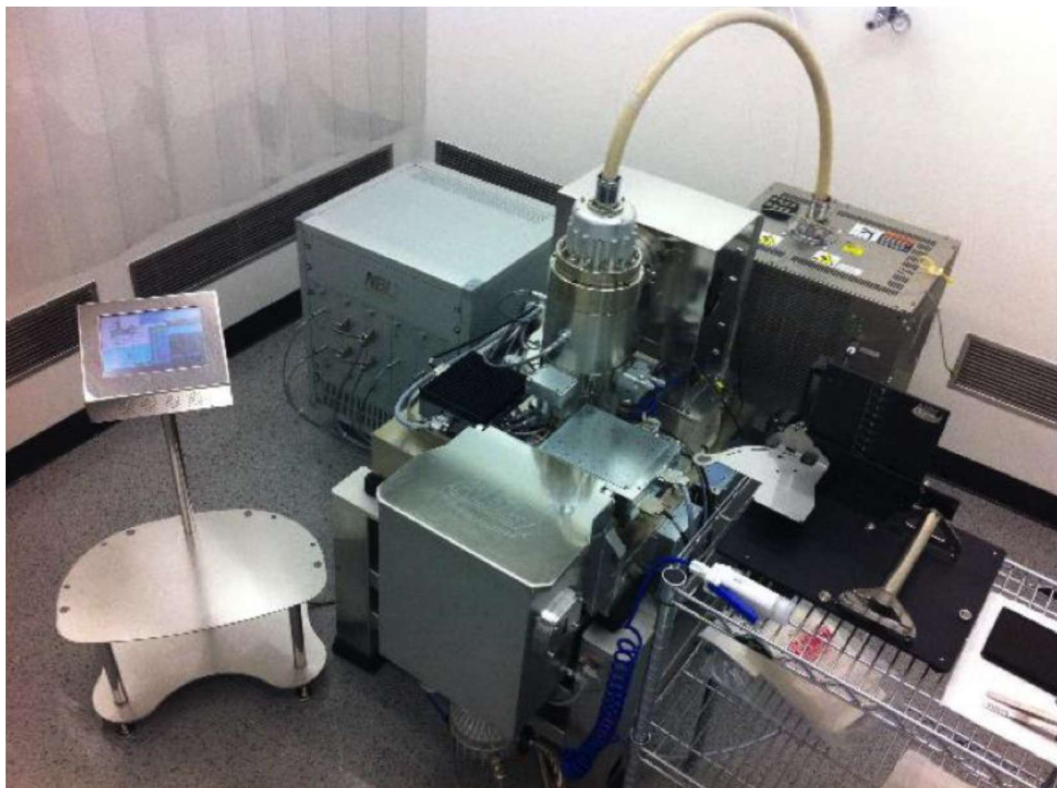




NanoBeam nB4

Standard Operating Procedure



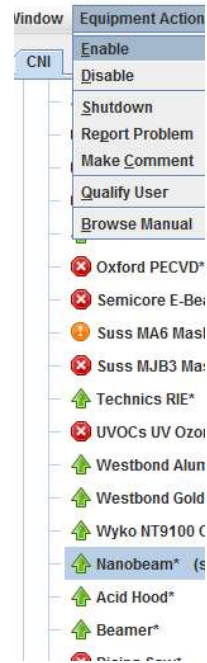
These instructions are intended for reference only, and will *not* replace the thorough training required for proper system operation. Contact a clean room staff member with questions or to report a system problem.

This documents is based on operating instructions written by Sunwoo Lee and Diego Scarabelli.





1. Enable the tool in BADGER



2. GOWNING Before entering the gowning room, apply disposable shoe covers and step on the sticky matt in front of the door. Wear the hood, a coverall, tack the hood inside the coverall. Wear booties on top of the coverall. Wear gloves. Wipe down everything brought into the room with Fab wipe soaked in IPA.





<p>3. CURRENT MEASUREMENT: Type “stage fc” in the terminal (moves the stage to the Faraday cage for current measurement). and open the current meter (“A”). Value should be 0.5-70 nA.</p>	
<p>4. UNLOAD CHUCK and TEMP CHECK: Unload the loaded chuck by clicking “Unload”. Return the stage to the load position by typing “stage load” in the terminal. Verify by going to stage control (green square icon”). Check the room temperature (“Pa”). Should be around 19 °C.</p>	
<p>5. VENT: enter the inner room (make sure door closes behind you) and vent the Air lock by pressing “VENT AIRLOCK” on the PLC (should be green) and confirm with “OK” (takes ~7min). An “Air lock vented” message will appear on the bottom left corner of the screen.</p>	





<p>6. LOAD SAMPLE: Carefully (two hands) lift the lid and open load lock. Take out the tray (handle should be on the left side) and load your sample. Lift the tray and place it on the table, plugging the three pins at the bottom in the three holes on the stage (small handle-lock facing you). Close the lid. Extract the desired chuck from the tray (do not use chuck #11). Load your sample in the appropriate space to its dimensions. No pressure should be put on the lid while loading your sample. Sample inserted into the Nanobeam should have a clean backside and should be prebaked for minimization of outgassing. Chuck #9 is recommended (with six 2 cm-slots, three 1 cm-slots, and three 0.5 cm-slots). Two tweezers may be of use when loading the sample.</p>	
<p>7. PUMP AIR LOCK: Reposition the chuck in the tray, open the lid and place the tray inside the airlock (make sure to insert the three pins inside their respective holes). Remove the handle and close the lid. Pump the load lock by clicking “Pump Air Lock” on PLC and confirm by “OK”.</p>	





	<p>Wait in the room until TP air steadily increases and you hear the sound of the turbo pump increasing in pitch. If the turbo fails to activate (TP air will not increase or PLC pump button turn green again) click on “RESET”, “PUMP DOWN” and “OK”.</p>																																																	
<p>8.</p>	<p>Wait until the pressure appears and decreases to $< 1.9 \times 10^{-6}$ mbar (10-20 minutes usually). LOAD CHUCK: go back to the control room. Choose the “CHUCK CONTROL” menu, choose the chuck that contains your sample and click on “LOAD”.</p>	<table border="1" data-bbox="909 724 1356 1344"> <thead> <tr> <th>Position</th> <th>Occupied</th> <th>Label</th> <th>Loaded</th> </tr> </thead> <tbody> <tr><td>1</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>2</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>3</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>4</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>5</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>6</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>7</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>8</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>9</td><td><input type="checkbox"/></td><td></td><td><input checked="" type="radio"/> Unload</td></tr> <tr><td>10</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> <tr><td>11</td><td><input type="checkbox"/></td><td></td><td><input type="radio"/> Load</td></tr> </tbody> </table>	Position	Occupied	Label	Loaded	1	<input type="checkbox"/>		<input type="radio"/> Load	2	<input type="checkbox"/>		<input type="radio"/> Load	3	<input type="checkbox"/>		<input type="radio"/> Load	4	<input type="checkbox"/>		<input type="radio"/> Load	5	<input type="checkbox"/>		<input type="radio"/> Load	6	<input type="checkbox"/>		<input type="radio"/> Load	7	<input type="checkbox"/>		<input type="radio"/> Load	8	<input type="checkbox"/>		<input type="radio"/> Load	9	<input type="checkbox"/>		<input checked="" type="radio"/> Unload	10	<input type="checkbox"/>		<input type="radio"/> Load	11	<input type="checkbox"/>		<input type="radio"/> Load
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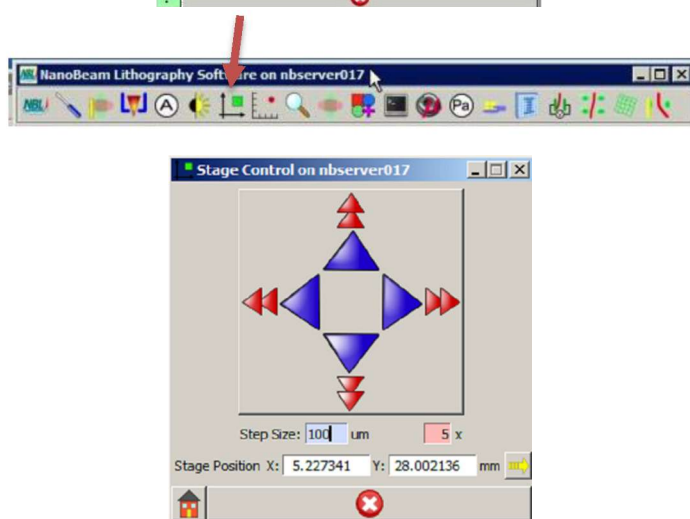
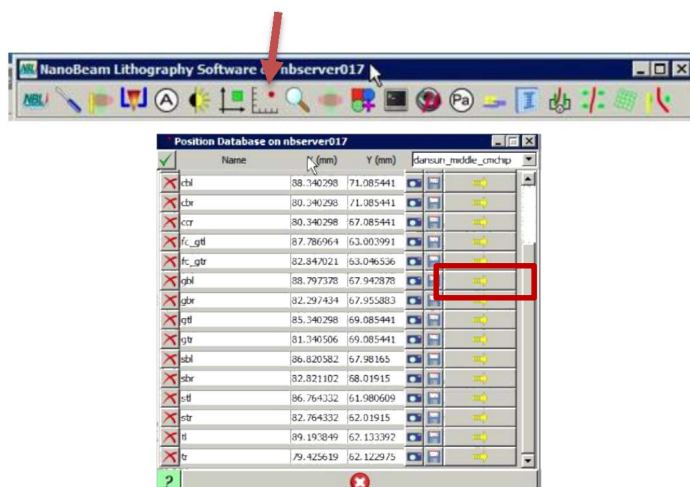


<p>9. ADJUST STEP HEIGHT: if you're using a sample 500 μm thick (standard 4" waters) skip to step 10. The stage has a built-in metal block for height adjustments, called "datumstep", in steps of 110 μm each. Datum 1 is for thickest sample and 11 the thinnest. Systate files may have a different datumstep corresponding calibration. Contact superusers for more information.</p>	
<p>10. SET BEAM CURRENT: In the terminal, press the button "Restore DB" and then type the number correspondent to the database file you intend to load.</p>	<pre> NanoBeam Terminal 01.01 on nbsrver017 File Edit History Help [Icons] Go Connecting to "nbsrver017"... Done. \$> run restore_db # log_file : </nanobeam/logs/db/db_restore.log> # machine: eb17 (2016-03-29 00:45:20) Current c=beam conditions: DB loaded: <1.1nA_80kV_datum6_16y03m22_2342.nrf> Select a DB to restore: No Settings 1 <0.6nA_80kV_datum6_16y03m19_1620.nrf> 2 <1.1nA_80kV_datum6_16y03m22_2342.nrf> 3 <30.3nA_80kV_datum6_16y03m19_1557.nrf> 4 <8.4nA_80kV_datum6_16y03m19_1606.nrf> restore_db> </pre>
<p>11. Click the C (Auto Conjugate) button in the terminal to run a calibration sequence – DO NOT run this until the system has reached the base pressure of 1.9×10^{-6} mbar.</p>	<pre> NanoBeam Terminal 01.01 on nbsrver017 File Edit History Help [Icons] Go corrections: 0x1 0 1 0 (-14628, -6074) duration: 14.0 sec ----- measured maximum stitching errors (nm): 500um main field: 12 20um subfield: 5 ----- loaded DB: 1.1nA_80kV_datum6_16y03m22_2342.nrf beam current: 1.078 nA calib level: 1 blanking: blanking ok (13.0 V) conjugate shift: 3 nm gun emission: 143.3 (uA) <foc= 3350 (V)> datum step at: 6 ----- starting time: 00:53:46-2016_Mar_29 finishing time: 00:55:50-2016_Mar_29 total duration: 124 (s) ----- auto_conjugate> \$> </pre>

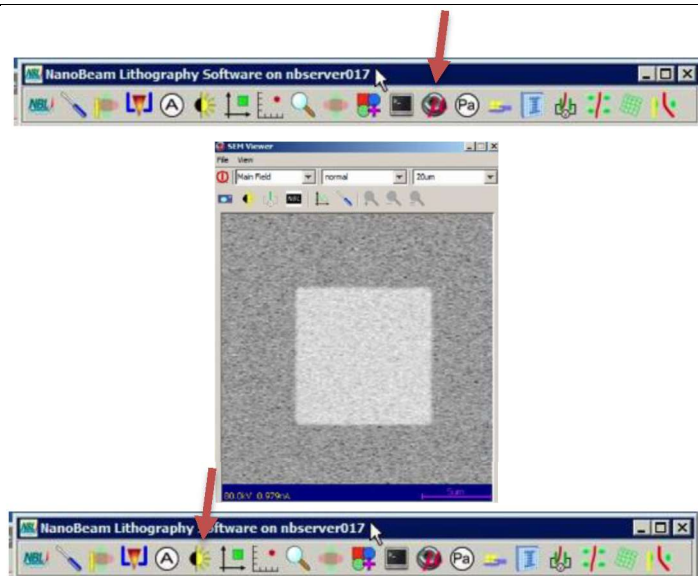




12. LOCATE ALIGNMENT MARKS:
From the main tool bar click on “Position Database” to open the position database window. Select the location of the bottom-left corner of the chip (from your stored in folder information) and press the yellow arrow to move the stage to that position. You can also move the stage directly by pressing the “Stage Control” button. To move by Step Size press blue arrow, to move by Step Size times Multiplier, press the red arrows.

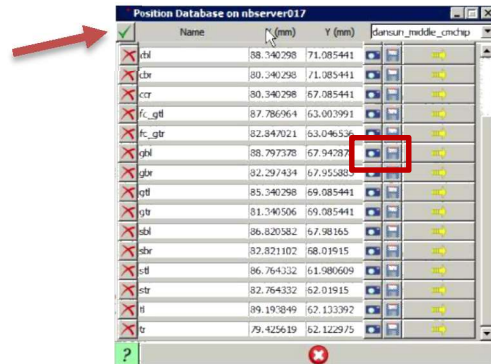


13. Click on “SEM View” to observe the sample and actual alignment marks present on it. Note that the top right corner of the chip when loading, will appear in the SEM as bottom left corner (the perspective is rotated by 180°). Contrast and brightness can be adjusted by clicking on “auto brightness”. It’s recommended to turn the SEM off when moving stage to minimize beam exposure of your sample.

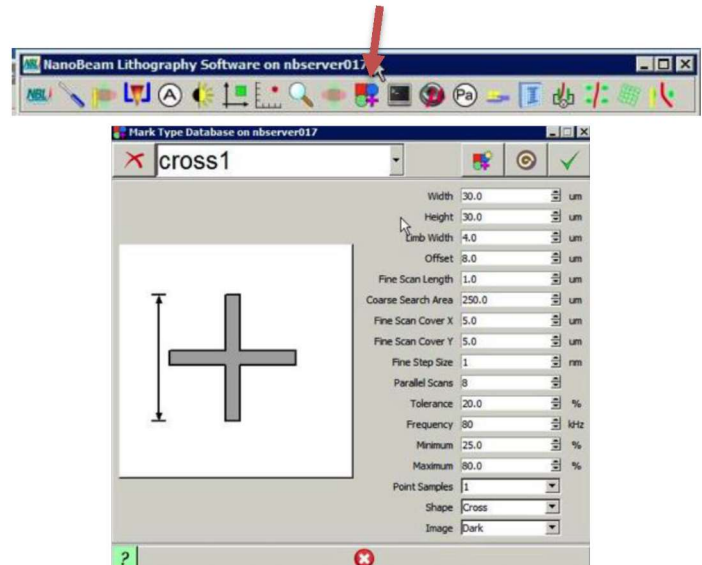




14. CENTER ALIGNMENT MARKS by pressing CTRL + mouse left click in the SEM view in correspondence with the center of your mark. To save a new position in the database, press on green “V” button (top left corner of the position database window), insert a name, click on the “camera” icon to acquire position and “save” icon to save it.

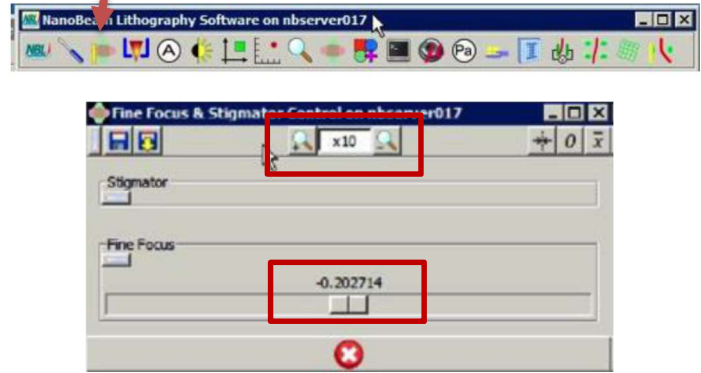


15. SEMIM-AUTOMATIC FOCUSING PROCEDURE is performed by typing in the terminal “af [markname]” to autofocus on the mark. You can check the procedure configuration clicking “Mark Type Database” from the main tool bar and choosing the name correspondent to the alignment mark utilized. This method is an alternative to the fully auto procedure (registration).

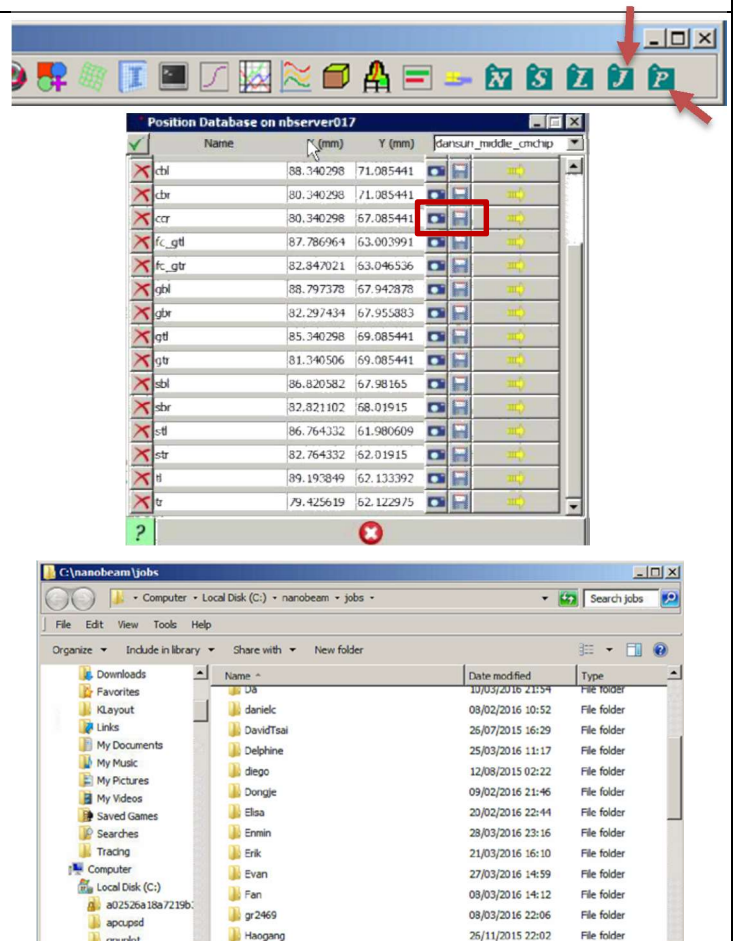




16. MANUAL FOCUSING can also be performed using the focus control available in the main tool bar. Multipliers at the top allow different focus adjustment finesse. You need at least three alignment marks. Store them in the position database then type “stage load” in the terminal to return to the home position.



17. OPEN JOB FILE. Click on the “J” icon in the main tool bar and select the file from your folder (with a “.njf” format). The job file uses patterns files with “.npf” format which should be saved under: Server/patterns/[yourname], accessible by clicking on the “P” icon in the main tool bar. Double check: marks names, block origins and pattern file names. Go to step 22 to learn how to create a job file.





18. RUN JOB: copy and paste the first line of the job into the terminal and press “enter” to run the job. The machine is reading the instructions present in your job file. Check for any mistake or error that could potentially show up. If everything is correct, confirm typing “2” and press enter.

```

NanoBeam Terminal 01.01 on nbsrver017
File Edit History Help
-----
starting time: 08:37:06-2016_Mar_29
finishing time: 08:39:01-2016_Mar_29
total duration: 115 (s)
-----
auto_conjugate>
$> run nwwrite diego/AG/AG-dosetest.njf -1-diego:onecm_top_mark22
# machine: eb17 (2016-03-29 09:06:27)
load jobfiles </nanobeam/jobs/diego/AG/AG-dosetest.njf> ...

setup position and beam for writing ...
check dose and pattern ...

nwwrite (AG-dosetest.njf) - 09:06:40 29-03-2016
<diego/AG/AG-dosetest.njf -1-diego:onecm_top_mark22>

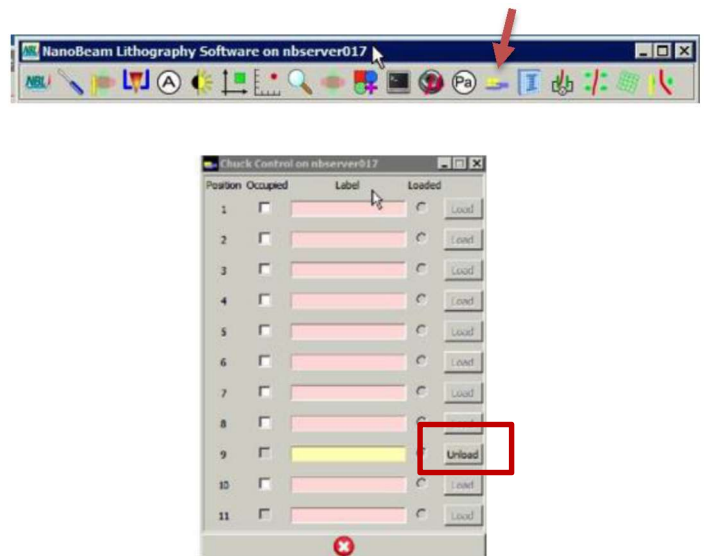
o1nhal ca1t1nax

NanoBeam Terminal 01.01 on nbsrver017
File Edit History Help
-----
write settings
beam current: auto (1.08 nA)

manual deflection corrections:
mf_trim: 1.0 1.0 0.0 0.0
sf_trim: 1.0 1.0 0.0 0.0

-----
Run Options <Enter to exit>:
1 Default - skip registration failed cells and write successful ones
2 All cells - skip bad marks and write all cells incl failed ones (-r)
3 Global run - perform global registration only
4 Test run - global and local registration without writing
5 1st local - apply 1st local registration to whole block (-s)
-----
nwwrite> 2
    
```

19. UNLOADING. After the job is done, unload your chuck using the “chuck control” window: Unload the loaded chuck by clicking “Unload”. Return the stage to the load position by typing “stage load” in the terminal. Verify by going to stage control (green square icon). Vent (by pressing “Vent Airlock”) in the PLC, unload the sample. Try to coordinate with the next user the loading and unloading of your samples.

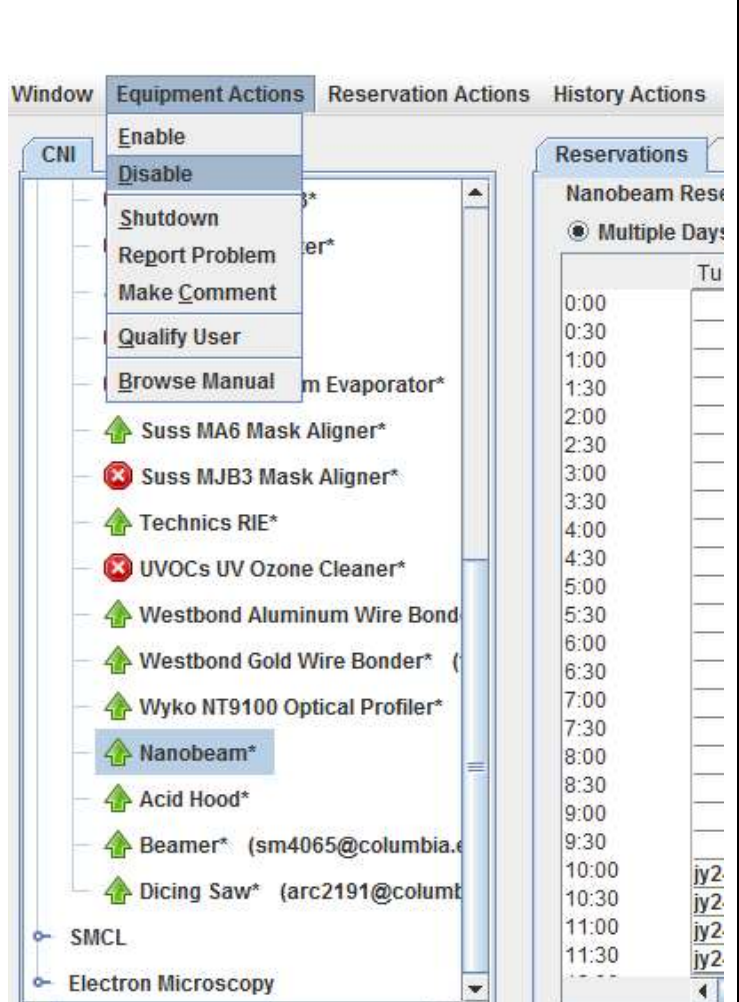




20. PUMP DOWN: the load lock by clicking “Pump Air Lock” on PLC and confirm by “OK”.



21. **BADGER LOGOUT:** Don't forget to disable the tool in badger after you're done.





22. CREATING A JOB FILE: using nB-Write software, a job file consists of several logical sections, each starting with a “.” Followed by section name, properties line, then “.end”. 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. Comments are inserted with “#” at the beginning of the line.

1. **.global:** contains properties affecting the whole job, such as registration points, mark type, focusing procedure, etc. You can either use a focus map with registration or at certain measured points.

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.

Global bottom left position (-1), saved origin position. This is the global origin.

JohnDoe folder

Global bottom right position (-2)

Example job file chipleads.nj

```
# run nbwrite JohnDoe/chipleads.njf -1=JohnDoe:cm_mid_gbl -2=JohnDoe:cm_mid_gbr
#
# define global properties
#-----
.global
registration (0,800000).....(800000,800000)
registration (0,0) (800000,0)
marktype cross50x10b
focus map1
.end

#alternatively if no registration is required:
.global
focus_map JohnDoe:onecm_middle_tempr 0.147384
focus_map JohnDoe:onecm_middle_tempr 0.157784
focus_map JohnDoe:onecm_middle_tempr 0.126467
focus_map JohnDoe:onecm_middle_tempr 0.136377
focus map1
.end

#-----
# define block default properties
#-----
.block_default
focus_global_map
stepsize (10000,10000)
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
```

Position of 4 global alignment marks, in nm, top left, top right, bottom left, and bottom right, relative to origin

Allows the repetition of a block or pattern in a specific array in (x,y) directions. "Stepsize" defines the distance between two grid points in nm

Allows the selection of specific grid cells or range of cells to be written. "Invert" means deselect

Dose in C/m². Dose_increment – if dose change (left to right, bottom to top) for every grid is needed. Dose increment acceptable formats are: 0.1, 1.05, -0.01, %0.025, *(1.1,1.01), %*(1.005,0.97)





4. **.pattern**: this section is where the properties of all patterns contained in the job file are defined. A specific block origin can be defined in the “.pattern” section. “id” links the pattern name to be called from the “.block” section. Note that “dose_increment” is not possible to use with “subgrid”, only with “grid”.

5. **.write**: properties related to the writing, such as what beam current to use. Adding “-r” as a final argument to the run command causes to skip the registration for any marks not found.

```

-----
# define block properties
#-----
.block
origin (1000000,4000000)
registration (0,2000000) (2000000,2000000)
registration (0,0) (2000000,0)
marktype      sqr10b
focus global_map
stepsize      (4000000,1000000)
grid (1,1)
base_dose     14
dose_increment 0
pattern      leads      (400000,400000)
pattern      extramarks (75000,25000)
.end

-----
# 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

```

leads

extramarks

Pattern file name

Dose ID, Dose factor, Pixel size (Step size) in nm (< half beam spot size)

Recommended to use when pattern area is small (creates an array repeating the pattern as indicated and increases the field size)





		<p>Beam spot size in nm as a function of the beam current in nA:</p> <pre> #----- # Writing conditions (auto-detect beam current) #----- .write current auto .end </pre>
<p>23.</p>	<p>CREATING A MARK TYPE mark type frequency has to be higher than 10 kHz. Do not change other users' files. When basing the new marktype on one already present, simply open the latter, modify as desired and then save with new name.</p>	





24. .GDS FILE CONVERSION:

.gds files can be converted to .npf by using the software nbPat. This also can be used to calculate writing time if base dose and beam current are indicated under “beam conditions”.

Minimum main field (mf) size: 50 μm , minimum subfield (sf) size 5 μm , and maximum clock frequency is 50 MHz. Suggested values are mf=250 μm , sf=10 μm . Under the tab “Pattern” you can view the layout, different layers in different colors, and check the position of main fields and subfields (mouse right button).

SAVE the .npf file, then **RE-OPEN** it and **SAVE AGAIN**, in order to avoid possible fracturing bugs.

