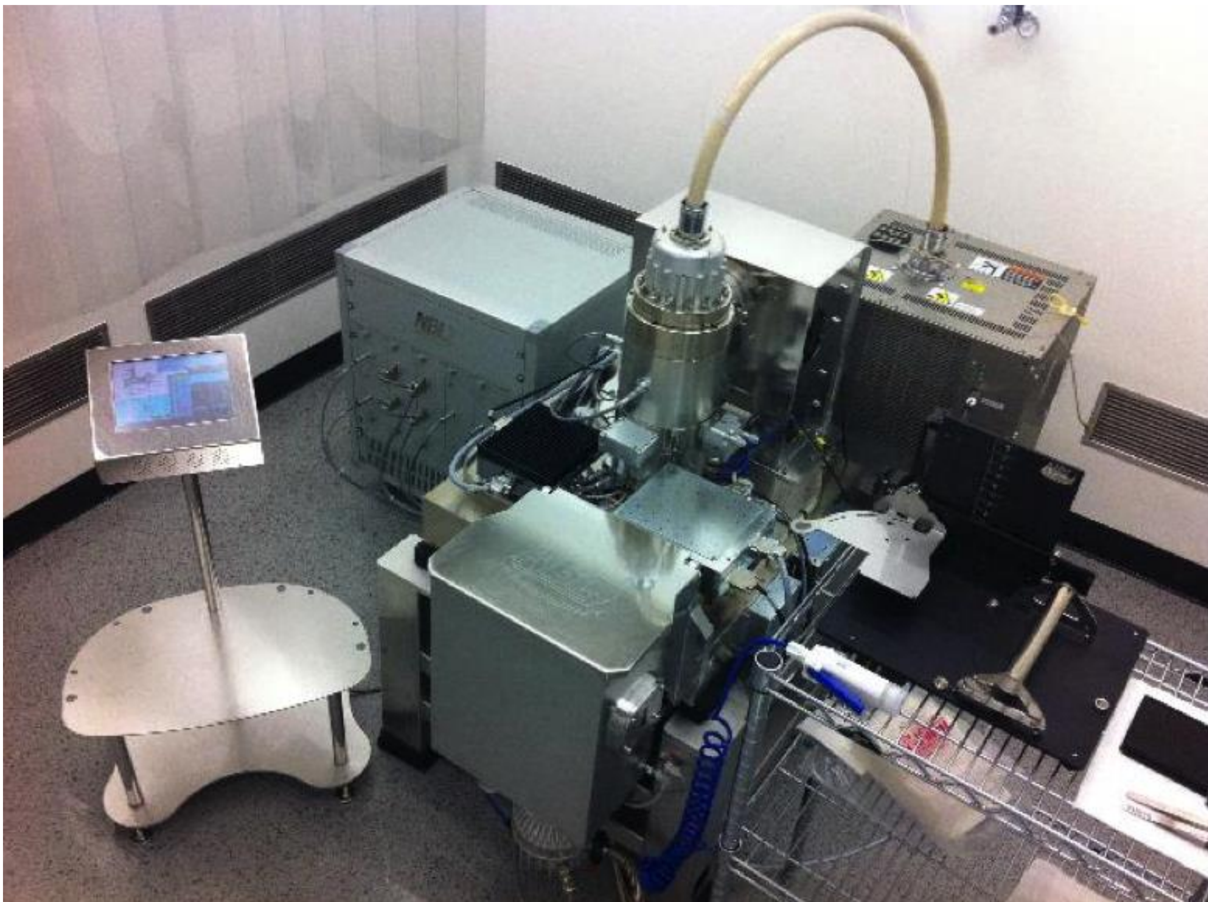
NanoBeam *n*B4

Electron Beam Writer

Standard Operating Procedures

July 2015



Introduction

NanoBeam *n*B4 is an electron beam writer located on the 7th floor of Northwest Corner (NWC) building of Columbia University Morningside Campus. The tool is housed in a class 100 cleanroom suit – a series of rooms with high fidelity dust/temperature/humidity controls – and its entrance is adjacent to the entrance to NWC 705.

Gowning procedure.

The NanoBeam lab is composed of 4 rooms and is a restricted area. In order to enter the most external room you need to swipe a card or enter a code that you will receive once certified. Before entering this room, apply the blue shoe covers and step on the sticky white adhesive matt located in front of the door. Put on a white head cap followed by a coverall, making sure that the lower part of the cap lies inside the coverall. Wear the white cleanroom covers on top of the coverall. Put on the cleanroom gloves and refrain from touching the outside of the gloves with your bare hands. Wipe down everything you are bringing into the room with Texwipe soaked in IPA to avoid contamination. You're now ready to enter the inner rooms.

1. Loading the sample for a write.

1.1. Assure that the beam is on by checking the current typing **stage fc** in the terminal and opening the current meter.
1.2. Unload all the loaded chucks
1.3. Check that the temperature of the room is stable around 19 °C.
1.4. Enter the room and **Vent** the airlock using PLC.
1.5. Load your sample. The sample must have a clean backside and must have been baked.
1.6. Pump down the airlock and wait until Airlock pressure appears.
1.7. Normally within 10 - 20 minutes, Airlock pressure should reach < 1.9×10^{-6} mbar. Select Chuck Control from main tool bar and press Load to load the chuck that contains your sample and wait till the **Loaded** indicator turns on.

Details

1.1. Assure that the beam is on by checking the current typing **stage fc** (moving to Faraday

cup) in the terminal and opening the current meter with the button **A** (Figure 1) to measure the current (the value should be in the range 0.5-70 nA).

Figure 1. Main Toolbar

1.2. **Unload** any possible loaded chuck(s), and make sure to return the stage to the load position by typing **stage load**. Check using the button in the main tool bar (Figure 1) – if the stage is not in load position you won't be able to vent the airlock and load your sample. Click on the **Chuck Control** button in the tool bar and check that no chuck is loaded – on each button on the right of the chucks should be visible ***Load***, if not proceed by checking the box relative to the chuck to be unloaded and press Unload (Figure 2). Check that the temperature of the room is stable around 19 °C (**PA** button in the main tool bar, and click on the detail button).

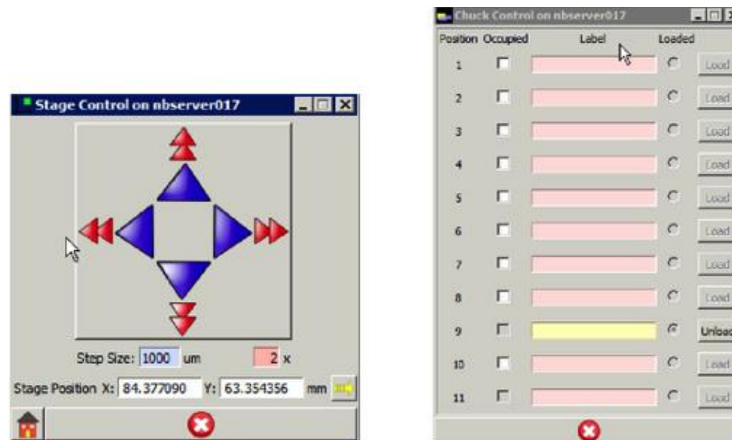


Figure 2. Stage Control Panel (Left) and Chuck Control Panel (Right)

1.3. Enter the room and vent the airlock by pressing **Vent** button on PLC. Enter the room of the e-beam writer and make sure to close the door behind you. Move towards the PLC screen right next to the machine (Figure 3). Check that the system is ready to be vented and press the **Vent Airlock** button and confirm by pressing **OK.** The airlock will now go to room pressure. The venting process will last approximately 7 minutes, and assure that the system is running correctly by staying in proximity of the machine until the PLC indicates ***Airlock Vented***.

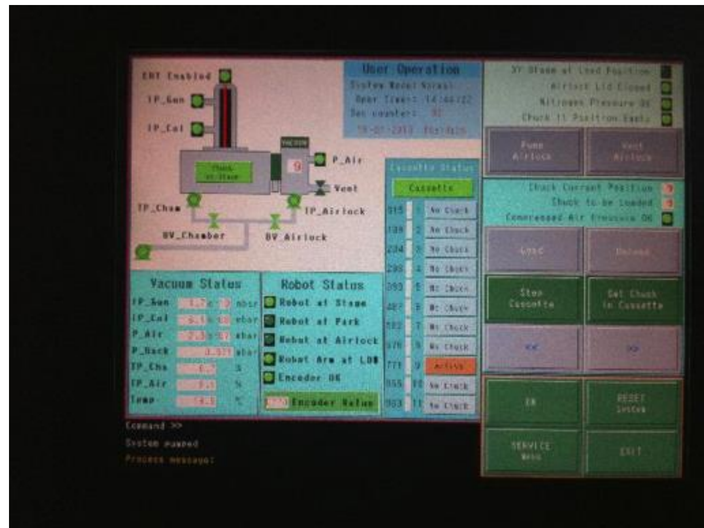


Figure 3. PLC Monitor Located Next to the Machine. In this particular case, chuck number 9 is loaded and the system is pumped down. The venting button is not activated (grey) because the stage is not in load position.

1.4. Once the airlock is at room pressure, you will see on the bottom left corner of the screen a message saying that the airlock has been vented. You can now lift carefully the lid of the airlock using two hands. Grab the handle and plug it in the four slots on the chuck tray (the small handle-lock must be on the left side). Make sure that the handle is well fixed, lift the tray and place it on the table, plugging the three pins at the bottom in the three holes on the stage (the small handle-lock must face towards you). Close the lid. Be aware of the chuck that you intend to use and extract it from the tray. Load your sample in the appropriate space according to its dimensions. Do not use the lid of the airlock as a loading stage – no pressure should be put on it. Make sure not to use the 11th chuck. Commonly, the 9th chuck is used (Figure 4), where you can find slots where to load your samples of different dimensions: six 2 cm-slots (three on the left column and the other three on the right column), three 1 cm-slots (central column) and three 0.5 cm-slots (central column). The backside of the sample you are going to load must be clean. Use a Q-tip soaked in acetone to remove residues of resist and bake it on a hot plate. PMMA, EL copolymer and HSQ are the only **Load** your sample. The sample must have a clean backside and must have been baked. For other kind of resists, check with the superusers. If you fail to do so you might incur in a period of suspension (Figure 5). Use two tweezers, one to hold the sample, one to slightly move the clip while sliding the sample in from a side. Assure that the sample is well fixed and touches the metal borders of the chuck. Make sure that the bottom of the sample is clean and the sample lies flat.

You can use the nitrogen gun to blow the chuck and the sample. Reposition the chuck inside the tray, open the lid and place the tray inside the airlock being careful to plug the three pins in the respective holes on the stage inside the airlock. Remove the handle and close the lid.

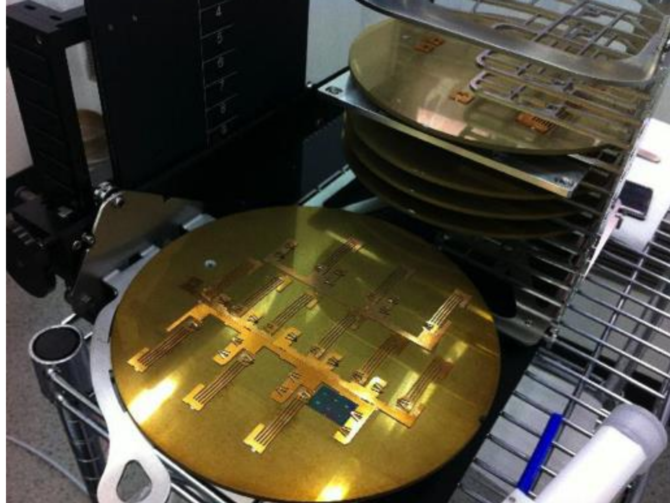


Figure 4. Chuck 9 Extracted from the cassette; a total of 10 slots are available for use.

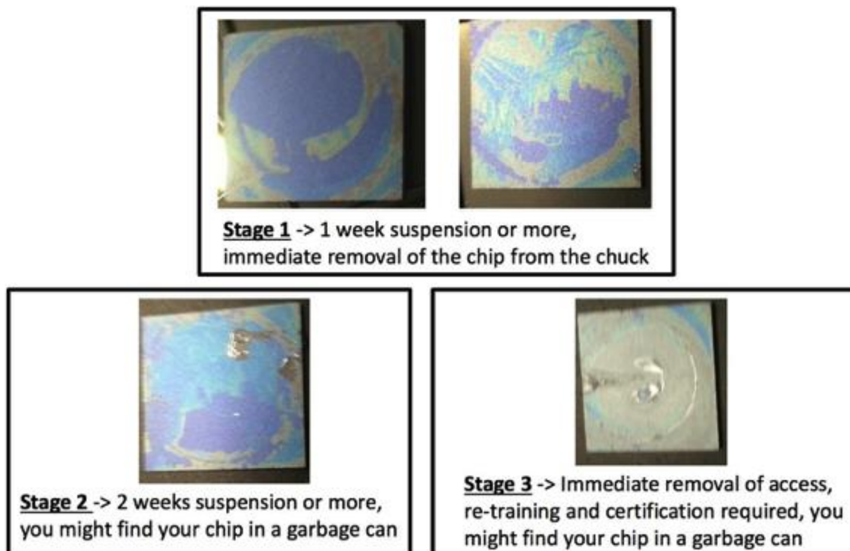


Figure 5. Examples of not cleaned backside and corresponding suspension periods.

1.5. Pump down the airlock by pressing **Pump** button on PLC and confirm by pressing **OK**. Wait till the airlock pressure appears on **Pa** window (it should take about 5-10 minutes). The machine will then start the pumping cycle consisting of vent and rough-pumping sequence repeated 3 times. After 100 mbar is reached, on the main screen, starting turbo pump will appear. Keep your eyes on TP AIR (unit = %) until you see it rising. TP AIR

shows the amount of load on turbo pump and you should see the percentage going up close to 100% on most cases, and back down, which you would expect from a starting turbo pump. If the pressure does not drop within a set time, the turbo pumps will halt as a precautionary measure (You will either see that from TP AIR not increasing or PLC pump button turn dark green again). In such cases (which can happen if your samples are outgassing more than usual or the loaded chuck(s) exposed in air for too long), hit **RESET**, **PUMP DOWN** and **OK** to initiate the pump down sequence again (Figure 6).

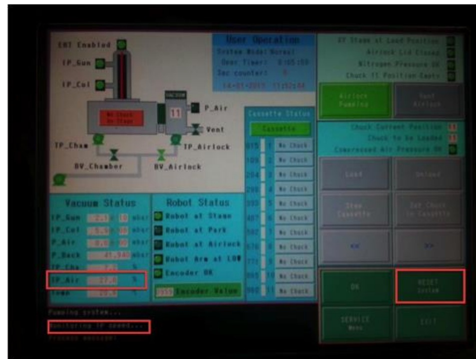


Figure 6. Resetting the system if the turbo pump fails to activate.

1.6. Exit the room and close the door behind you. The pumping process will take approximately 10-20 minutes to reach $1.9\text{x}10^{-6}$ mbar at which you can load the chuck and proceed – again, depending on how many chucks are loaded on the cassette and how well your chips are baked.

1.7. In about 10-20 minutes, the airlock pressure should reach its base pressure, **< $1.9\text{x}10^{-6}$ mbar**. Select **Chuck Control** from main tool bar and press **Load** to load the chuck that contains your sample and wait till the ***Loaded*** indicator turns on – do not run any other operations meanwhile.

2. Setting the beam current and calibrating the system.

2.1. Open the folder **Sysstate** that contains the set current files on the desktop and open the file that corresponds to the desired current.

2.2. **Copy/Paste** the last line of this into the terminal to set the current. (run sys_restore 80.0KV-xxnA...). Wait until you see system prompt '$>' again.

2.3. Click the **C** (Auto Conjugate) button in the terminal – **DO NOT** run this until the system has reached the base pressure of $1.9\text{x}10^{-6}$ mbar.

Details

2.1. In case your sample has a different height from a normal 4 inch silicon substrates (500 μm), you might need to change *datum(step)* in order to focus the beam on the sample – the xy stage assembly has a metal block built in called datumstep, which has 11 steps with a height difference of 110 μm per step to accommodate various sample heigts. The first step, datum 1, is the highest available (thickest sample) while the datum 11 being the lowest (thinnest sample). Calibrations such as auto_conjugate are applied in reference to a datum and therefore the reference datum cannot deviate excessively from your sample thickness. The fine focus value should be lower than 0.3, which is about 120 μm. To write on a sample with a height over this range (> 0.3), users will have to change the datumstep or load a different sysstate file with better fitting datumstep. Contact superusers if the existing sysstate files cannot accommodate your needs.

    *The sensitivity of the fine focus is about 0.0025 – 0.0030 per μm in sample height. For a main-field size of 500 μm, the beam-landing angle at the corner of the field is about 0.8 to 0.85 degrees, or 14 mrad.

2.2. Open a **Sysstate** folder and choose the file relative to the desired current, copy and paste in the terminal the last line of this file which is the command to change the current. Open the current meter by pressing **A** button and check that the current is right.

2.3. Run a calibration package by pressing the **C** button (Auto Conjugate) in the terminal tool bar. The system will perform a set of operations (2-3 minutes). Always wait at least one minute between loading up a **Sysstate** file and before hitting **Auto_Conjugate** for system to equilibrate. Failure to do so could result in FPGA error, which requires a server reboot.

    *If you are running a batch file pertaining different current files, you can add a line "sleeps 15" between the **Sysstate** load and the **Auto_Conjugate** command to create the delay.

3. Locating the sample and positioning the alignment marks.

3.1. Open **Stage Control** from main control bar. Select the location of the bottom-left corner of the chip from the **Position Database** and press the **yellow arrow** to move the stage to that position.

3.2. Open the SEM view by pressing **NanoBeam SEM** button on the main control bar and

Zoom Out**. Press **Start/Stop** button to turn on the beam. Press **Auto Brightness** and check that the corner is visible, in focus and centered.

3.3. **Move** to the first alignment mark you will use in your job file using the Position Database with SEM. Turn SEM on and make sure you can see the alignment mark and center it.

3.4. Select **Mark Type Database** from the main control bar. In the terminal type **af MarkName** to autofocus on the mark.

3.5. **Save the location** of the alignment mark in the Stored Position Database. Repeat this procedure for the other alignment marks present in the job.

Details

3.1. This step aims at defining the marks that the system will use to create a focus map. Click on the button **Position** Database (Figure 7) that you find in the main tool bar. You should already have created a folder with your name where you store the position of the chips on the chuck and the alignment marks on these chips. Press the button **Stage Control**. It's now possible to move the stage by setting the step size and the multiplier and read the x-y position. The stage will move in the direction of the arrow (*note that on SEM view, it will appear as if the stage is moving in an opposite direction to your command – this is normal, as the SEM and stage coordinates are off by 180 degrees by convention). To move by Step Size press blue arrow, to move by Step Size X Multiplier, press the red arrows. Depending on where you loaded your chip, go to the position database and click on the yellow arrow in correspondence to the position of the chip you want to write.

Position Database on nbserver017

dansun_middle_cmchip

Name	X (mm)	Y (mm)
cbl	88.340298	71.085441
cbr	80.340298	71.085441
ccr	80.340298	67.085441
fc_gtl	87.786964	63.003991
fc_gtr	82.847021	63.046536
gbl	88.797378	67.942878
gbr	82.297434	67.955883
gtl	85.340298	69.085441
gtr	81.340506	69.085441
sbl	86.820582	67.98165
sbr	82.821102	68.01915
stl	86.764332	61.980609
str	82.764332	62.01915
tl	89.193849	62.133392
tr	79.425619	62.122975

Figure 7. Positions Database

3.2. Press the button **SEM** in order to open the SEM view and check if the chip is where

expected to be. Zoom out selecting the largest field size. Press the **On/Off** button to turn on/off the beam (Figure 8). Press the **Auto Brightness** button to adjust the contrast and brightness. Remember that the view in the SEM in flipped both vertically and horizontally with respect to what you could see while loading the sample; for instance the top right corner of the chip when loading, will be viewed as the bottom left corner at the SEM. Always remember to turn the SEM off when not used, in order to minimize unwanted exposure of the sample (avoid moving the stage when the SEM is on).

3.3. At this point you should move to the position of the first alignment mark used in your job file, the location of which is stored in the Position Database. As described previously click on the yellow arrow next to the stored position and turn the SEM on to check. You should see the mark, center accurately by pressing **ctrl + mouse left click**.

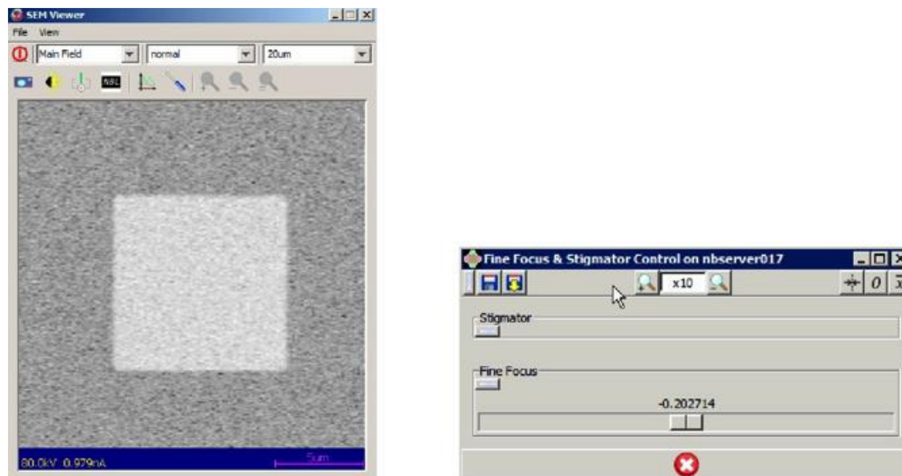


Figure 8. SEM view and fine focus control.

3.4. According to your job file (regarding the focusing and registration options) you might need to use the automatic procedure and the database containing the various mark types. Select **Mark Type Database** from the main tool bar and choose the type of alignment mark you centered on in the previous step. In the naming convention, 'b' means bright for bright contrast, e.g. metal marker (Figure 9). Now in the terminal type **af [markname]** to autofocus on the mark. This is an optional step, in case you want to perform directly the automatic focusing on the mark. Otherwise a fully automatic procedure is included in the registration option of the job file (for details see section "how to create a job" regarding mark type and registration). Also you can repeat [af markname] a few times or verify by manually checking the focus with **Focus Control** button from the main tool bar and adjusting the knob (mind the multiplier at the top) in order to find the right focus (Figure 8).

It is suggested to use the minimum field size of the SEM (maximum magnification) in order to have a better focus adjustment.

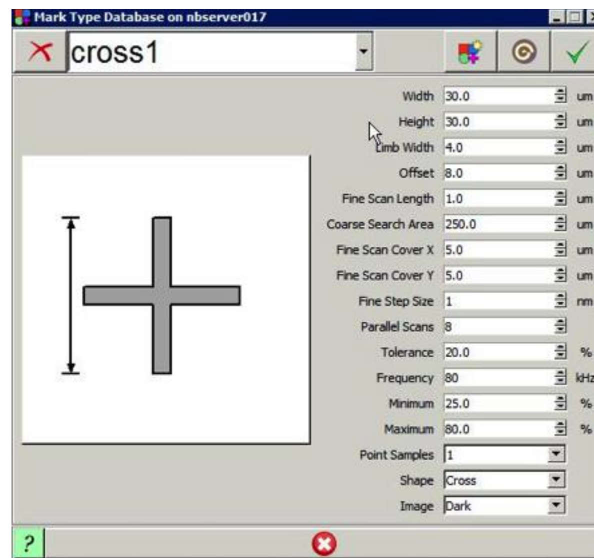


Figure 9. Mark Type Database

3.5. When the mark in centered and in focus, store its position in the Position Database creating a new entry with a temporary name (the same as in the job file), click on the **camera** button to acquire position and **save** button to save it. Repeat the same procedure for the other marks present in your job file (at least 3) and when finished type in the terminal **stage load** to return to the default position.

4. Running the job.

4.1. Open your **job file** from the Jobs folder on the Desktop.

4.2. **Copy/Paste** first line of the job file to the terminal to run the job.

Details

4.1. During writing, close all the GUIs, including the vacuum and chuck control.

4.2. In the folder **Jobs** on the desktop you should find a folder with your name where you saved your job file in the format .njf. The job file uses patterns files ending with a .npf which is present in the folder Server/patterns/[yourname]. Open the job file and make sure that the names of the marks are correct and the block origins are consistent with the alignment marks used to create the focus map. Check that the name of the pattern file is

correct and that file is present in the patterns folder.

4.3. Proceed by copying and pasting the first line of the job into the terminal and press enter to run the job. After a few seconds you will be asked to confirm - typically the second option is utilized to run a job.

Unloading

Following the same procedure described earlier, unload the chuck using the **Chuck Control** button. Vent, unload the sample, pump down the airlock, and wait until the **Airlock** pressure appears.

How to create a job file

The writing is carried out with the software package **nB-Write**. It performs some rudimentary corrections to account for wafer rotation and to accordingly “distort” the exposure layout. It is also capable of some pattern manipulation, so that a small pattern can be replicated over a larger area. **nB-Write** accepts instructions in the form of job files. A job file consists of several logical sections. A section will start with a “.” followed by the section name, then have several lines of properties (each on a separate line), then finish with “.end”. There are five sections:

1. **.global:** contains properties affecting the whole job, such as registration points, mark type, focusing procedure, etc.
2. **.block_default:** defines default properties common to all blocks (if not redefined in the .block section). Specifying a property in this section is equivalent to writing the same definition in every block section of the job file.
3. **.block:** here you find the list of patterns to be written together with the optional definition of local registration and mark type. There can be multiple blocks in a job file.
4. **.pattern:** this section is where the properties of all patterns contained in the job file are defined.
5. **.write:** properties related to the writing, such as what beam current to use.

Job files must start with a global section, then optionally block_default, then as many block sections as required, then one pattern section for every pattern referenced in the blocks, and finish with a write section. Properties are defined only within one of the previous sections and comprise a single word identifier followed by various parameters. Some properties can be

defined in more than one section. In addition, job files may contain comments, inserting "#" or ";" at the start of the line containing the comment. Here is an example of job file, followed by the explanation.

Example job file chipleads.njf

```
# run nbwrite JohnDoe/chipleads.njf -1=JohnDoe:cm_mid_gbl -2=JohnDoe:cm_mid_gbr
#--------------------------------------------------------
# define global properties
#--------------------------------------------------------
.global
registration          (0,8000000)  (8000000,8000000)
registration          (0,0)  (8000000,0)
marktype              cross50x10b
focus                 map
.end

#alternatively if no registration is required:

.global
focus_map          JohnDoe:onecm_middle_tempbl 0.147384
focus_map          JohnDoe:onecm_middle_tempbr 0.157784
focus_map          JohnDoe:onecm_middle_temptl 0.126467
focus_map          JohnDoe:onecm_middle_temptr 0.136377
focus                 map
.end
```

The first commented line is the command that you copy and paste in the terminal when you want to run the job. The argument "JohnDoe/chipB12leads.njf" says that this .njf (NanoBeam job file) is located within the "JohnDoe" folder of the "jobs" folder on the client desktop (the software already knows to look in "jobs"). The argument "-1=JohnDoe:onecm_mid_gbl" and "-2=JohnDoe:onecm_mid_gbr" specify the global bottom left (-1 position) and global bottom right (-2 position) positions (the second is optional). In this case, "onecm_mid_gbl" is a saved position of the "JohnDoe" set of positions in the position database. The first position is the global origin, and is the reference point for most of the subsequent coordinates. The second position, if specified, is used to calculate the wafer/chip rotation, allowing registration and pattern coordinates to be automatically compensated. The first two "registration" lines specify the positions of 4 global alignment marks used to measure the chip/wafers position and orientation. Their coordinates are in nanometer units and are relative to the position specified by "-1=JohnDoe:onecm_mid_gbl", the global origin. The first contains the top left and top right mark coordinates, the second contains the bottom left and bottom right mark coordinates. Remember that these coordinates are oriented according to the SEM view, which mirrors the stage position (at the SEM you will see as bottom left what is actually top right as for stage coordinates). After locating all of the global registration marks, the coordinates of the global origin (which will have been approximated on the command line) will be corrected so that the center of the bottom left

global mark is at the specified distance from the global origin. It is possible to add “-r” at the end of the of the writing command to recover the job from a failed registration forcing the machine to continue using the parameters of the last successful registration. The property “**marktype**” followed by a name present in the mark type database defines the type of the mark on which the registration is performed. The name is arbitrary (user defined) and simply refers to a saved group of settings relative to that specific mark (shape, scan size, frequency, contrast, etc.).
Figure 10 shows how to create a mark type and define different properties affecting the way the machine looks for the mark and focuses on it (analyzing shape, mean position, focus value...). Notice that you want to minimize the exposed area during this procedure in order not to expose the region where the pattern might be written. Remember that the mark type frequency has to be higher than 10 kHz. Do not change and save parameters of marks created by others, create your own instead “focus” is a property that sets the focus value for the write. It can be defined in the global or in the block environment. When you use “**focus map**” after registration, the registration points will be used together with the value of the focus at those points to create an interpolation map that sets the value of the focus within the area included within the marks. If no registration is needed you can alternatively directly indicate the value of the focus at specific points (for instance positions stored in the database) where the focus has been measured directly by the user. Additionally you can use “focus” followed by “auto” and the first registration mark is used to perform an auto focus, or “**hsmap**” where a map of heights is calculated and the focus determined from it (together with the use of “hmap_range” and “hmap_size” in the “write” section), or directly enter a numeric value.

```
#-------------------------------------------------------
# define block default properties
#-------------------------------------------------------
.block_default
stepsize (100000,100000)
grid (3,3)
select (1,1):(2,2) (3,2)
select (3,3) invert
base_dose 7.8
dose_increment 3.5
pattern ciao (0,0)
.end
```

If “registration” is used in the “.global” section then a registration is required also in the “.block” section (or “.block_default”). Remember that the coordinates here specified are referred to the local origin of each “.block”. Within the “block” or “pattern” sections (or “block default”) you can use a very useful property: the “**grid**”. It allows to repeat a block or a pattern in a specific array. It can be used in the “block” or the “pattern” section and it repeats the same block at each point of the array. Notice that into brackets the first number indicates how many times the pattern will

be repeated in x, the second in y. It comes together with the property “**stepsize”** which defines the distance between two grid points in unit of nm. Using the property “**select**”, it is possible to write only specific cells (or a range of cells) in the grid using the format select (< x >; < y >). Adding the property “**invert**” will deselect the indicated cell or range of cells. When “**origin**” is defined in .block specifies the block origin relative to the global origin. For .pattern, this specifies the pattern origin relative to block origin in units of nm. In the “block" section, the property “**base_dose**” defines the base dose (in C/m^2) the pattern will be written with. Using “**dose increment**” (within “block” or “pattern”) it is possible to change the dose at each grid point starting from the specified “base dose”. This will be applied only where “grid” and “stepsize” are used. The dose changes from the left to right, bottom to top. Possible formats following “dose_increment” are: 0.1, 1.05, -0.01, %0.025, *(1.1,1.01), %*(1.005,0.97). “**pattern**” specifies a pattern that should be written in the block.

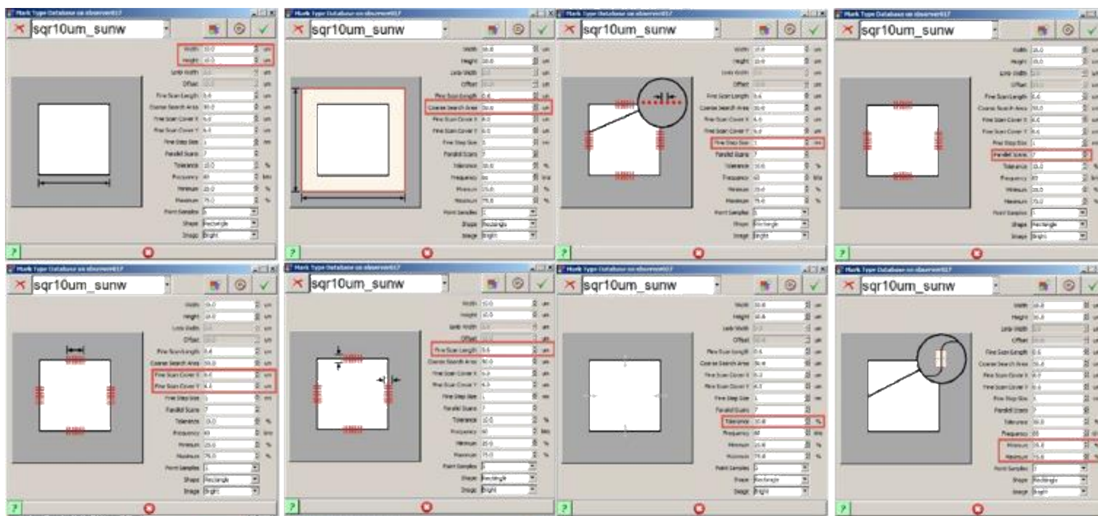


Figure 10. List of images showing the various parameters that can be set in the definition of a mark type.

```
#--------------------------------------------------------
# define block properties
#--------------------------------------------------------
.block
origin (1000000,4000000)
registration (0,2000000)  (2000000,2000000)
registration (0,0)  (2000000,0)
marktype     sqr10b
focus  map
stepsize     (4000000,1000000)
grid   (1,1)
base_dose    14
dose_increment      0
pattern      leads        (400000,400000)
```

```
pattern      extramarks   (75000,25000)
.end
```

There can be as many pattern properties in a block section as you like. It is followed by an ID, a unique pattern name defined using the “id” property in a pattern section. The offset (x, y) is the position of the pattern with respect to the pattern origin in nm. Notice that if a “registration” is performed in the “block” section, local marks will be used for the local correction of the pattern (scale, rotation, shear) and if “focus_map” is also indicated, this will have priority on the one defined in the .global section.

```
#---------------------------------------------------------
# Define pattern properties
#---------------------------------------------------------
.pattern
id 1
filename JohnDoe/chipB12_1.npf
dose 1 1 2
.end

.pattern
id leads
filename JohnDoe/chipB12leads.npf
stepsize (500000,500000)
grid (1,1)
dose_increment 10
dose 1 0 2
dose 2 1 2
dose 3 1.5 2
.end

.pattern
id extramarks
filename JohnDoe/twobytwo.npf
substepsize (500000,500000)
subgrid (1,1)
dose 1 1 2
.end
```

Within the .pattern section first you may define an “origin” that will be referred to the origin of the block where the pattern is included. Then an “id” links the name used in the .block section to the list of properties present in this section. Each pattern must have its own id specified in a different .pattern section. The “**filename**” refers to a file .npf (NanoBeam pattern file) present in the “pattern” folder on the server (link on the desktop of the client pc). Besides the definition of a “grid”, within this environment it is possible to define a “**subgrid**” with a “**substepsize**”. Basically this property allows to create an array of a pattern and to treat the resulting “subgrid” as a single

pattern itself. For example, imagine that a pattern is constituted of one main field. When the “grid” function is used, the array will contain as many main fields as the number of grid points. Instead, when “subgrid” is used, the main field size will be the size of the whole array. This is very important when the pattern is small (a few μm), since it is highly suggested to use a few hundred μm main field size, and the use of a “subgrid” instead of a “grid” is essential. Also, remember that it is not possible to use “dose_increment” with “subgrid”.

Still within the .pattern section, the “**dose**” is defined: the first number is the dose id (usually corresponding to the layer number in the pattern file), the second number is a dose factor (a proportion of the base dose) assigned to that dose id. The last number is the pixel size in nm, that is the minimum deflection of the beam during the write. It is commonly considered acceptable to use a pixel size that is less than half the spot size of the beam (Figure 11). A pattern section can have as many dose properties as it likes.

```
#---------------------------------------------------------
# Writing conditions (auto-detect beam current)
#---------------------------------------------------------
.write
current                 auto
.end
```

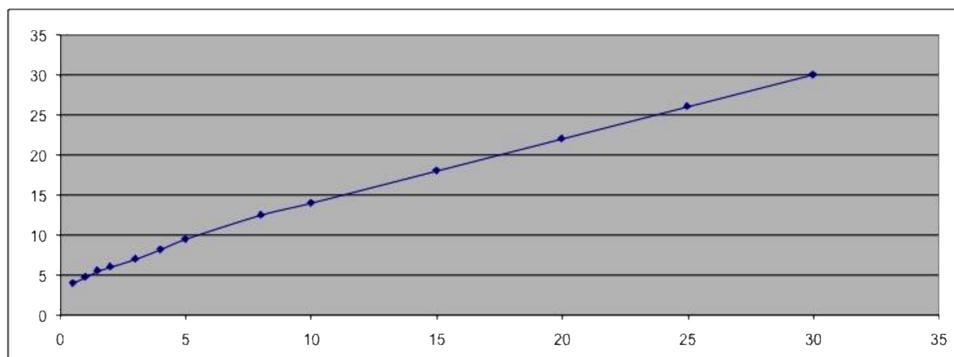


Figure 11. Beam spot size in nm as a function of the beam current in nA.

Finally the last section “write” specifies writing conditions, specifically the current to be used. For this example, the current is set to “**auto**”, indicating that the tool should use the current it was set to before the write.

Additionally, adding “-r” as a final argument to the run command causes to skip the registration for any mark it cannot find. This option can be exploited to effectively skip the registration for the blocks when mark type is defined as tiny marks with little search areas. The machine will fail to find these tiny marks and by default use the global alignment for the block writes. Starting with a .gds file, you will have to convert it into a .npf file by means of the software nbPat that can be

opened using the relative button in the main tool bar (Figure 12). This software allows to set the subfield and main field size, the center of the pattern, and calculate the writing time and the clock frequency by setting the beam current and dose that will be used. Remember that there are limits for the main field (mf) and subfield (sf) dimensions and clock frequency: minimum mf size is 50 μm, minimum sf size is 5 μm, and maximum clock frequency is 50 MHz. Suggested values are 250 μm for the mf and 10 μm for the sf. You can also view and measure the pattern, showing subfields and main fields, and finally “save as fractured pattern”.

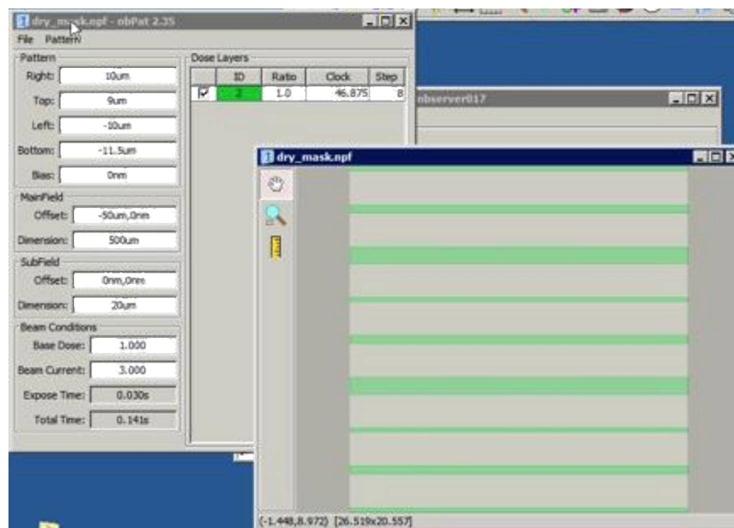


Figure 12. NanoBeam Pattern Generator - nbPat is the software that converts the .gds file into an .npf, the only format that the machine recognizes. It performs the fracturing of the pattern and its division into main fields and subfields.

Additional information

NanoBeam scheduling

1. Regular hours are Monday through Friday 7 am - 6 pm. After hours is Monday through Friday 6 pm – 7 am and weekends.
2. A session is **limited to 3 hours every day of the week between 7 am and 10 pm**. Instead, from 10 pm to 7 am reservations have no time limit.
3. A user can only have one reservation at a time. You must wait for your session to complete before making another reservation.
4. Do not book the tool more than 72 hours in advance.

Pattern overlap with microscope photos

Microscope photos of pattern results including graphene deposits can be copied into some drawing/pattern editors. For example you can follow the following procedure:

1. Take a photo of graphene deposits on a sample with a microscope.
2. Paste the photo into AutoCAD.
3. Scale the photo to match up the true dimension
4. Draw the required overlay patterns on the photo
5. Overlay writing with the nB system using a proper registration procedure.

The nB system is capable to write with < 20 nm overlay accuracy over 15 mm registration area. The registration marks can be designed at a position of 10 mm away from the graphene area.

Troubleshooting

Cassette misaligned with encoder: request Auto Align/Failed to unload substrate

If while transferring the chuck between the airlock and the stage (or vice versa), the following error appears: “Cassette misaligned with encoder: request Auto Align” or “Failed to unload substrate: FAULT:0x3405305a: NAME:NBVC_090 MSG:Arm not at stage position”, try the following and then try to load the chuck again.

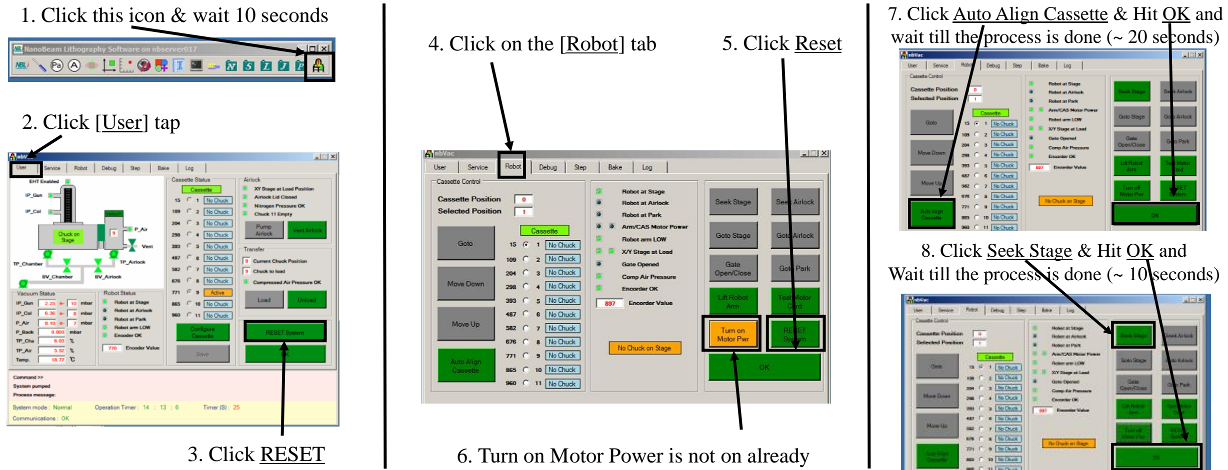


Figure 13. Stage Error Correction

Writing took longer than expected

The max writing time per shape within one sub field is 10 s. When the shape is large and beam current is low, the writing time may be over the 10 s limit, therefore an error massage “error: Pattern writing took longer than expected”. Before the time limit is modified in software, large shapes have to be sorted as follows: fracture with 5 μm sf size and save as a .npf file then load the saved .npf file back and re-fracture it as 20 μm sf size and save it. This trick can be used also to make sure that the .npf file contains only shapes that the machine can correctly write.