucsc.edu/cgi-bin/>, build 19). Of the CGIs represented on the array, 26% is located in promoter regions. Many studies have shown that aberrant methylation of CGIs in promoter regions represents one of the most frequent epigenetic events associated with gene silencing in

cancer. In our analysis we observed that there was no specific preference for methylation of promoter regions. Instead, methylation was distributed proportionally over CGIs in promoter regions, within genes and in intergenic regions (Table 11). Examples are shown for CGIs in two of the selected genes, MEIS1 and NR4A2 (Figure 1). To investigate whether methylation outside promoter regions also repressed gene expression, we next compared genes with methylated CGIs with available genome-wide expression profiles of bladder cancer using the Oncomine database [Blaveri et al. 2005. Clin Cancer Res 11: 4044; Dyrskjot et al. 2004. Cancer Res 64: 4040; Dyrskjot et al. 2003. Nat Genet 33: 90; Lindgren et al. 2006. Oncogene 25: 2685; Modlich et al. 2004. Clin Cancer Res 10: 3410; Sanchez-Carbayo et al. 2006. J Clin Oncol 24: 778]. This information could be obtained for 54 genes. Out of these 54 genes, 22 showed promoter CGI methylation and a positive correlation with low expression was observed in 17 genes (77.3 %). The remaining 32 genes showed methylation of CGIs within introns. Interestingly, 23 of these genes also showed low expression (71.9 %) in bladder cancers. These data suggest that not only promoter CGI methylation but also methylation of intronic CGIs leads to reduced gene expression. The expression profile box plots of MEIS1, NR4A2 and HOXA9 are shown in Figure 1.

Analysis of individual subgroups shows NMI-wt tumors to have a highly methylated profile

To explore whether global DNA methylation can identify subgroups of bladder cancer, we performed an unsupervised analysis by means of a principal component analysis (PCA) using all probes on the array (244K) (Figure 2A). The first three components of the PCA explained 42.4% of the variability between the samples suggesting that there is a reasonable discrimination between the subgroups. This unsupervised analysis indicates the presence of two clusters of bladder cancer patients. The NMI-wt tumors (in green) clustered closely together and separate from the NMI-mt (in blue) and MI tumors (in red). Furthermore, we looked at the individual subgroups of

bladder tumors. NMI-wt tumors showed a 2.7 to 4.6 times higher number of hypermethylated probes compared to the NMI-mt and MI groups (Figure 2B). A list of genes differentially methylated between subgroups is given in Table 12.

We next clustered the different subgroups of bladder tumors based on all probes that were differentially methylated between two groups with a p value of <0.05 , regardless of the log fold change. For clustering of probes differing between NMI-mt and MI tumors, we had to use a p-value <0.5 because not many differences exist between these two groups. We employed a hierarchical clustering algorithm choosing Euclidian distance and complete linkage to organize the three different comparisons (Figure 3). We then performed principal component analysis on the same data. The probes along with gene names and p-values are listed in Table 12. These semi-supervised analyses showed clearly that the different bladder cancer subgroups can be identified based on their methylation pattern.

Genes hypermethylated in bladder cancer often are PcG target genes

Polycomb group (PcG) proteins function as transcriptional repressors of genes that have been implicated in stem cell self renewal and differentiation. These PcG target genes have been shown to be particularly prone to DNA methylation in cancers [Ohm et al. 2007. Nat Genet 39: 237; Widschwendter Met al. 2007. Nat Genet 39: 157; Schlesinger et al. 2007. Nat Genet 39: 232]. We investigated whether DNA hypermethylation in bladder cancer was more present in PcG target genes by matching our list of 71 genes from Table 10 with recent studies showing that 8-14% of all genes in the genome to be PcG regulated [Bracken et al. 2006. Genes Dev 20: 1123; Lee et al. 2006. Cell 125: 301]. Notably, we found that 63.3% of the hypermethylated genes in bladder cancer were PcG target genes, with a representation factor of more than 3 (<http://elegans.uky.edu/MA/progs/representation.stats.html>) (Figure 4A). This was approximately the same for all different tumor subsets. Twenty-two PcG

regulated genes were methylated in all three subtypes, while a striking 81 genes were specific to NMI-wt tumors (Figure 4B). A list of the PcG target genes methylated in bladder cancer is given in Table 8.

Genes methylated in blood compared to bladder cancer

We also observed 21 CGIs that were methylated in blood but not in bladder tumors. These are listed in Table 9. We compared our results with a study based on methylated DNA immunoprecipitation (MeDIP), in which the genome-wide methylation pattern in blood was investigated [Rakyan et al. 2008. *Genome Res* 18: 1518]. We found a 90 % correlation with their study..

Validation of hypermethylation and markers for diagnosis and progression

Next we set out to validate the selected significant CGIs on a custom Illumina platform based on bisulfite conversion of tumor DNA. The following CGIs were included in the custom array:

- 1) Differential methylation between tumors and blood (Tables 9 and 10);
- 2) Probes that could be of use as biomarkers to distinguish the subgroups. There were 7 CGIs representing 6 genes found to differentiate between NMI-mt and NMI-wt tumors. In the MI versus NMI-wt comparison, we found 17 CGIs representing 13 genes to be significant. No significant probes were found between the MI versus NMI-mt subgroups at a p-value < 0.05. Therefore we decided to include probes from 6 CGIs representing 6 genes with a p-value < 0.5;
- 3) CGIs that were associated with progression and survival. In all cases the CGI to be validated had at least 3 CpGs that were highly methylated.

We employed a hierarchical clustering algorithm on the average beta values per subgroup with all 384 probes on the array choosing Euclidian distance and complete linkage. The analysis clearly separated the bladder tumors from normal urine and blood (Figure 5A). We were able to validate

more than 70% of the probes hypermethylated in all bladder tumors. For example, in the custom 384-plex GGMA, there were 205 probes which were methylated in bladder cancer but not in blood based on our Agilent array data. Of these, 147 probes were also methylated in bladder cancer but not in blood in the GGMA. These probes are shown in the heat map (Figure 5B). We also included DNA isolated from cells present in urine of healthy individuals, which most likely are derived from normal urothelial cells. Eighty % of the probes validated against blood were also not methylated in urine. For the different subgroups of bladder tumors, the number of probes validated varied between 65-75% of probes compared to blood and 76-83% compared to urine.

CGIs that are differentially methylated between tumors and urine from non-bladder cancer controls represent potential biomarkers for urine tests (Table 12). We validated several of these using a bisulfite specific PCR followed by a Snapshot assay for the CpG. The results of these analyses are shown in Figure 5C. We were able to detect methylation in urine DNA quantitatively using this method. We investigated MEIS1 gene methylation at two CpG sites using different probes (MEIS1 A and B). The black peak (Cytosine) represents methylation and red peak (Thymine) represents no methylation. In vitro-methylated DNA (IM), BC patient urine sample (PU) and bladder cancer cell lines (RT112, T24, J82) showed a strong methylation signal while normal urine (NU) and blood DNA (NB) were not methylated.

Next we analyzed the CGIs that were included on the GGMA as potential markers for progression. To this end the 6 best CGIs that were methylated in non-progressors vs progressors and similarly, 6 CGIs that were methylated in progressors vs. non-progressors were analyzed separately and in several combinations (Table 12B). The Kaplan-Meier curves depicted in Figure 5D show that a combination of CGIs in the GPR103, DBC1 and GATA2 genes can significantly predict progression ($p=0.001$). Interestingly, methylation of the GPR103 and DBC1 CGIs was inversely correlated with progression and methylation of GATA2 was strongly indicative for progression. The DBC1

associated CGI overlaps with the promoter of this gene, whereas the GATA2 and GPR103 CGIs are located in introns.

Discussion

We report an investigation of bladder cancer-associated aberrant DNA methylation. To our knowledge this is the first study that addresses genome-wide methylation in bladder cancer. The major goal of this work was the identification and validation of methylated CGIs that could serve as biomarkers for the early detection of primary and recurrent tumors as well as markers that are predictive of disease course. The genome-wide screen resulted in the selection of 177 CGIs that significantly differed in methylation in tumors when compared to blood. About 70% of these CGIs could be validated in a custom GGMA assay. This analysis also showed that most of these CGIs were not methylated in urine-derived DNA from age matched non-bladder cancer controls. This group of CGIs represents markers for urine based assays. Methylation of some of these markers was confirmed on urine samples. Another important finding is that a combination of CGIs from the GPR103, DBC1 and GATA2 genes is able to predict progression to muscle – invasive disease. Loss of heterozygosity or homozygous deletions of DBC1 (also called DBCCR1) gene (deleted in bladder cancer 1) have been observed in many bladder tumors, as well as methylation of the promoter. Methylation has so far not been correlated to disease course. In our study methylation of the promoter CGI of the DBC1 gene was associated with a decreased risk of progression. The role of the GATA 2 transcription factor in cancer is contradictory. Decreased expression was found to be correlated with proliferation in monocyte progenitors, whereas high expression seems to poise prostate cancers for a more aggressive phenotype and gain-of-function point mutations have been found in chronic myeloid leukemia. In bladder tumors a lower expression of this protein has been observed in MI vs. NMI-BC, which correlates with methylation and the positive association with progression. The GPR103 (QRFPR) gene encodes a G protein-coupled receptor and hence the

protein is involved in signal transduction, however, but no further data about the gene or its product can be found in the literature.

Most genes discovered in the present study have never been shown to be methylated in bladder cancer or in other types of cancer. Some of the previously described methylated CGIs in bladder cancer that are associated with the SOX9, CDKN2A, TERT, DAPK1, EDNRB, and LAMB3 genes were also found to be methylated in our study, although only SOX9 and CDKN2A made it to the list of our 177 highly methylated CGIs.

To our surprise we observed that NMI-BCs with a wild-type FGFR3 gene have more methylated CGIs and the intensity of methylation is more profound than in the FGFR3 mutant NMI-BC and MI-BC groups. The difference in methylation presents additional evidence that the two subgroups of NMI-BC develop along different pathogenesis pathways. WT NMI-BCs also have more wide spread chromosomal aberrations than FGFR3 MT NMI-BCs. The extensive methylation in WT NMI-BC is reminiscent of the CpG island methylator phenotype (CIMP) that characterizes a subset of colorectal cancers (CRC). CIMP in CRC also identifies a subset of CRCs as it is associated with BRAF mutations, microsatellite instability and occurs more often in elderly females. No large-scale genome-wide study on DNA methylation has been performed for CRC, however, CIMP has been studied using a 1536-plex GGMA array.

When comparing the genes methylated in this study with those found by us, there was hardly any overlap. This confirms that CGI methylation is tissue and tumor type specific.

In line with previous reports in solid tumors, a high proportion of the genes we find *de novo* methylated in bladder cancer are repressed by polycomb complexes (PcG) in embryonic stem cells. PcG target genes are as much as 12 times as likely to be silenced by DNA methylation in cancer as non-PcG target genes. The association between DNA methylation and PcG has further been substantiated by the finding of interactions between DNMT1, DNMT3A, DNMT3B and several PcG complex subunits like EZH2 and BMI1. Another

recent study showed that 49% of the genes methylated in colon cancer are polycomb targets in embryonic stem cells, agreeing with other reports showing that genes prone to tumor specific hypermethylation in colon cancer were more likely to be marked by H3K27 methylation in normal tissues than genes lacking H3K27 methylation. Another study reported that many genes hypermethylated in a prostate cancer cell line were bound by PcG in normal cells but lost PcG binding upon acquiring DNA methylation in cancer. In this perspective we found that 60% of the hypermethylated genes in bladder cancer are PcG targets in embryonic stem cells. These epigenetic alterations occurring in early development specifically in stem or progenitor cells might be bladder cancer specific and this strengthens the further understanding of bladder cancer tumorigenesis. Besides finding 92 commonly PcG regulated genes in bladder cancer subgroups, a group of 336 genes regulated by PcG complexes are found to be specific to NMI-wt tumors. Besides a possible CIMP phenotype being the cause for the extensive methylation in this group, another possible explanation for this finding could be that the cell from which the WT NMI-BCs originate is more closely related to the embryonic or bladder stem cell than the founder cells of the MT NMI and MI-BCs. In general it is thought that lineage-specific genes are activated during subsequent differentiation steps and during this process the PcG complexes will be replaced by cell fate specific transcription factors. Hence, fewer possible methylation targets will remain after every differentiation step.

Our data clearly shows that adjacent loci within a certain CGI are co-methylated, while neighbouring CGIs of a certain gene can have a very different methylation level. Significant association among the methylation states of adjacent CpG sites and a high frequency of short-range co-methylation was reported previously. Another interesting finding in this study is that our data shows no preference for methylation of CGIs in promoter regions compared to gene bodies, since the location of the significant CGIs is distributed over the genome in accordance to the distribution of CGIs on the array. The effects of promoter methylation on chromatin organization and gene

expression have been well documented in various types of cancer. In our study, besides promoter methylation, we found more than 50% of all significant probes to be located in CGIs located within gene bodies. The influence of this on gene expression is not fully known. Previous reports in *Arabidopsis* have shown that gene body methylation was low in genes transcribed at low levels, higher in highly transcribed genes, and absent in genes that were not transcribed. By comparing our methylation results with gene expression studies, we show that for 70% of our genes there is an inverse correlation with gene expression, suggesting that intragenic methylation also contributes to gene silencing.

In summary we have identified hypermethylated CGIs in bladder cancer. The aberrant DNA methylation in bladder cancer seems to be very selective and could be the first step in tumor initiation, especially for the WT NMI-BCs. The study also illustrates an interesting biological finding: besides the promoter methylation intragenic methylation observed to the same extent in bladder cancer and it also appear to influence the gene expression. Many discovered methylated CGIs represent putative biomarkers for early detection in urine-based assays. The combination of CGIs from the *GRP103*, *DBC1* and *GATA2* genes predicts progression to muscle-invasive disease. Thus, the CGIs identified in this study will be of considerable interest for further investigation of their clinical and functional relevance and will provide advance insights into the pathogenesis of bladder cancer.

Claims

1. A method for diagnosing bladder cancer in a subject comprising the steps of:

- obtaining DNA from a urine sample of a subject;
- detecting in the DNA obtained from the urine sample of said subject a hypermethylated CpG island associated with said cancer, wherein an elevation in the level of methylation in said CpG island of said subject, relative to the level of methylation in said CpG island of a control subject, is indicative of said CpG island being hypermethylated, and wherein said CpG island is the CpG island of OTX-1 present in chr2:63134539-63134851 as comprised in the Human Genome Assembly hg18 of March 2006.

2. The method according to claim 1, wherein said bladder cancer is recurrent bladder cancer; and wherein the step of obtaining DNA from a urine sample of a subject comprises isolating DNA from a tumor cell fraction from said urine sample.

3. The method according to claim 1, wherein said bladder cancer is a primary form of bladder cancer in a subject, and wherein the step of obtaining DNA comprises isolating DNA from a tumor cell fraction from said urine sample.

4. The method according to any one of claims 1-3 wherein said bladder cancer is non muscle-invasive bladder cancer.

5. A method for the prediction of the recurrence or prognosis of bladder cancer, comprising detecting in the DNA of a subject a hypermethylated CpG island associated with said cancer, wherein an elevation in the level of methylation in said CpG island of said subject, relative to the level of methylation in said CpG island of a control subject, is indicative of said CpG

island being hypermethylated, and wherein said CpG island is the CpG island of OTX-1 present in chr2:63134539-63134851 as comprised in the Human Genome Assembly hg18 of March 2006.

6. The method of any one of claims 1-5, wherein said step of detecting comprises determining the methylation level of said CpG island through methylation-specific PCR (MSP).

7. The method of any one of claims 1-5, wherein said step of detecting comprises determining the methylation level of said CpG island through multiplex ligation-dependent probe amplification (MLPA).

8. The method according to claim 1, wherein the step of obtaining DNA comprises extracting DNA from a tumor cell fraction from said urine sample.

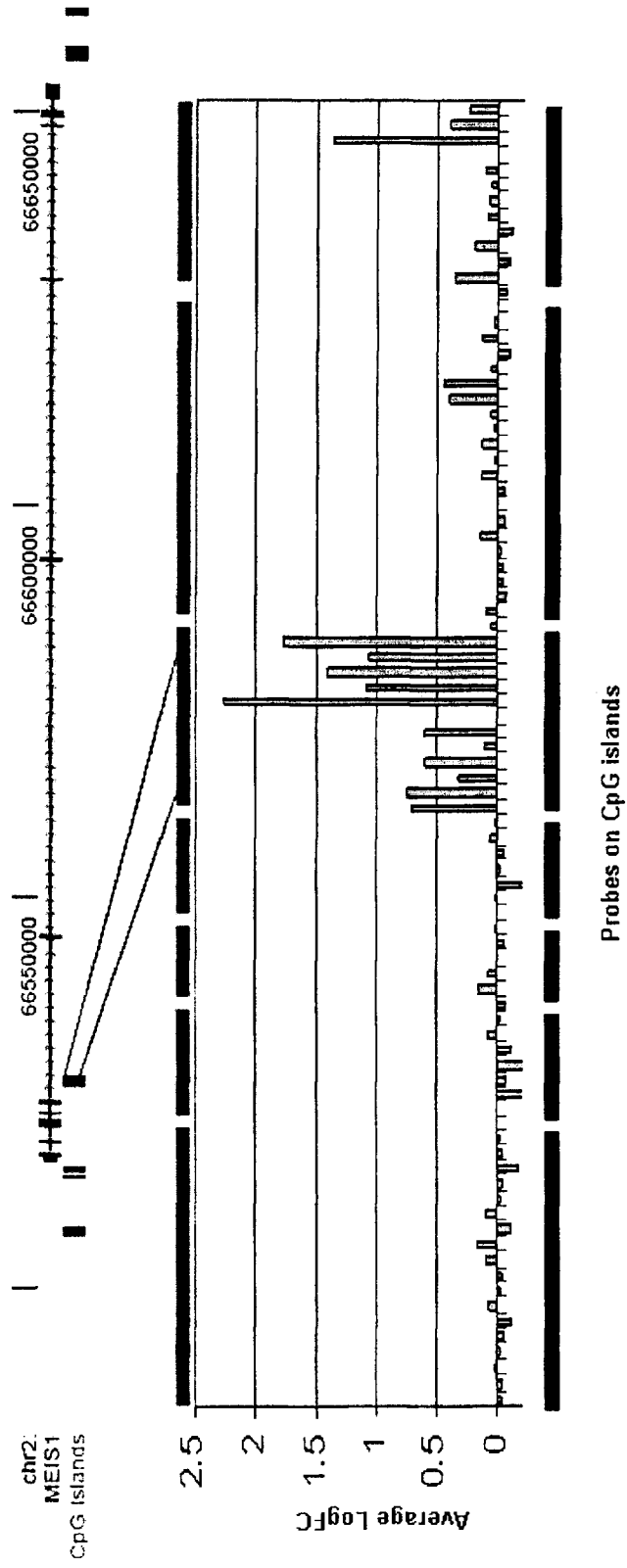


Fig. 1A

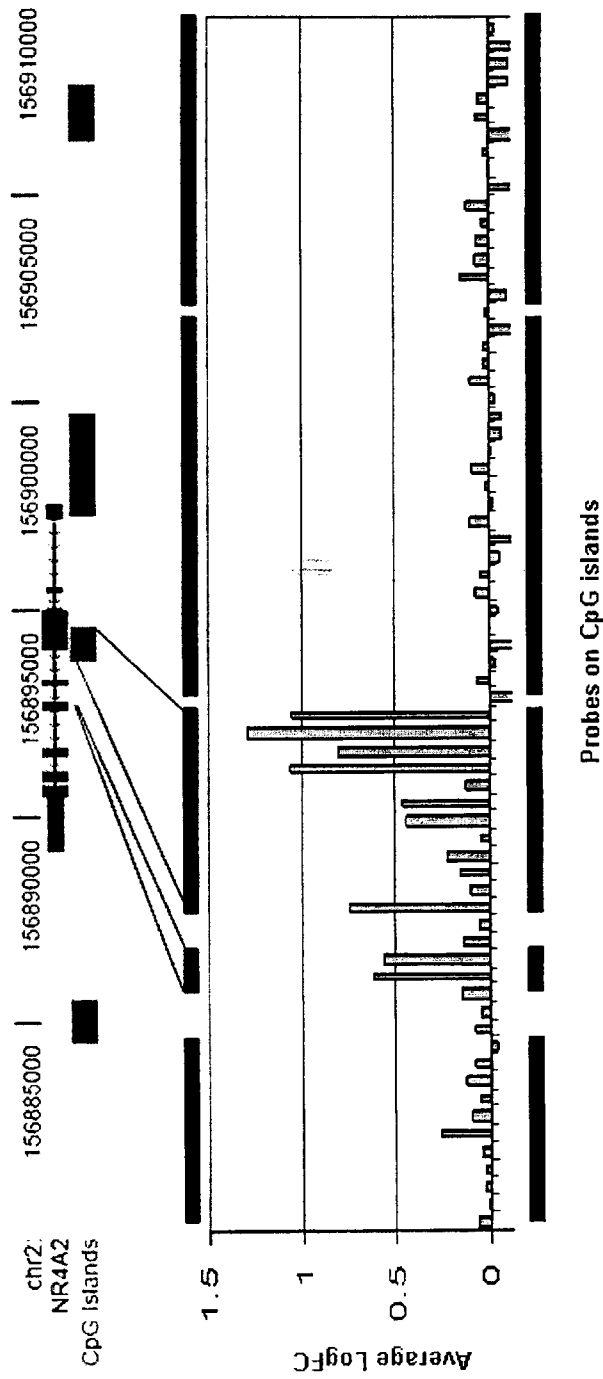


Fig. 1B

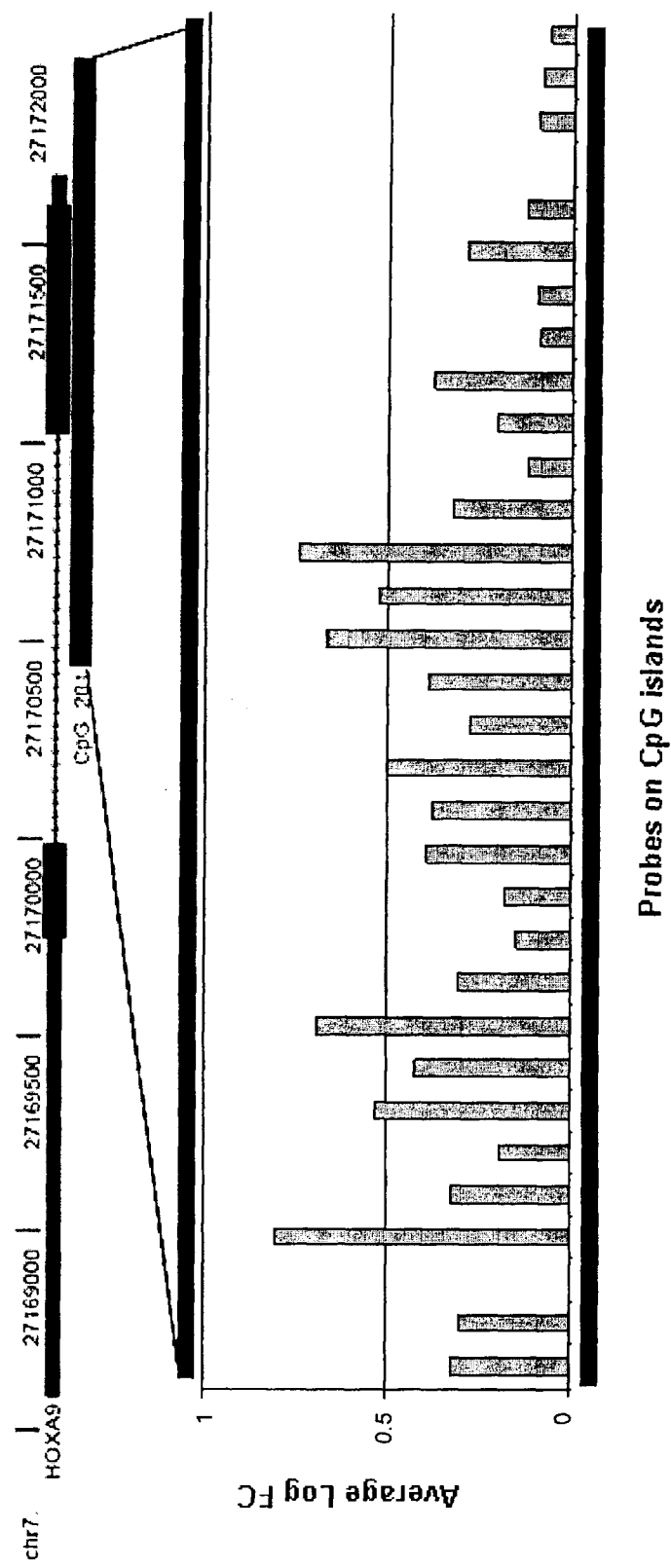


Fig. 1C

4/15

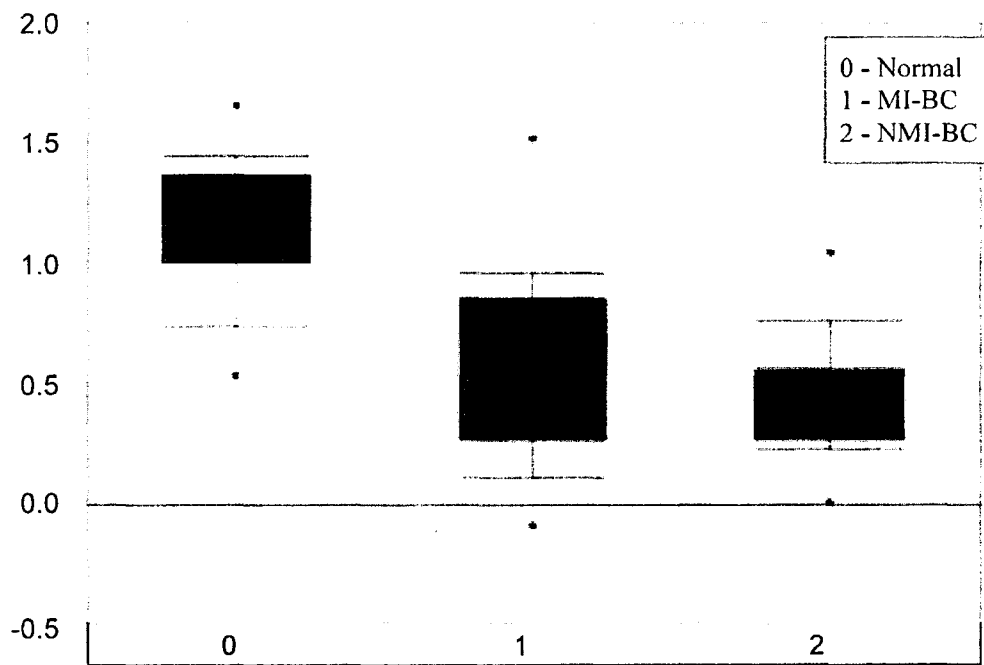


Fig. 1D

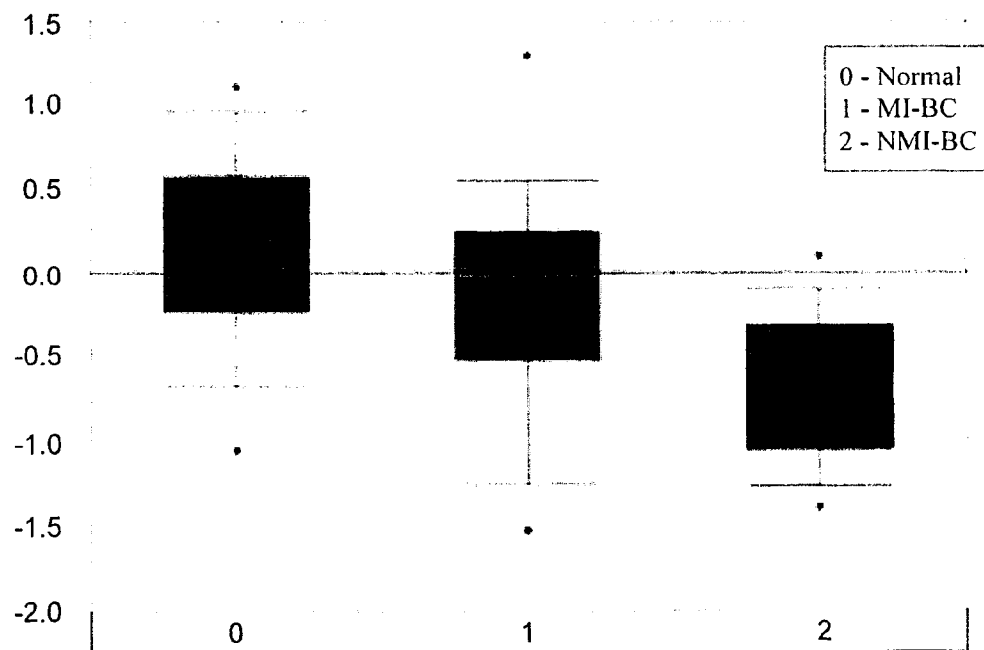


Fig. 1E

5/15

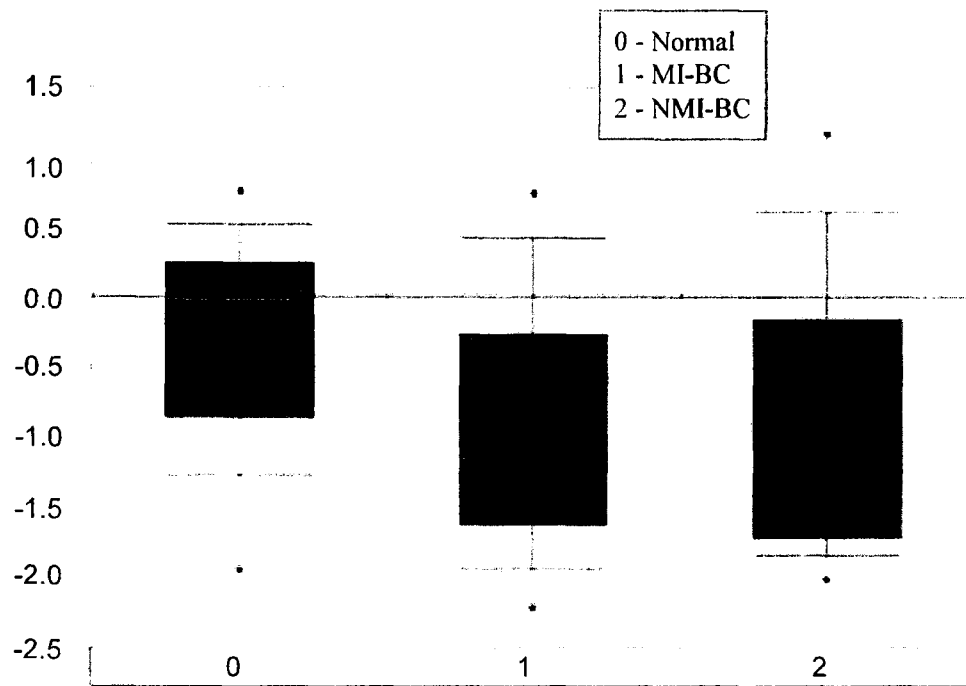


Fig. 1F

6/15

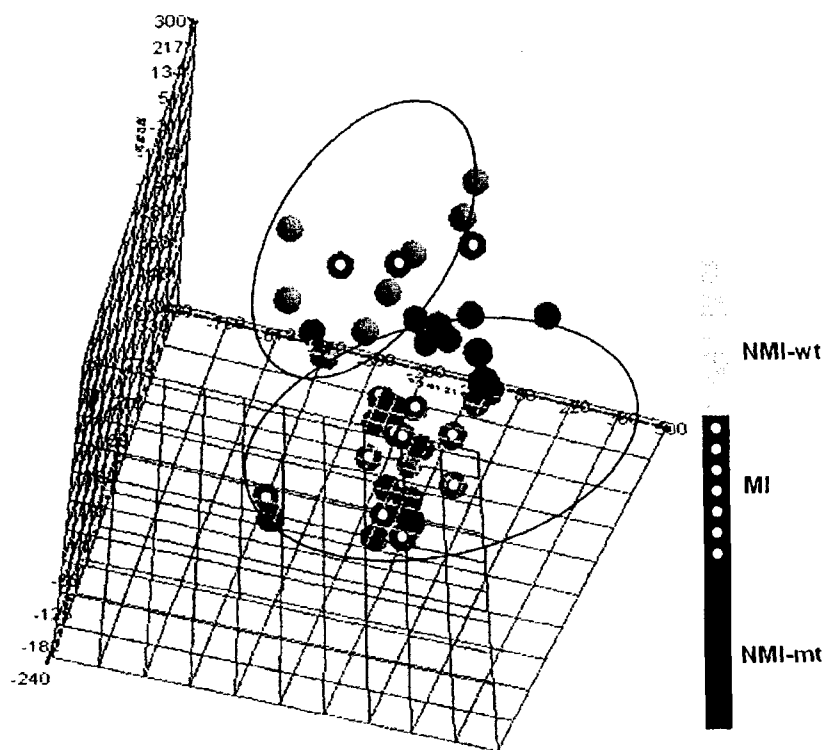


Fig. 2A

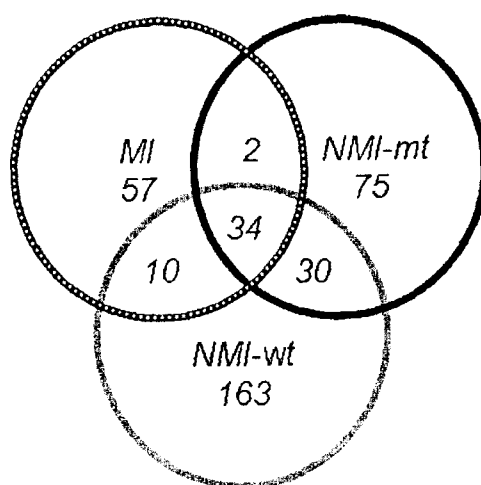


Fig. 2B

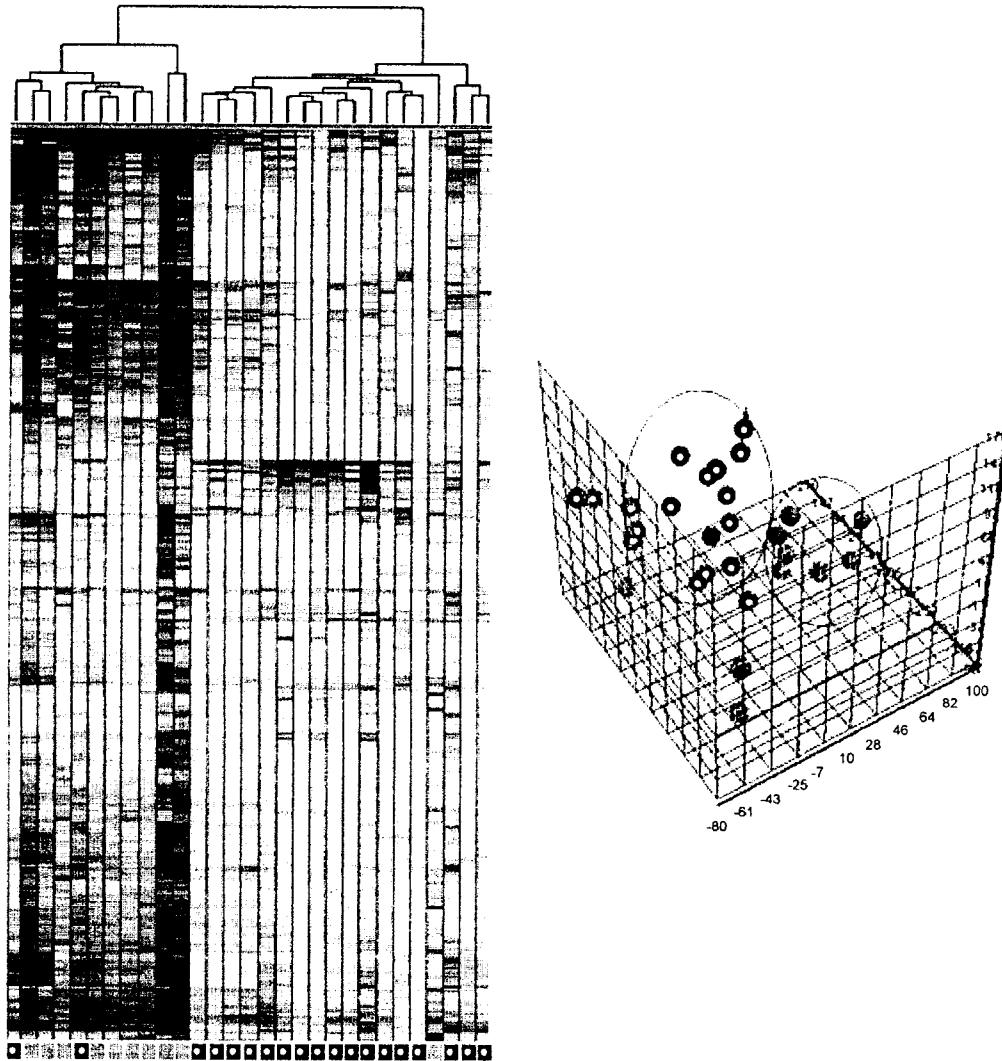


Fig. 3A

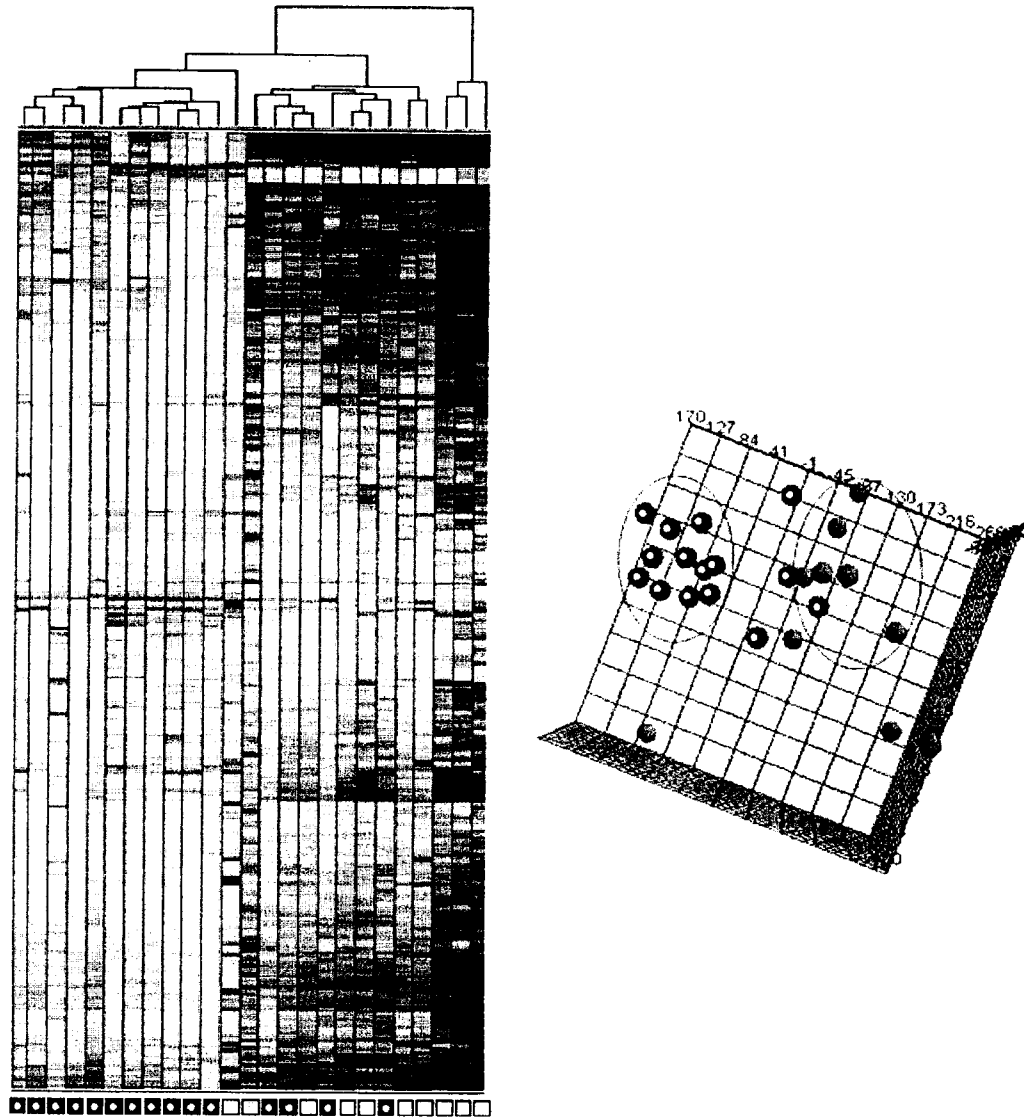


Fig. 3B

9/15

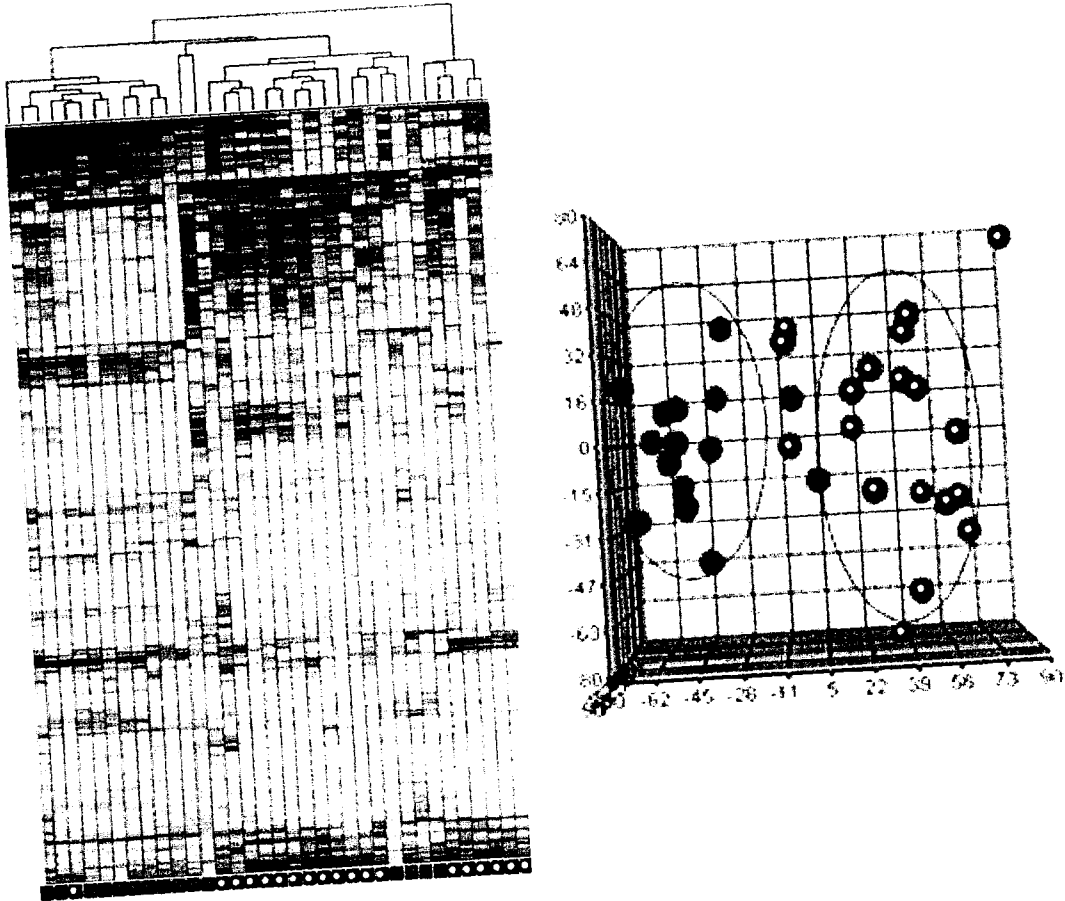


Fig. 3C

10/15

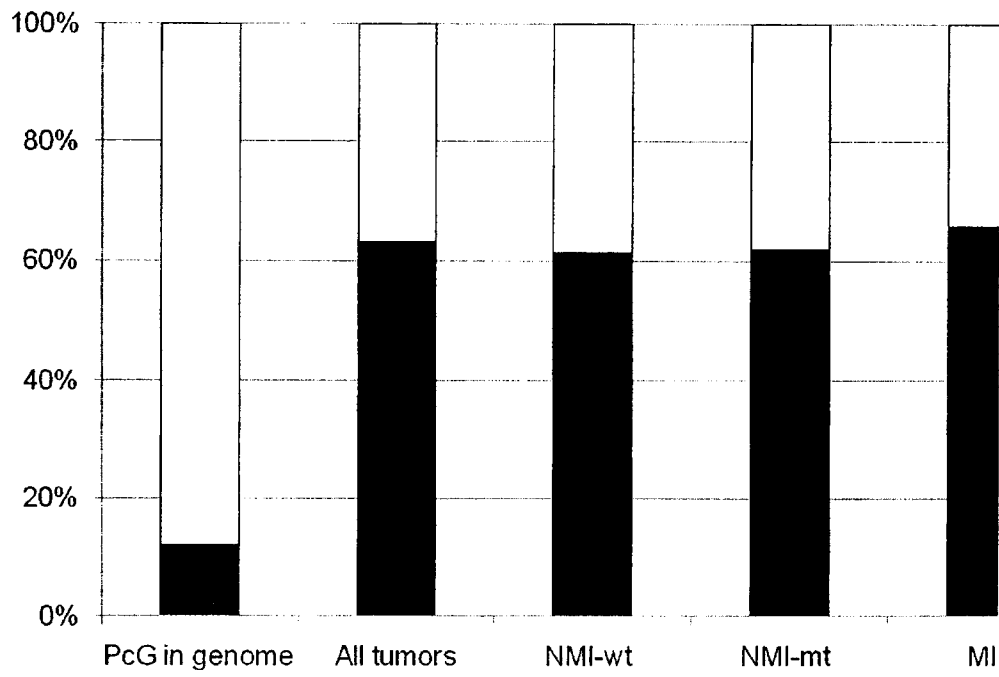


Fig. 4A

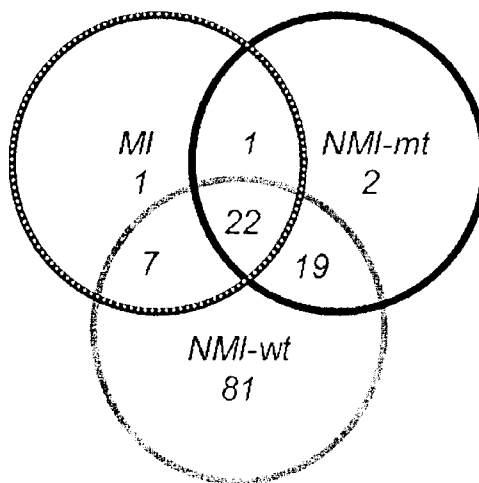
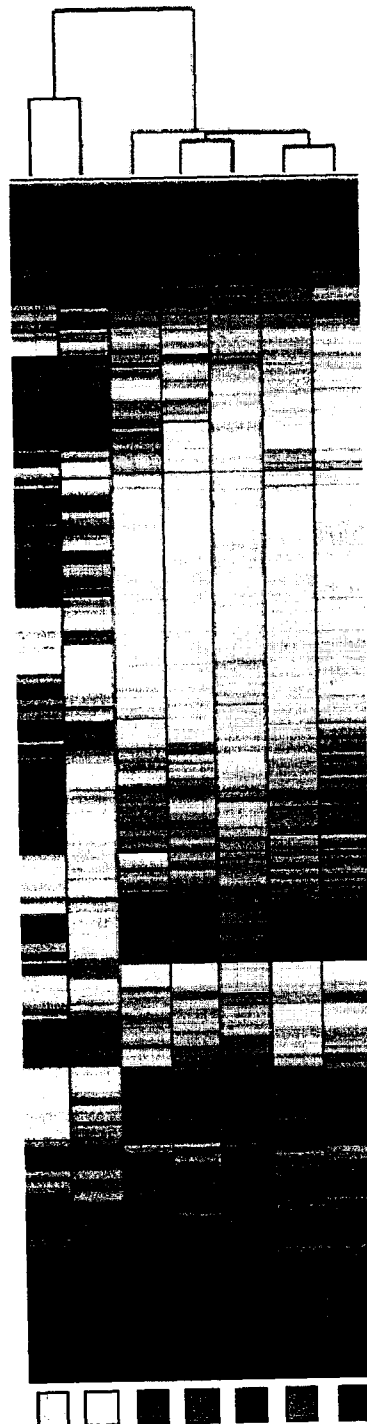


Fig. 4B

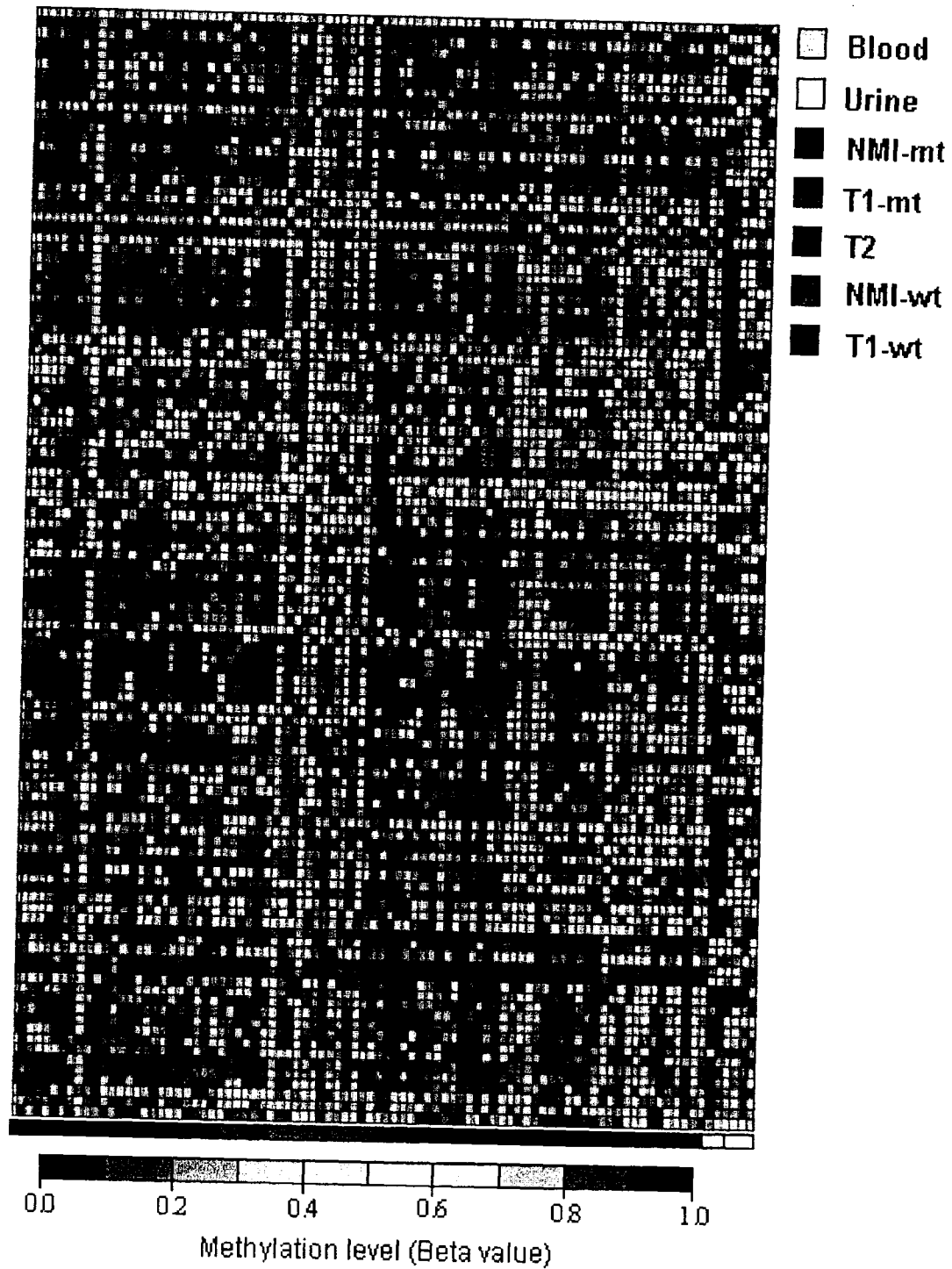
11/15

Fig. 5A



12/15

Fig. 5B



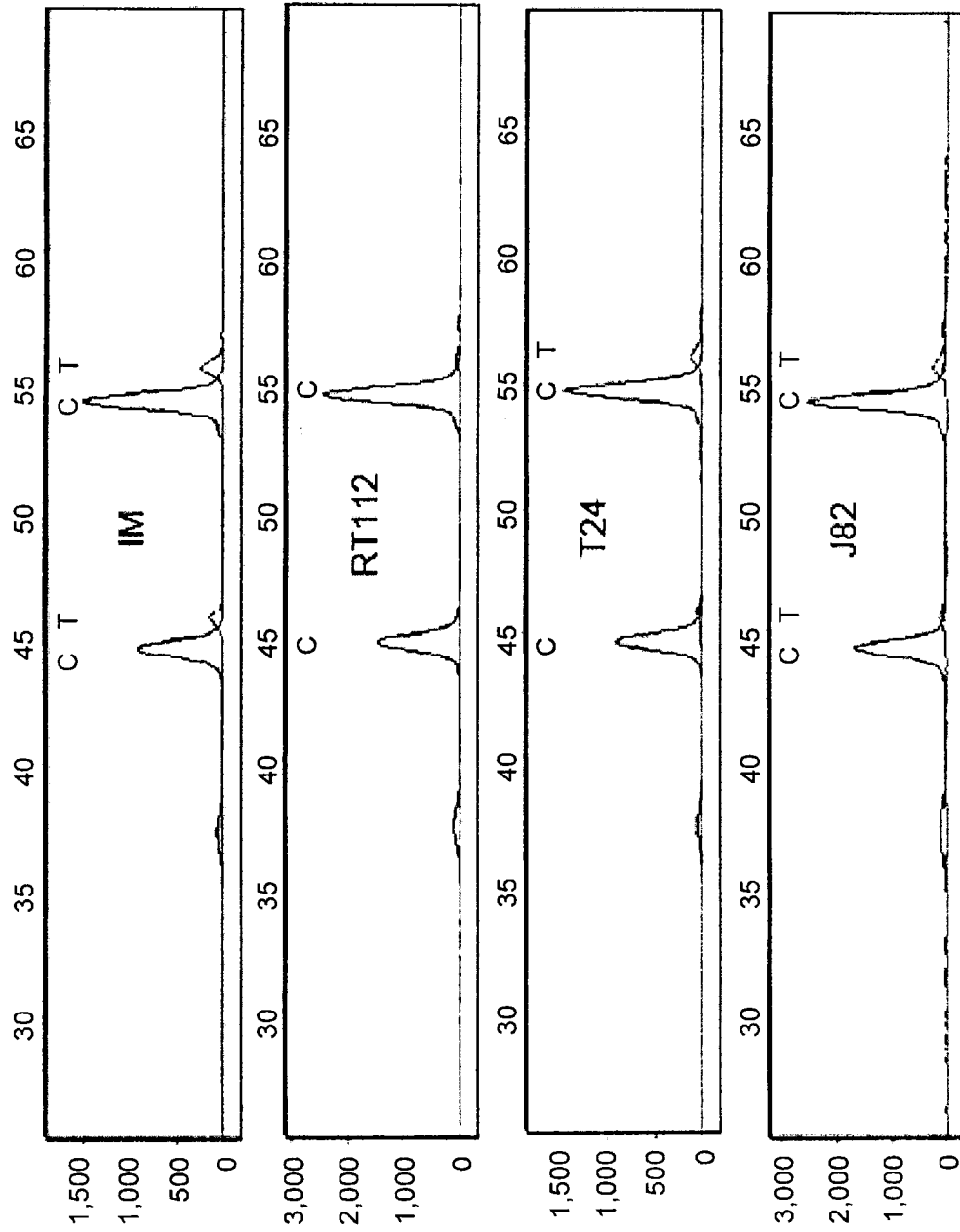


Fig. 5C

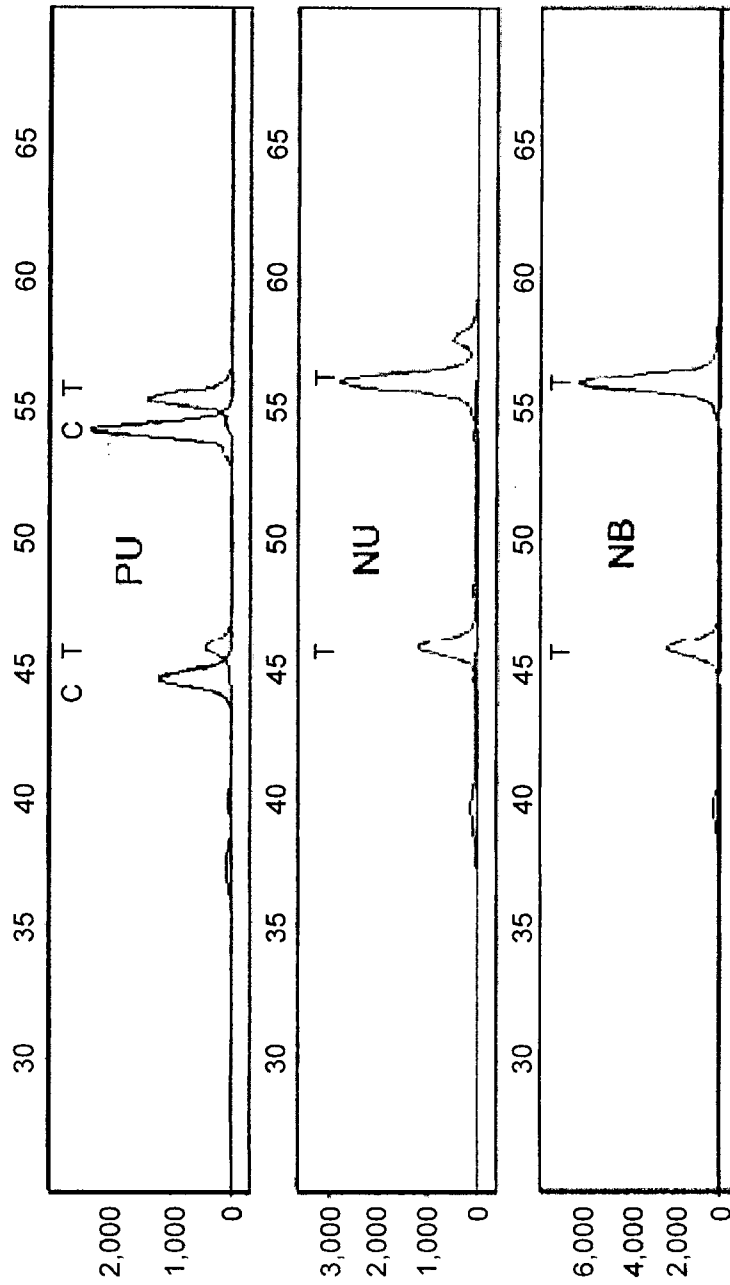


Fig. 5C, cont'd.

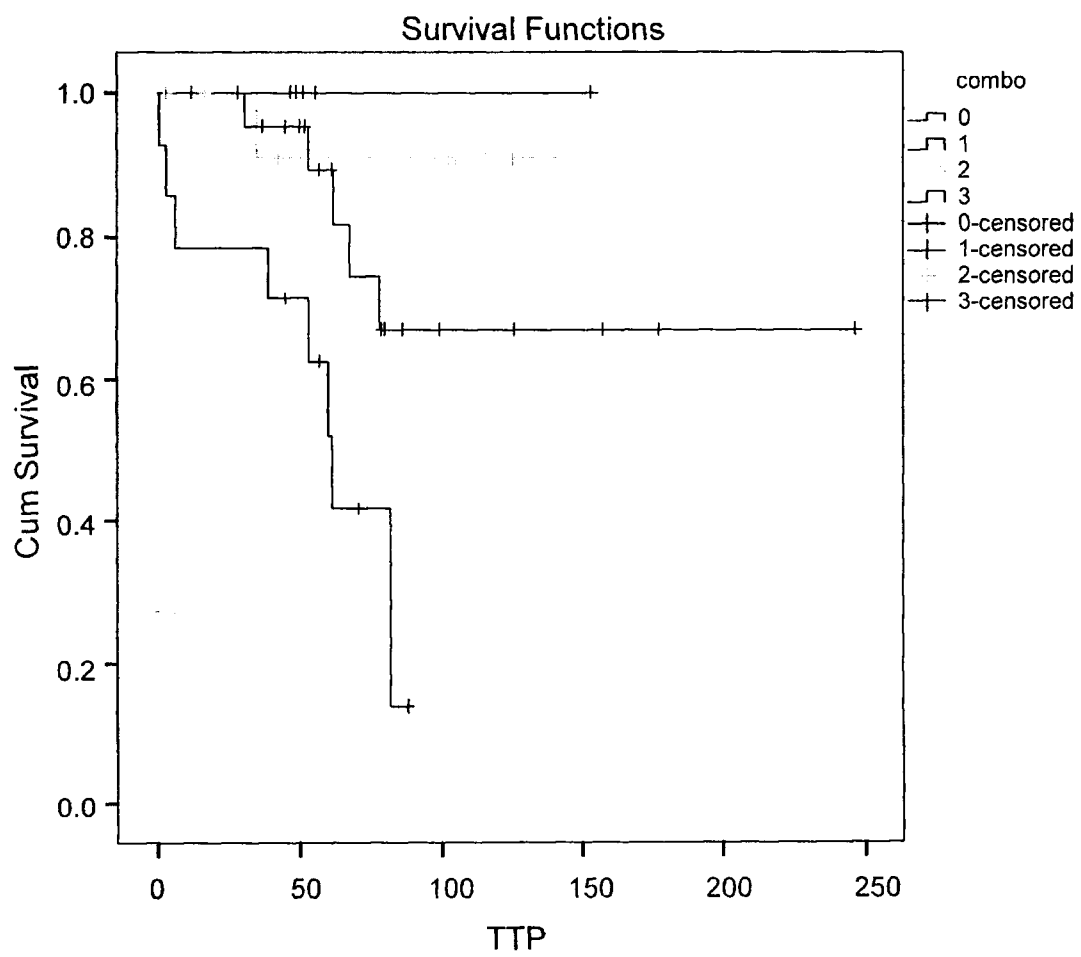


Fig. 5D