diagenode

Innovating Epigenetic Solutions

AUTO MethylCap KIT MANUAL

Auto MethylCap kit x48

New Cat. No. C02020011; Old Cat. No. AF-Auto01-0048

Version 4 I 16.01.14

Technical Assistance & Ordering Information

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Introduction

Overview

Methylation of CpG dinucleotides is generally associated with epigenetic silencing of transcription and is maintained through cellular division. Multiple CpG sequences are rare in mammalian genomes, but frequently occur at the transcriptional start site of active genes, with most clusters of promoter CpGs being hypomethylated (1).

The binding specificity of the H6-GST-MBD fusion protein to un-, hemi- and fully methylated DNA was evaluated using synthetic DNA that either contained three methylated CpGs (GAM3), three hemimethylated CpG's or no methylated CpGs (GAM). Hemimethylated DNA does not stably interact with the MBD of MeCP2. A single fully methylated CpG is sufficient for the interaction between the H6-GST-MBD fusion protein and methylated DNA, whereas there is little binding to a hemimethylated target sequence (1).

Reference:

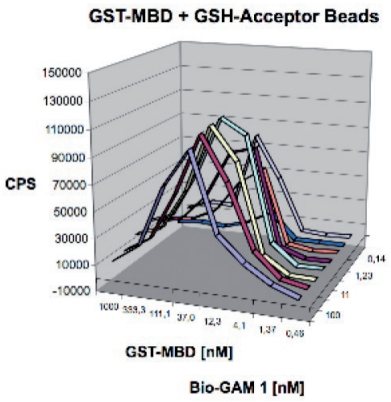
1. Kangaspeska S, Stride B, Métivier R, Polycarpou-Schwarz M, Ibberson D, Carmouche RP, Benes V, Gannon F, Reid G. 2008 Transient cyclical methylation of promoter DNA. Nature 452(7183):112-5.

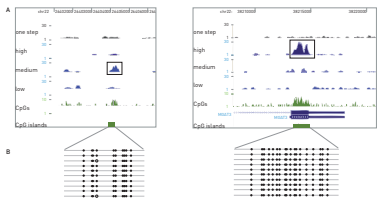
Product description

This H6-GST-MBD fusion protein (cat# mbd-001-100) has been extensively validated. It consists of the methyl binding domain (MBD) of human MeCP2, as a C-terminal fusion with Glutathione-S-transferase (GST) containing an N-terminal His6-tag. The H6-GST-MBD fusion protein can be used to specifically isolate DNA containing methylated CpGs. See overview and protocol below.

GST protein (cat# gst-001-050) can also be purchased, to be used as negative control in the MBD pull-down experiment.

Results of QC on the H6-GST-MBD fusion protein





The Diagenode H6-GST-MBD fusion protein (cat# mbd-001-100) contains two tags: the GST which can bind to GSH and the His6-tag which can bind to nickel. A cross titration of BioGAM1 (oligonucleotide) and the MBD fusion protein was performed using serial dilutions in an alpha-screen assay. Results are shown in the two Figures above. The Figures show the interaction between BioGAM1 and the H6-GST-MBD fusion protein, using the GSH-Acceptor beads (left side). Interaction between BiOGAM1 and the H6-GST-MBD fusion protein is also seen using the Nickel-Acceptor beads (right side).

SX-8G IP-Star® and SX-8G IP-Star® Compact Systems for automation of epigenetic applications

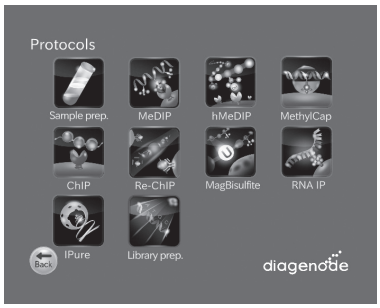
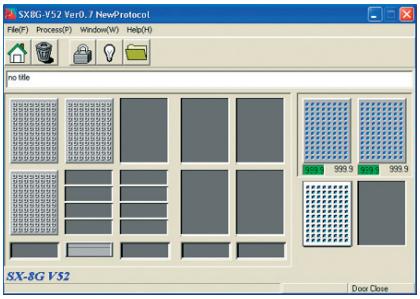
Diagenode has developed two automated platforms (SX-8G IP-Star® and SX-8G IP-Star® Compact) designed to increase your lab's productivity, efficiency and experimental reproducibility. The two automated platforms are capable of processing up to 16 samples per cycle. The automated systems processes sheared chromatin (or DNA) to deliver purified DNA ready for qPCR, amplification, microarray and sequencing analysis. Both, the SX-8G IP-Star® and SX-8G IP-star® Compact have an easy-to-use open software that provides you with flexibility. This allows you to create your personal protocol according to your specific needs.

Major benefits of Diagenode Automated Platforms

SX-8G IP-Star® Compact

SX-8G IP-Star®

- → High resolution ChIP-seq and MeDIP-seq profiles
- → Automated library preparation for Next Generation sequencing
- → Reduces hands on time to just 30 minutes
- → Reduces variability between operators and labs
- → Ideal for low sample starting amounts
- → Compatible with Diagenode Kits (Auto ChIP kit, Auto Histone ChIP-seq kit, Auto Histone ChIP-seq kit, Auto MeDIP kit, Auto MethylCap kit, Auto hMeDIP, Auto IPure kit)
- → Reduces cross-contamination

	SX-8G IP-Star® Compact	SX-8G IP-Star®
Applications	**ChIP-seq, MeDIP-seq, MethylCap-seq, hMeDIP, IPure, Sample preparation, Re-ChIP, MagBisulfite, RNA-IP, Library preparation for NGS platforms.**	**ChIP-seq, MeDIP-seq, MethylCap-seq, hMeDIP, IPure, Sample preparation, Re-ChIP, MagBisulfite, RNA-IP.**
Software		
User interface	Intuitive touch screen panel	PC Software
User friendly	Software training not required	Software training before use
Dispensing	Automated dispension of assay reagents	Manual dispension of assay reagents
Protocol optimization (flexible parameters)	Antibody coating (temperature, time, mixing speed) Immunoprecipitation (temperature, time, mixing speed) Washes (temperature, time, mixing speed)	Antibody coating (temperature, time) Immunoprecipitation (temperature, time)
New protocol development	Achievable by Diagenode product specialist	Achievable by customer after training
Characteristics	750W x 740 D x 610 H | 100 kg 8 Nozzles X-Y-Z axis | 4 – 95°C	1070W x 650 D x 780 H | 130 kg 8 Nozzles X-Y-Z axis | 4-95°C

Improved reproducibility

Our SX-8G IP-Star will increase the immunoprecipitation reproducibility between IPs performed by the same as well as by different operators (see figure 1 and 2 below). Reagents (Antibodies, buffers,...) and sheared chromatin were identical for "ManChIP" and "AutoChIP". The SX-8G IP-Star Automated system removes variation that can be created by manual handling and allows you to optimize and standardize your assay within a lab. The SX-8G IP-Star is designed to improve the accuracy and the reproducibility of any immunoprecipitiation experiment.

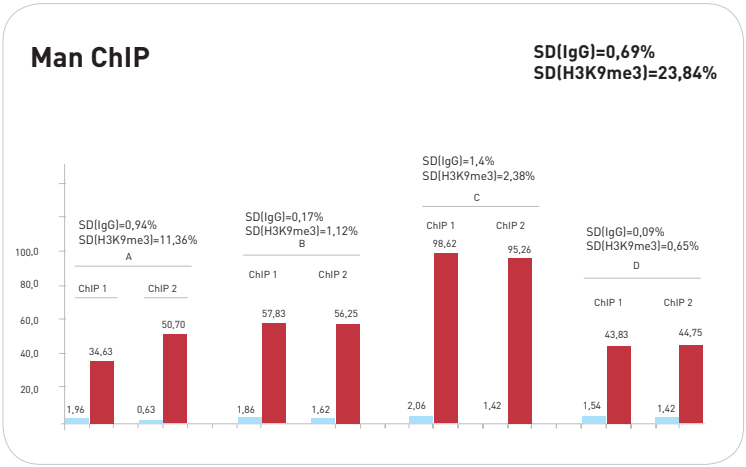


Figure 1: Manual ChIP. Four different operators have each performed two ChIP experiments using H3K9me3 antibody on the genomic region SAT2 (positive locus). 10,000 Hela cells have been used per IP. Reagents and sheared chromatin were identical per assay. The standard deviations between the ChIPs performed by the same operator and between the four different operators are displayed.

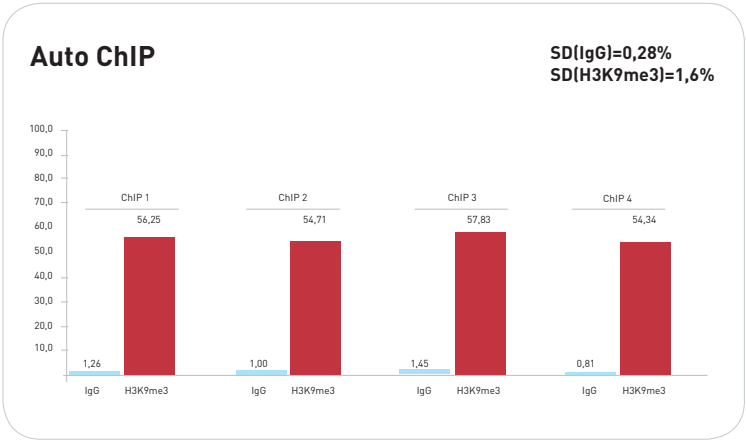
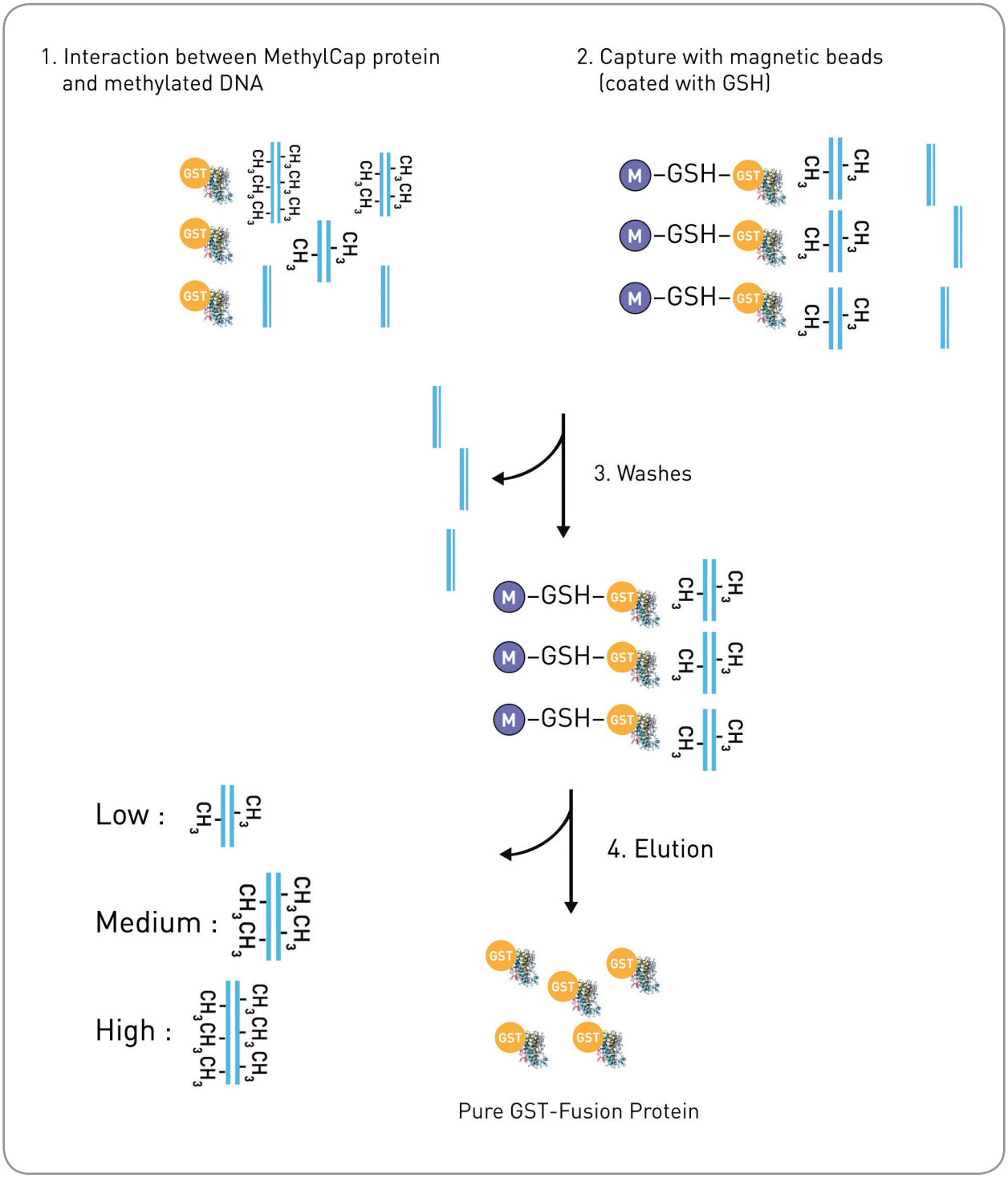


Figure 2: Automated ChIP. Four ChIP experiments using H3K9me3 antibody on the genomic region SAT2 (positive locus) have been performed by the SX-8G IP-Star. 10,000 Hela cells have been used per IP. Reagents and sheared chromatin were identical per assay. The standard deviations between the four ChIPs performed by the SX-8G IP-Star are displayed.

Kit Method Overview



Kit Materials

Kit Content

Table 1. Kit content

meDNA Capture Module (48 reactions)			
Component	Description	Format	Storage
Buffer A (Fusion protein Dilution)		100 µl	4°C
Buffer B (Capture)		40 ml	4°C
Wash Buffer 1		16 ml	4°C
Wash Buffer 2		32 ml	4°C
MethylCap Beads	Do not freeze	1700 µl	4°C
H6-GST-MBD		11 µl	-20°C/-80°C
Low Elution Buffer		16 ml	4°C
Medium Elution Buffer		16 ml	4°C
High Elution Buffer		32 ml	4°C
hum meDNA primer pair (TSH2B)		500 µl	-20°C
hum unDNA primer pair (GAPDH)		500 µl	-20°C

Table 2. Components available separately

Component	Description	Format	Storage
hum meDNA primer pair (TSH2B)	pp-1041-500	500 µl	-20°C
hum unDNA primer pair (GAPDH)	pp-1044-500	500 µl	-20°C
mouse meDNA primer pair (TSH2B)	pp-1042-500	500 µl	-20°C
mouse unDNA primer pair (GAPDH)	pp-1045-500	500 µl	-20°C
rat meDNA primer pair (TSH2B)	pp-1043-500	500 µl	-20°C
rat unDNA primer pair (GAPDH)	pp-1046-500	500 µl	-20°C
H6-GST-MBD-protein	Mbd-001-050	50 rxns	-20°C/-80°C
GST protein	Gst-001-050	25 rxns	-20°C/-80°C
200 µl tube strips (12 tubes/strip) + cap strips	WA-001-0080	80	RT
200 µl tube strips (8 tubes/strip) + cap strips for SX-8G IP-Star® Compact	WA-002-0120	120	RT
Tips (bulk)	WC-001-1000	1000	RT
Tips (box)	WC-002-0960	10x96	RT

Table 3. Modules available separately

Description	Comments	Reference	Quantity
XL GenDNA Extraction Module	For easy and fast DNA extraction	mc-magme-003	60 rxns

How to prepare Automated MethylCap in the SX-8G IP-Star®

A) Prepare reagents

1. Prepare H6-GST-MBD protein

   a. Thaw on ice the H6-GST-MBD fusion protein.

   b. Keep the H6-GST-MBD fusion protein on ice and add 44 µl of buffer A (fusion protein dilution). Vortex, for 5 seconds, at medium power (4°C).

   - Make 5 aliquots of 11 µl (10 capture reactions per aliquot) to avoid multiple freeze-thaw cycles.
   - Store quickly at -80°C

2. Prepare DNA mix tube without H6-GST-MBD fusion protein

   a. In a new 1.5 ml tube, prepare the capture reaction mix without H6-GST-MBD fusion protein. For one reaction, see volume needed below (Table1). Vortex for 5 seconds, at medium power and keep on ice.

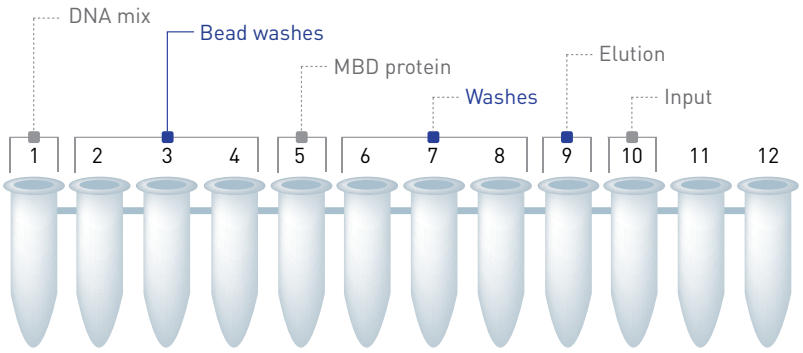
Reagent	Volume per capture reaction and INPUT sample (1 µg of DNA)
Sheared DNA (0.1 µg/µl)	12 µl
Buffer B	129.8 µl
TOTAL VOLUME	141.8 µl

B) Dispense prepared reagents into the corresponding tubes

Loading reagents: make sure that all reagents are in the bottom of the tubes (especially magnetic beads) before starting the protocol.

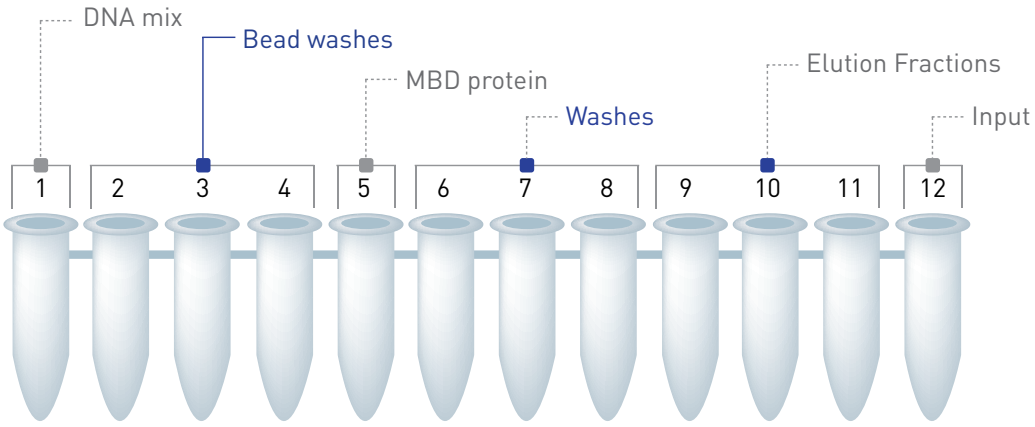
a. One Elution Protocol

Tube #	Description	Volume
1	DNA mix	119 µl
2	Buffer B (120 µl) + beads (30 µl)	150 µl
3	Buffer B	150 µl
4	Buffer B	150 µl
5	Buffer B + GST-MBD (1 µl)	50 µl
6	Wash Buffer 1	150 µl
7	Wash Buffer 2	150 µl
8	Wash Buffer 2	150 µl
9	High Elution Buffer	150 µl
10	High Elution Buffer (input)	138.1 µl
11	-	-
12	-	-



b. Fractionated Elution Protocol

Tube #	Description	Volume
1	DNA mix	119 µl
2	Buffer B (120 µl) + beads (30 µl)	150 µl
3	Buffer B	150 µl
4	Buffer B	150 µl
5	Buffer B + GST-MBD (1 µl)	50 µl
6	Wash Buffer 1	150 µl
7	Wash Buffer 2	150 µl
8	Wash Buffer 2	150 µl
9	Low Elution Buffer	150 µl
10	Medium Elution Buffer	150 µl
11	High Elution Buffer	150 µl
12	High Elution Buffer (input)	138.1 µl



Loading and running protocol

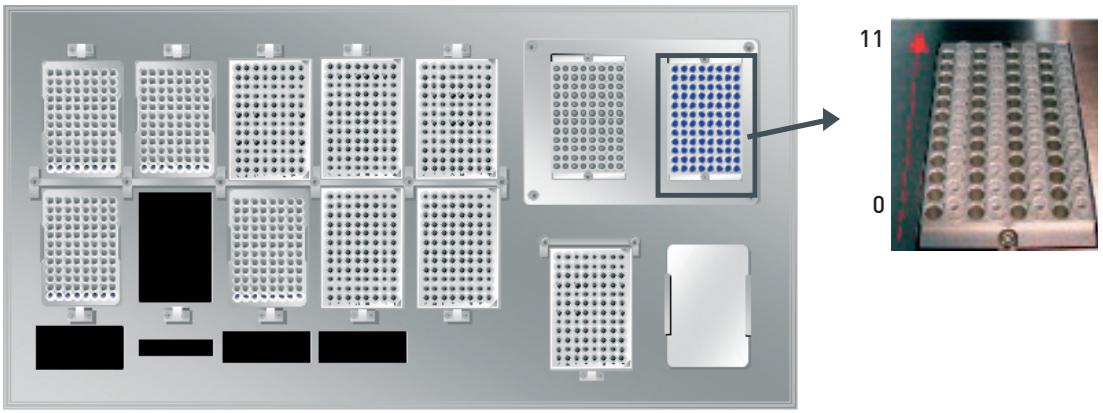
Be sure that the computer connected to the robot never switches to the standby modus. (standby modus has to be inactivated). Standby of the computer will lead to the abort of the protocol.

Table 3.

Protocol Name	Elution	Fractionated Protocol
Reagent Preparation*	30 min	30 min
Magnetic Bead Washes	20 min	20 min
MBD DNA Binding	2h	2h
Complex capture	1h	1h
Washes	30 min	30 min
Elution	20 min	50 min
Total Time	**4h40 min**	**5h10 min**
* Input required is sheared DNA ready-to-MethylCap		

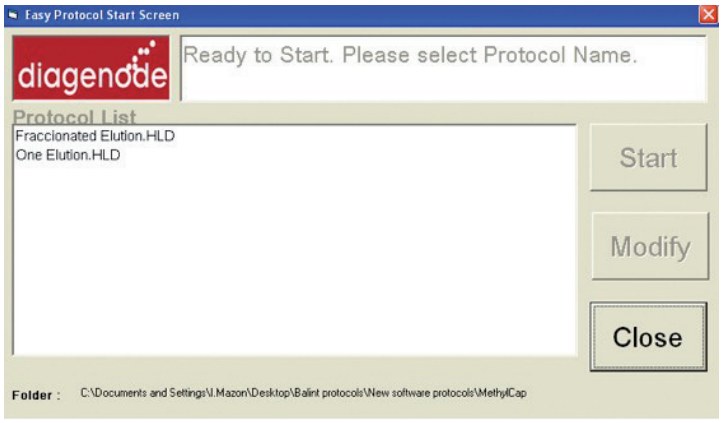
Note: Hands-on-work time is reduced to 30 min !

1. Switch on the IP Star. The power switch is on the right side of the instrument.
2. Switch on the computer.
3. Start SX-8G V52 software through SX-8G V52 the following icon 
4. Place the prepared tube strip on the right cooling / heating block of the workstation

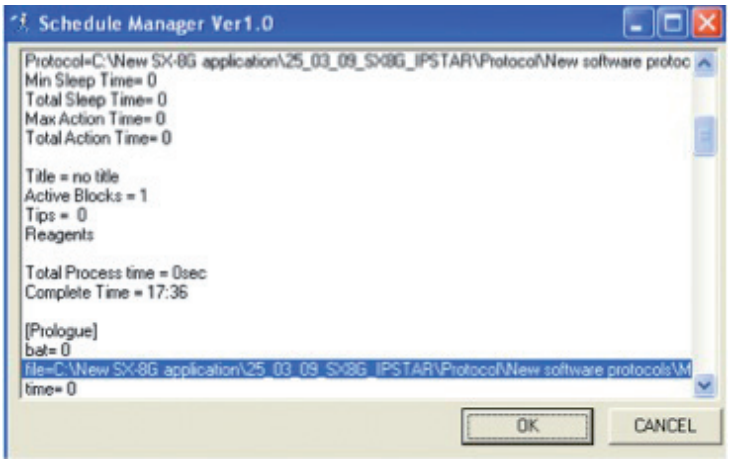


5. Close the workstation door and lock it using the following icon 
6. Press the following icon 

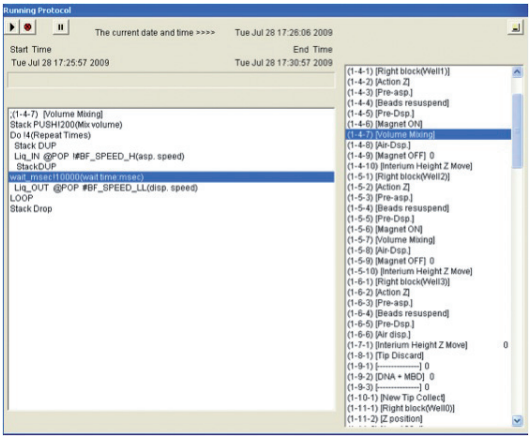
   Select the protocol of interest. Press start.



Before starting the protocol a start confirmation window will appear. Press OK and the protocol will run.



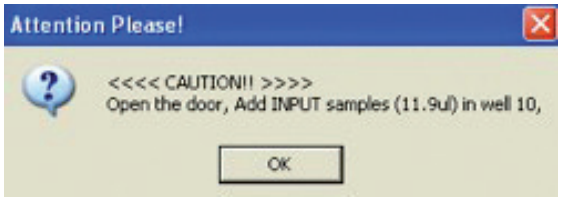
7. The program will run through the following steps: magnetic bead washes, IP and IP washes.



During protocol the next window will be displayed indicating the current protocol step.

8. After the IP washes the following window will be appear.

One Elution Protocol



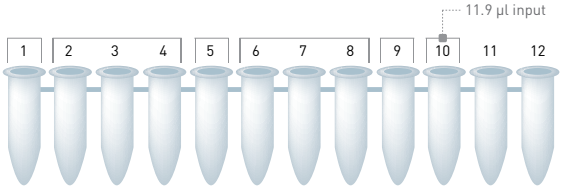
Fractionated Elution Protocol

Follow the next instructions:

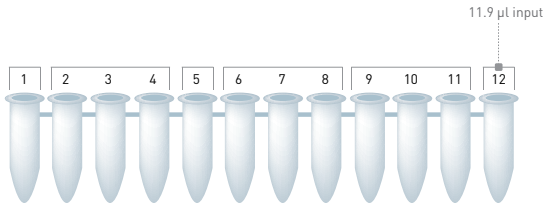
1. Add 11.9 µl DNA Mix (input)

2. Press OK

One Elution Protocol



Fractionated Elution Protocol



9. The following window will appear:

Close the workstation door and press OK.

The program will move forward to the next steps of the MethylCap protocol.

10. The IP-Star software indicates the end of the protocol.

Collect your immunoprecipitated and isolated DNA.

11. Discard magnetic beads by using the DiaMag02 (cat# kch-816-001) or by centrifugation.

12. Purification of all fractions and INPUT by using one of the following techniques:

- Purification using Phenol/Chloroform/Isomamyl alcohol (see additional protocol for instructions).
- The QIAquick PCR purification columns (QIAGEN cat# 28106).
- The DNA Clean & Concentrator™-5 (ZYMO RESEARCH cat# D4003S).

Shutting down the IP-Star

1. Click on File and press End to close the software correctly.
2. Switch off the computer and its monitor.
3. Switch off the IP-Star Robot (power switch on the right side).

Note: Ensure that the door is closed!

How to perform Automated MethylCap in the SX-8G IP-Star® Compact

Prepare reagents

1. Prepare H6-GST-MBD protein

   a. Thaw on ice the H6-GST-MBD fusion protein.

   b. Keep the H6-GST-MBD fusion protein on ice and add 44 µl of buffer A (fusion protein dilution). Vortex, for 5 seconds, at medium power (4°C).

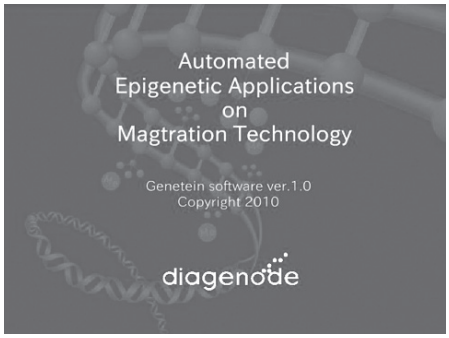
   - Make 5 aliquots of 11 µl (10 capture reactions per aliquot) to avoid multiple freeze-thaw cycles.
   - Store quickly at -80°C

2. Prepare DNA mix tube without H6-GST-MBD fusion protein

   a. In a new 1.5 ml tube, prepare the capture reaction mix without H6-GST-MBD fusion protein. For one reaction, see volume needed below (Table1). Vortex for 5 seconds, at medium power and keep on ice.

Reagent	Volume per capture reaction and INPUT sample (1 µg of DNA)
Sheared DNA (0.1 µg/µl)	12 µl
Buffer B	129.8 µl
TOTAL VOLUME	141.8 µl

Running a protocol



Diagenode Splash Screen – A0

After the software start-up screen disappears, the Diagenode splash screen is displayed for several seconds, and then disappears.

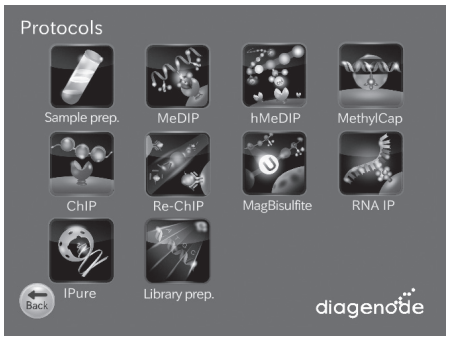
Start Screen – Top menu

After the Digenode splash screen disappears, the start screen is displayed. This is the first active window; it allows the user to enter into three different parts of the software.

USER ACTIONS:

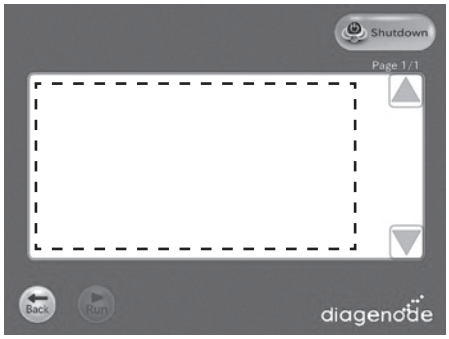
Buttons:

- Protocols
- Maintenance (for technical service)
- Information (Diagenode contact details)



Protocols screen

All available protocols are displayed on this screen.

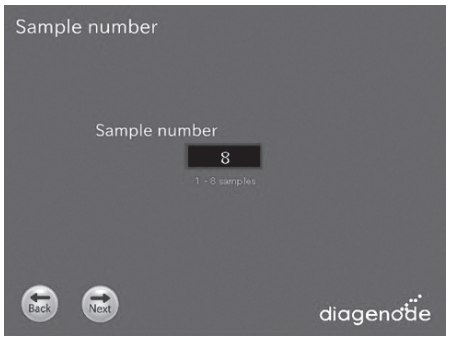


Screen – [Categories Name] Protocol List

After the user presses the "[Categories Name]" button, the "[Categories Name]" appears. When selected the protocol on the protocol list, the "Run" button shall turn executable.

Buttons:

- The user presses the "Back" button. The user returns to the "Protocols" screen.
- The user presses the "Shutdown" button. The screen shall be changed to "Power Off".
- The user presses the "Run" button. The screen shall be changed to "Sample number".
- ▲ Page up the list box.
- ▼ Page down the list box

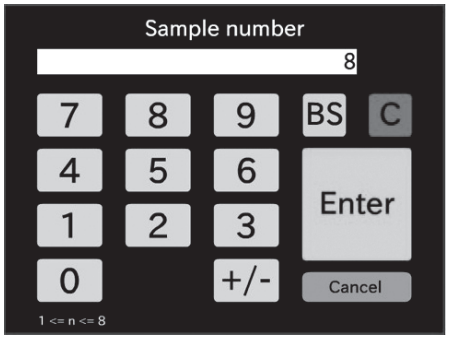


Screen – Sample number

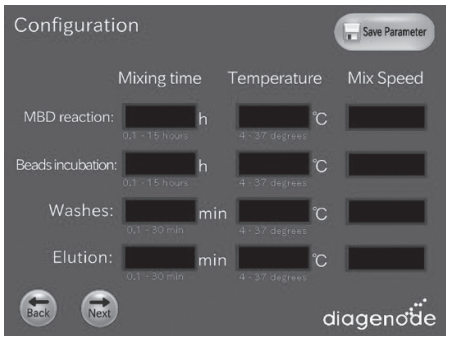
After the user presses the "Run" button, the "Sample number" appears.

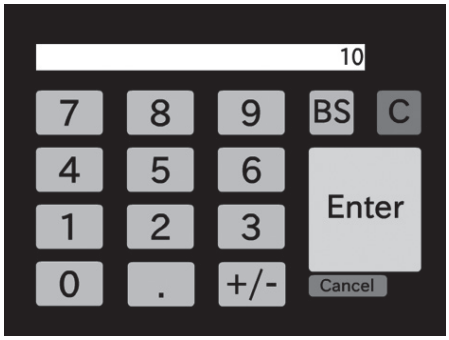
Buttons:

- The user presses the "Sample number" Text box. The screen will be changed to keyboard.
- The user presses the "Back" button. The user returns to the "Protocol List" screen.
- The user presses the "Next" button. The screen shall be changed to "Configuration" or "Layout information".

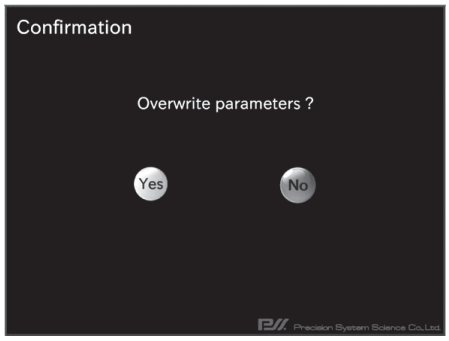


Keyboard





Keyboard



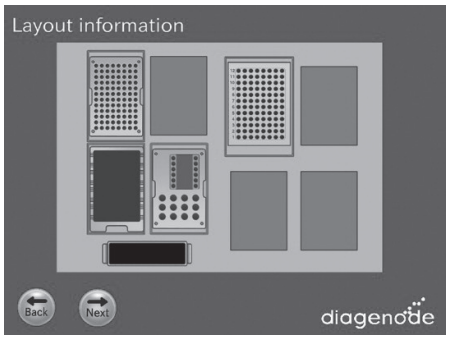
Screen – Configuration

After the user presses the next button from the "Sample number" screen, the "Configuration" screen appears.

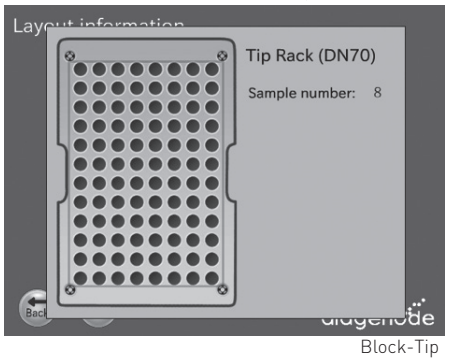
Buttons:

- The user presses the "Back" button. The user returns to the "Protocol List" screen.
- The user presses the "Next" button. The screen shall be changed to "Layout information".
- The user presses the "Save Parameter" button. The screen will be changed to "Save Parameter - Confirmation".
  - OK – Current parameters shown in the Display View will be stored to the [Protocol].ptd. And, returns the user to the display of the "Configuration" screen.
  - No – Returns the user to the display of the "Configuration" screen.
- The user presses the Text box. The screen will be changed to Keyboard or Speed list menu.

Speed list menu



Layout information



Block-Tip

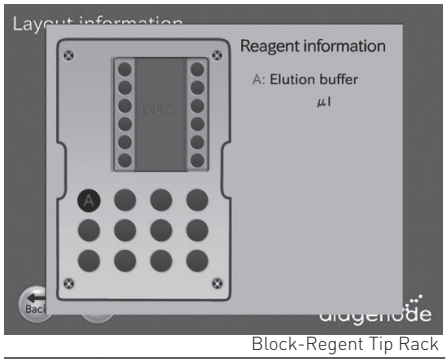
Screen – Layout Information

After the user presses the "next" button from "Sample number" screen or "Configuration" screen, the "Layout Information" screen appears.

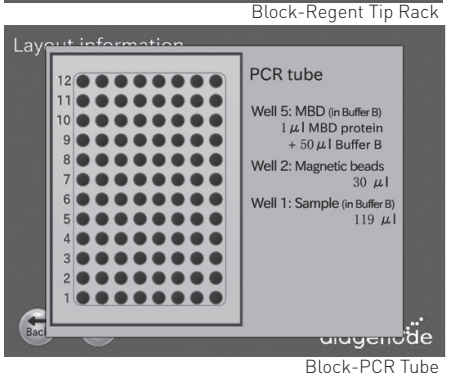
Buttons:

- The user presses the "Back" button. The user returns to the previous screen.
- The user presses the "Next" button. The screen changed to "Set confirmation".
- When the user presses a block, that block is magnifies on the work surface layout background. The magnified view provides a better display of the correct method setup for that block on the work surface.
- Based on the selected protocols, the user follows the indications provided in the screens to set up correctly the different reagents and samples.

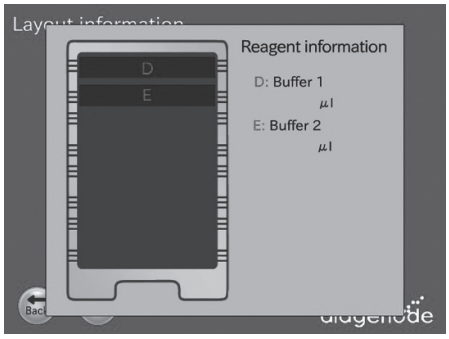
ONE ELUTION



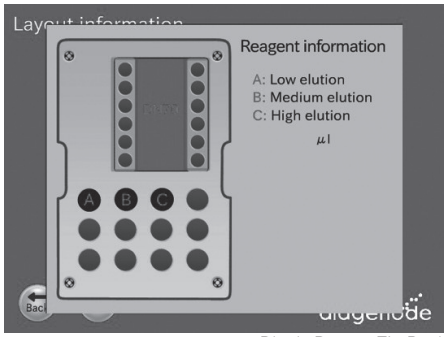
Block-Regent Tip Rack



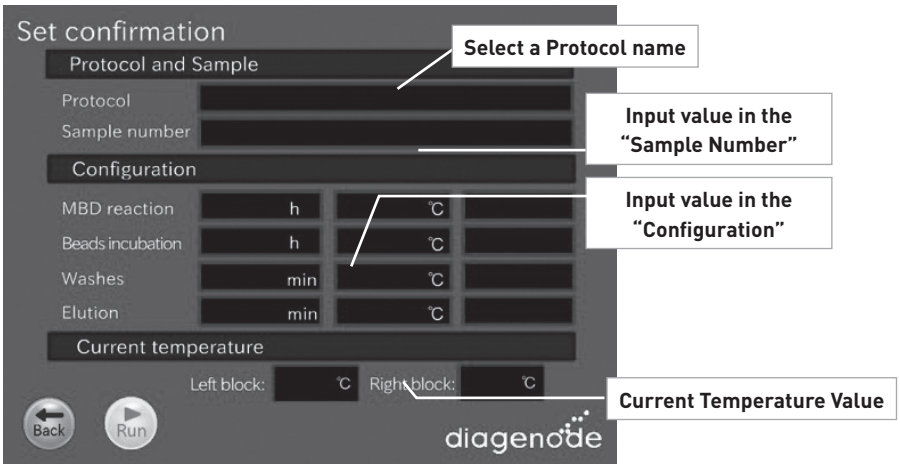
Block-PCR Tube



FRACTIONATED ELUTION



Block-Regent Tip Rack



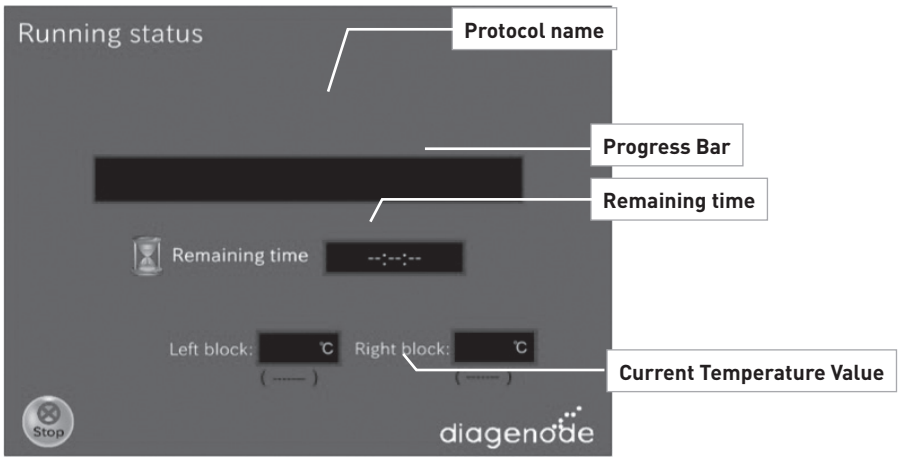
Screen – Set confirmation

After the user presses the "next" button in the "Layout information" screen, the "Set confirmation" screen appears.

At this point, user is expected to be ready to press RUN.

Buttons:

- The user presses the "Back" button. The user returns to the Layout information screen.
- The user presses the "Run" button. This is the expected action when user gets to this display after reviewing blocks. Runs the protocol.



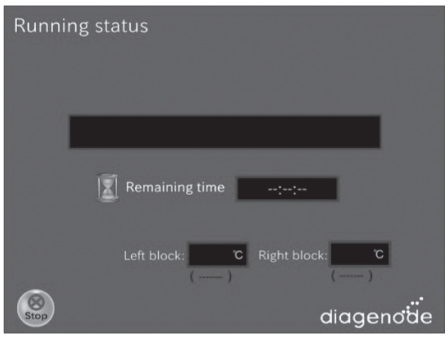
Screen – Running

After the user presses the "Run" button in the "Set confirmation" screen, the "Running" screen appears.

Buttons:

- The user presses the "Stop" button. The screen changes to "Stop Dialog".

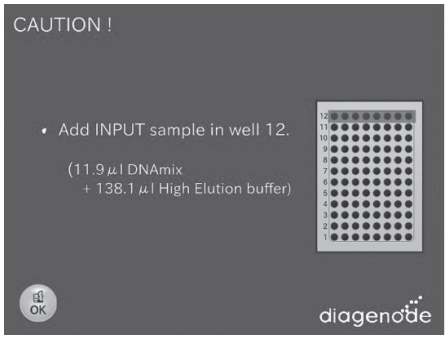
Status screen is preferred as a progress bar that moves across the screen as the step progresses

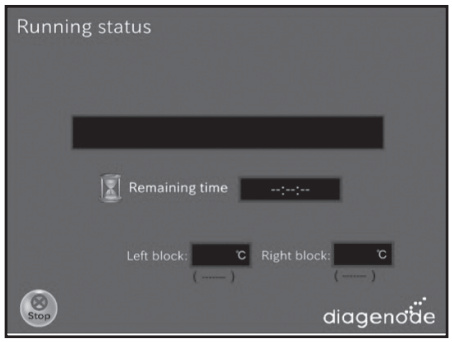


Screen – Running status

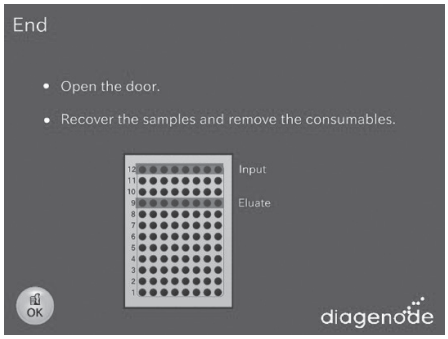
This screen gives informations about the current running step of the protocol.

The user can check through this screen the passed and remaining time of the experiment.

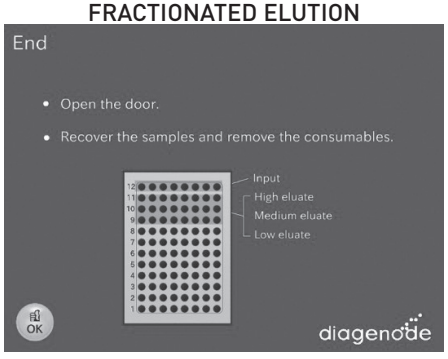




ONE ELUTION



FRACTIONATED ELUTION



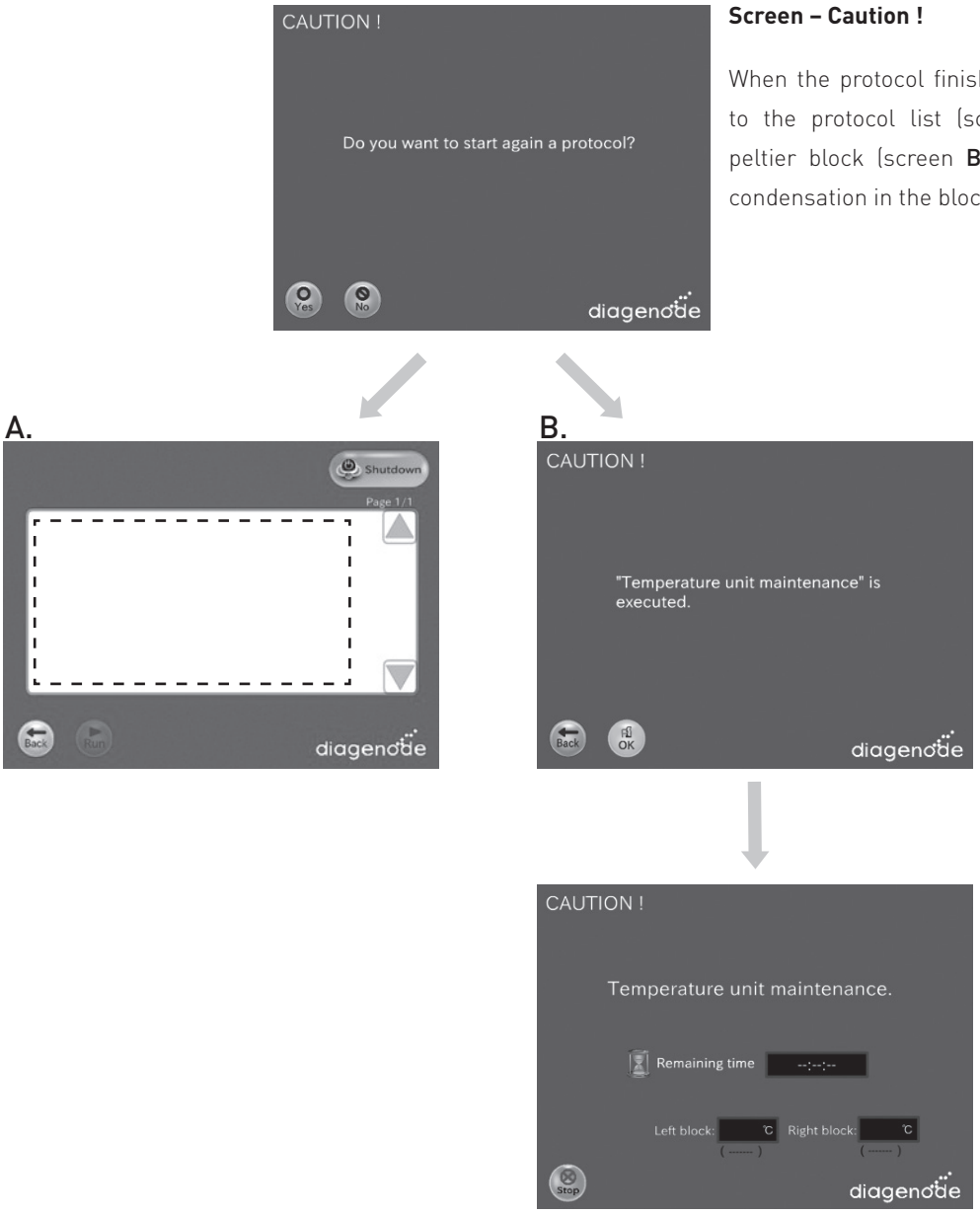
Screen – Finish/End

When the protocol is complete, a window appears telling user the run is over. The screen behind this window should be the Startup screen. When OK is pressed, then the Startup screen appears and the user can immediately begin to remove their sample and prepare the next run.

At this point, user is expected to be ready to press RUN.

Buttons:

- The user presses the "OK" button. Then screen shall be changed to "[Categories Name] Protocol List".



Screen – Caution !

When the protocol finishes the user can return to the protocol list (screen **A.**) or warm the peltier block (screen **B.**) to eliminate possible condensation in the block.

Quantitative PCR & Data Analysis

The Methylated DNA IP module includes four validated primer pairs specific to four types of DNA:

1) methylated human DNA region (testis-specific H2B, TSH2B)
2) unmethylated human DNA region (GAPDH promoter)

Note: Primer pairs for mouse and rat are available! Please visit www.diagenode.com

1. Prepare your **qPCR mix** using SYBR Green PCR master mix and start out qPCR.

qPCR mix (total volume of 25 µl/reaction:

- 1.00 µl of provided primer pair (stock: 10 µM each: reverse and forward)
- 12.50 µl of master mix (e.g.: iQ SYBR Green supermix)
- 5.00 µl of isolated DNA or diluted purified DNA sample (see above for DNA dilutions)
- 6.50 µl of water

Table 1. qPCR cycles:

	Temperature	Time	Cycles
PCR Amplification	95°C	7 minutes	x1
	95°C	15 seconds	x40
	60°C	60 seconds	
	95°C	1 minute	x1
Melting curve	65°C and increment of 0.5°C per cycle	1 minute	x60

2. When the PCR is done, analyse the results. Some major advices are given below.

- **Data interpretation**

The efficiency of methyl DNA immunoprecipitation of particular genomic locus can be calculated from qPCR data and reported as a recovery of starting material: % (meDNA-IP/ Total input).

% (meDNA-IP/ Total input)= 2^[(Ct(10%input) - 3.32) - Ct(meDNA-IP)]x 100%

Here 2 is the AE (amplification efficiency), Ct (meDNA-IP) and Ct (10%input) are threshold values obtained from exponential phase of qPCR for the methyl DNA sample and input sample respectively; the compensatory factor (3.32) is used to take into account the dilution 1:10 of the input. The recovery is the % (meDNA-IP/ Total input).

- **Background determination**

The final goal of IP is to calculate the enrichment in the same IP sample of: 1/ the specific DNA fragments (corresponding to the hydroxymethylated DNA) in comparison with 2/ non-methylated DNA (i.e. negative unDNA control).

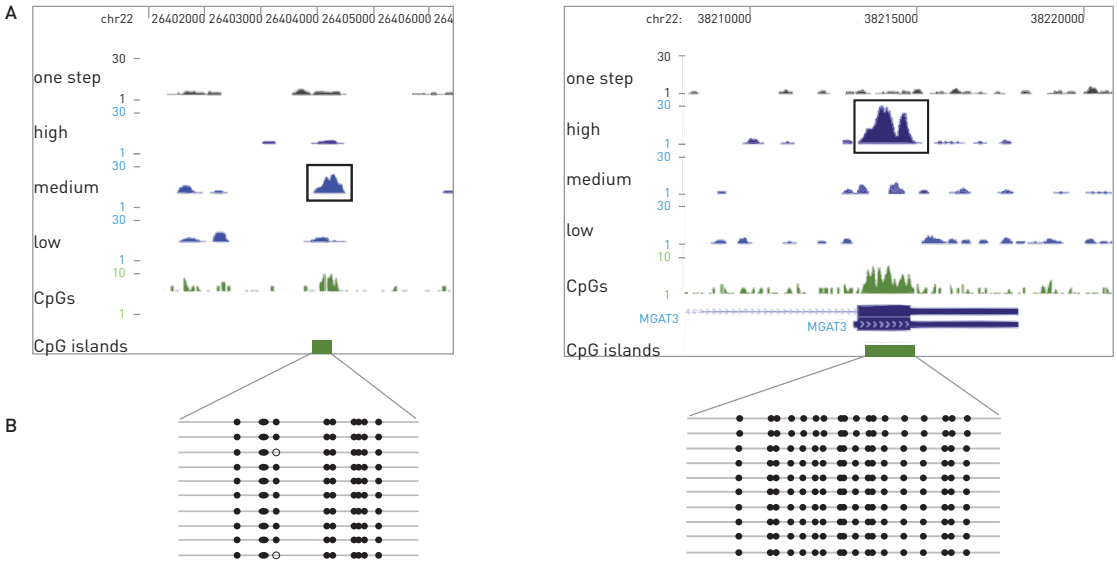
- **Relative occupancy can be calculated as a ratio of specific signal over background.**

Occupancy= % input (specific loci) / % input (background loci)

Relative occupancy is then used as a measure of the hydroxymethylation of a specific locus; it provides clues about specificity of the IP. (background loci) corresponds to the signal obtained with one of the unmethylated DNA kit control.

Results

MBD-seq (Methylbinding domain - sequencing) allows for detection of genomic regions with different CpG density

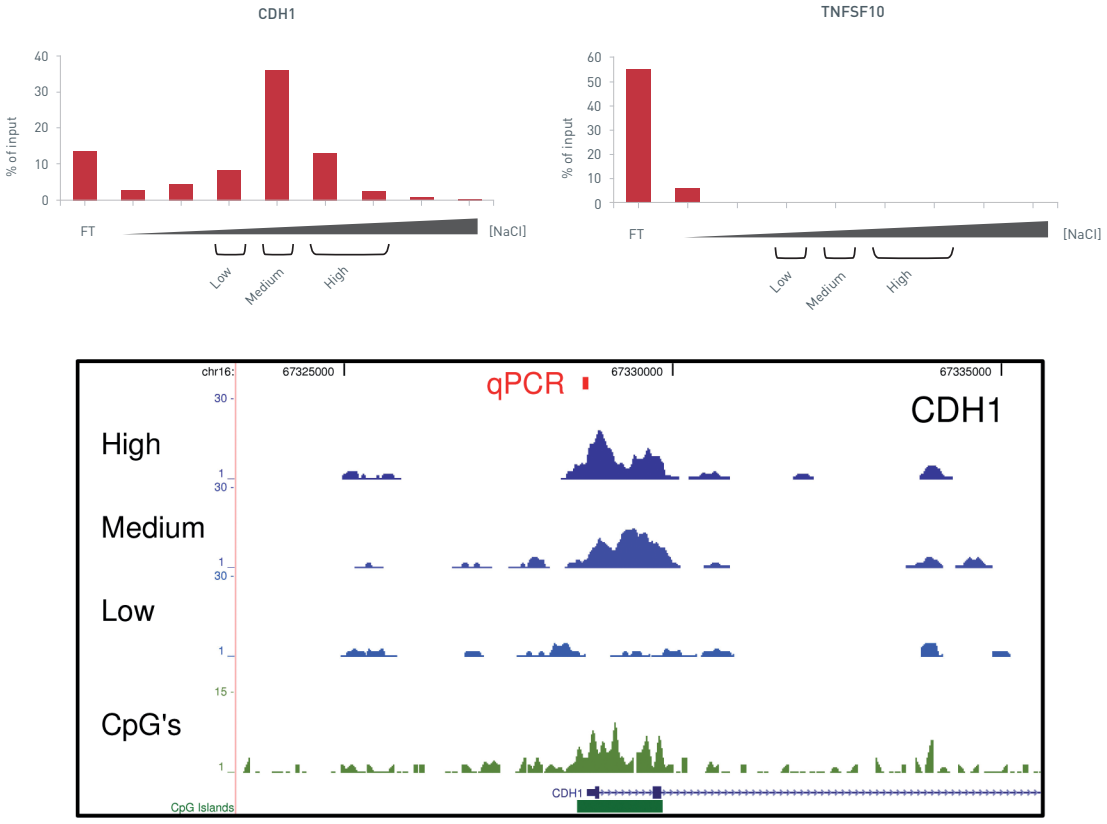


Data provided by Henk Stunnenberg (Nijmegen Center for Molecular Life Sciences - The Netherlands)

Figure 1.

Using MBD-seq, two methylated regions were detected in different elution fractions according to their methylated CpG density (A). Low, Medium and High refer to the sequenced DNA from different elution fractions with increasing salt concentration. Methylated patterns of these two different methylated regions were validated by bisulfite conversion assay (B).

MethylCap results



Data provided by Henk Stunnenberg (Nijmegen Center for Molecular Life Sciences - The Netherlands).

Figure 2.

MethylCap assays were performed using DNA from NB4 cells and the MethylCap kit (Diagenode). Differential fractionation of double stranded DNA based on CpG methylation density was performed using increasing salt concentration during the elution steps. (A) qPCR results in a methylated (CDH1-CpG) and a unmethylated (TNFSF10) region show the % of recovery of captured DNA compared to the input in the different fractions. (B) Results have been confirmed by sequencing the captured DNA in the different elution fractions.

Troubleshooting Guide

Error Cause	Remedy
SX-8G IP-Star cannot be switched on	SX-8G IP-Star is not receiving power. Check that the power cord is connected to the workstation and to the wall power outlet.
Computer cannot be switched on	Computer is not receiving power. Check that the power cord is connected to the computer and to the wall power outlet.
SX-8G IP-Star shows no movement when a protocol is started	SX-8G IP-Star is not switched on. Check that the SX-8G IP-Star is switched on.
SX-8G IP-Star shows abnormal movement when a protocol is started	The pipettor head may have lost its home position. In the Software, select "Manual Operation/Home". After confirming that the pipettor head moves to the home position, run the protocol again.
Aspirated liquid drips from the disposable tips	Dripping is acceptable when ethanol is being handled. For other liquids: air is leaking from the syringe pumps. Grease or replace the O-rings. If the problem persists, contact DIAGENODE Technical Services.

Technical Assistance

At DIAGENODE we pride ourselves on the quality and availability of our technical support. Our Technical Services Departments are staffed by experienced scientists with extensive practical and theoretical expertise in molecular biology and the use of DIAGENODE products. If you have any questions, or experience any difficulties regarding the SX-8G IP-Star or DIAGENODE products in general, do not hesitate to contact us.

DIAGENODE customers are a major source of information regarding advanced or specialized uses of our products. This information is helpful to other scientists as well as to the researchers at DIAGENODE. We therefore encourage you to contact us if you have any suggestions about product performance or new applications and techniques.

For technical assistance and more information call the DIAGENODE Technical Service Department or contact your local distributor.

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Ordering information

Description	Cat. No. (NEW)	Cat. No. (OLD)	Format
SX-8G IP-Star® Compact	B03000002	UH-002-0001	1 unit
Auto True MicroChIP kit	C01010140	/	16 rxns
Auto True MicroChIP & MicroPlex Library Prep Package	C01010141	/	16 ChIP rxns & 12 library prep rxns
MicroPlex Library Preparation kit x12	C05010010	AB-004-0012	12 rxns
Auto Histone ChIP-seq kit protein A x16	C01010020	AB-Auto02-A016	16 rxns
Auto Histone ChIP-seq kit protein A x100	C01010022	AB-Auto02-A100	100 rxns
Auto Histone ChIP-seq kit prowwtein G x16	C01010021	AB-Auto02-G016	16 rxns
Auto Histone ChIP-seq kit protein G x100	C01010023	AB-Auto02-G100	100 rxns
Auto Transcription ChIP kit protein A x16	C01010030	AB-Auto03-A016	16 rxns
Auto Transcription ChIP kit protein A x100	C01010032	AB-Auto03-A100	100 rxns
Auto Transcription ChIP kit protein G x16	C01010031	AB-Auto03-G016	16 rxns
Auto Transcription ChIP kit protein G x100	C01010033	AB-Auto03-G100	100 rxns
Auto ChIP kit protein A x100	C01010011	AB-Auto01-A100	100 rxns
Auto ChIP kit protein G x100	C01010013	AB-Auto01-G100	100 rxns
Auto MeDIP kit x16	C02010011	AF-Auto01-0016	16 rxns
Auto MeDIP kit x100	C02010012	AF-Auto01-0100	100 rxns
Auto hMeDIP kit x16	C02010033	AF-Auto02-0016	16 rxns
Auto MethylCap x48	C02020011	AF-Auto01-0048	48 rxns
Auto IPure kit	C03010010	AL-Auto01-0100	100 rxns

Visit us at one of Diagenode's demo sites or discover our Automated Systems by performing some assays with the help of our R&D and Technical Department.

www.diagenode.com

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